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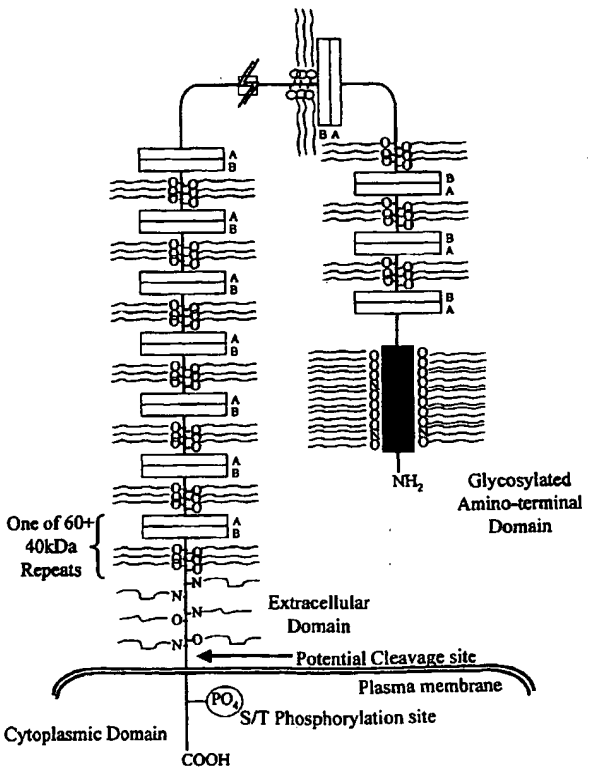

(57) Abstract: The CA125 gene has been cloned and multiple repeat sequences including the carboxy terminus have been identified. The CA125 molecule comprises three major domains: an extracellular amino terminal domain (Domain 1); a large multiple repeat domain (Domain 2); and a carboxy terminal domain (Domain 3) which includes a transmembrane anchor with a short cytoplasmic domain. An amino terminal extension is present. The structure is dominated by a repeat domain comprising 156 amino acid repeat units, which encompass the epitope binding sites. More than 60 repeat units have been identified. The repeat units encompass the site of OC125 and M11 binding. Expression of the repeats was demonstrated. Any one of the repeat domains has the potential for use as a new gold standard for detecting and monitoring the presence of the CA125 antigen. The repeat domains and other domains also provide a basis for the development of a vaccine.

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REPEAT SEQUENCES OF THE CA125 GENE AND THEIR USE FOR DIAGNOSTIC AND THERAPEUTIC INTERVENTIONS

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application Serial No. 60/284,175 filed April 17, 2001, U.S. Provisional Application Serial No. 60/299,380 filed June 19, 2001, U.S. Non-Provisional Application Serial No. 09/965,738 filed September 27, 2001, and U.S. Provisional Application Serial No. 60/345,180 filed December 21, 2001, which are incorporated by reference in their entirety.

BACKGROUND OF THE INVENTION

The present invention relates generally to the cloning, identification, and expression of the CA125 gene's glycosylated amino terminal domain, the multiple repeat domain, and the carboxy terminal doman *in vitro* and, more specifically, to the use of recombinant CA125 with epitope binding sites for diagnostic and therapeutic purposes.

CA125 is an antigenic determinant located on the surface of ovarian carcinoma cells with essentially no expression in normal adult ovarian tissue. Elevated in the sera of patients with ovarian adenocarcinoma, CA125 has played a critical role for more than 15 years in the management of these patients relative to their response to therapy and also as an indicator of recurrent disease.

It is well established that CA125 is not uniquely expressed in ovarian carcinoma, but is also found in both normal secretory tissues and other carcinomas (i.e., pancreas, liver, colon) [Hardardottir H *et al.*, Distribution of CA125 in embryonic tissue and adult derivatives of the fetal periderm, *Am J Obstet. Gynecol.* 163;6(1):1925-1931 (1990); Zurawski VR *et al.*, Tissue distribution and characteristics of the CA125 antigen, *Cancer Rev.* 11-12:102-108 (1988); and O'Brien TJ *et al.*, CA125 antigen in human amniotic fluid and fetal membranes, *Am J Obstet Gynecol.* 155:50-55, (1986); Nap M *et al.*, Immunohistochemical characterization of 22 monoclonal antibodies against the CA125 antigen: 2nd report from the ISOBM TD-1 workshop, Tumor Biology 17:325-332 (1996)].

Notwithstanding, CA125 correlates directly with the disease status of affected patients (i.e., progression, regression, and no change), and has become the "gold standard" for monitoring patients with ovarian carcinoma [Bast RC *et al.,* A radioimmunoassay using a monoclonal antibody to monitor the course of epithelial ovarian cancer, *N Engl J Med.* 309:883-887 (1983); and Bon GC *et al.,* Serum tumor marker immunoassays in gynecologic oncology: Establishment of reference values, *Am J Obstet. Gynecol.* 174:107-114 (1996)]. CA125 is especially useful in post-menopausal patients where endometrial tissue has become atrophic and, as a result, is not a major source of normal circulating CA125.

During the mid 1980's, the inventor of the present invention and others developed M11, a monoclonal antibody to CA125. M11 binds to a dominant epitope on the repeat structure of the CA125 molecule [O'Brien TJ *et al.*, New monoclonal antibodies identify the glycoprotein carrying the CA125 epitope, *Am J Obstet Gynecol* 165:1857-64 (1991)]. More recently, the inventor and others developed a purification and stabilization scheme for CA125, which allows for the accumulation of highly purified high molecular weight CA125 [O'Brien TJ *et al.*, More than 15 years of CA125: What is known about the antigen, its structure and its function, *Int J Biological Markers* 13(4):188-195 (1998)].

Considerable progress has been made over the years to further characterize the CA125 molecule, its structure and its function. The CA125 molecule is a high molecular weight glycoprotein with a predominance of O-linked sugar side chains. The native molecule exists as a very large complex (~2-5 million daltons). The complex appears to be composed of an epitope containing CA125 molecule and binding proteins which carry no CA125 epitopes. The CA125 molecule is heterogenous in both size and charge, most likely due to continuous deglycosylation of the side chains during its life-span in bodily fluids. The core CA125 subunit is in excess of 200,000 daltons, and retains the capacity to bind both OC125 and M11 class antibodies. While the glycoprotein has been described biochemically and metabolically by the inventor of the present invention and others, no one has yet cloned the CA125 gene, which would provide the basis for understanding its structure and its physiologic role in both normal and malignant tissues.

Despite the advances in detection and quantitation of serum tumor markers like CA125, the majority of ovarian cancer patients are still diagnosed at an advanced stage of the disease--Stage III or IV. Further, the management of patients' responses to treatment and the detection of disease recurrence remain major problems. There, thus, remains a need to significantly improve and standardize current CA125 assay systems. Further, the development of an early indicator of risk of ovarian cancer will provide a useful tool for early diagnosis and improved prognosis.

SUMMARY OF THE INVENTION

The CA125 gene has been cloned and multiple repeat sequences as well as the glycosylated amino terminal and the carboxy terminus have been identified. CA125 requires a transcript of more than 35,000 bases and occupies approximately 150,000 bp on chromosome 19q 13.2. The CA125 molecule comprises three major domains: an extracellular amino terminal domain (Domain 1); a large multiple repeat domain (Domain 2); and a carboxy terminal domain (Domain 3) which includes a transmembrane anchor with a short cytoplasmic domain. The amino terminal domain is assembled by combining five genomic exons, four very short amino terminal sequences and one extraordinarily large exon. This domain is dominated by its capacity for O-glycosylation and its resultant richness in serine and threonine residues. Additionally, an amino terminal extension is present, which comprises four genomic exons. Analysis of the amino terminal extension revealed that its amino acid composition is consistent with the amino acid composition of the amino terminal domain.

The extracellular repeat domain, which characterizes the CA125 molecule, also represents a major portion of the CA125 molecular structure. It is downstream from the amino terminal domain and presents itself in a much different manner to its extracellular matrix neighbors. These repeats are characterized by many features including a highly-conserved nature and a uniformity in exon structure. But most consistently, a cysteine enclosed sequence may form a cysteine loop. Domain 2 comprises 156 amino acid repeat units of the CA125 molecule. The repeat domain constitutes the largest proportion of the

CA125 molecule. The repeat units also include the epitopes now well-described and classified for both the major class of CA125 antibodies of the OC125 group and the M11 group. More than 60 repeat units have been identified, sequenced, and contiguously placed in the CA125 domain structure. The repeat sequences demonstrated 70-85% homology to each other. The existence of the repeat sequences was confirmed by expression of the recombinant protein in *E. coli* where both OC125/M11 class antibodies were found to bind to sites on the CA125 repeat.

The CA125 molecule is anchored at its carboxy terminal through a transmembrane domain and a short cytoplasmic tail. The carboxy terminal also contains a proteolytic cleavage site approximately 50 amino acids upstream from the transmembrane domain, which allows for proteolytic cleavage and release of the CA125 molecule.

The identification and sequencing of multiple repeat domains of the CA125 antigen provides potentially new clinical and therapeutic applications for detecting, monitoring and treating patients with ovarian cancer and other carcinomas where CA125 is expressed. For example, the ability to express repeat domains of CA125 with the appropriate epitopes would provide a much needed standard reagent for research and clinical applications. Current assays for CA125 utilize as standards either CA125 produced from cultured cell lines or from patient ascites fluid. Neither source is defined with regard to the quality or purity of the CA125 molecule. The present invention overcomes the disadvantages of current assays by providing multiple repeat domains of CA125 with epitope binding sites. At least one or more of any of the more than 60 repeats shown in Table 16 can be used as a "gold standard" for testing the presence of CA125. Furthermore, new and more specific assays may be developed utilizing recombinant products for antibody production.

Perhaps even more significantly, the multiple repeat domains of CA125 or other domains could also be used for the development of a potential vaccine for patients with ovarian cancer. In order to induce cellular and humoral immunity in humans to CA125, murine antibodies specific for CA125 were utilized in anticipation of patient production of anti-ideotypic antibodies, thus indirectly allowing the induction of an immune response to the CA125 molecule. With the availability of recombinant CA125, especially domains

which encompass epitope binding sites for known murine antibodies, it will be feasible to more directly stimulate patients' immune systems to CA125 and, as a result, extend the life of ovarian carcinoma patients.

The recombinant CA125 of the present invention may also be used to develop therapeutic targets. Molecules like CA125, which are expressed on the surface of tumor cells, provide potential targets for immune stimulation, drug delivery, biological modifier delivery or any agent which can be specifically delivered to ultimately kill the tumor cells. Humanized or human antibodies to CA125 epitopes could be used to deliver all drug or toxic agents including radioactive agents to mediate direct killing of tumor cells. Natural ligands having a natural binding affinity for domains on the CA125 molecule could also be utilized to deliver therapeutic agents to tumor cells.

CA125 expression may further provide a survival or metastatic advantage to ovarian tumor cells. Antisense oligonucleotides derived from the CA125 repeat sequences could be used to down-regulate the expression of CA125. Further, antisense therapy could be used in association with a tumor cell delivery system of the type described above.

Recombinant domains of the CA125 molecule also have the potential to identify small molecules, which bind to individual domains of the CA125 molecule. These small molecules could also be used as delivery agents or as biological modifiers.

In one aspect of the present invention, a CA125 molecule is disclosed comprising: (a) an extracellular amino terminal domain, comprising 5 genomic exons, wherein exon 1 comprises amino acids #1-33 of SEQ ID NO: 299, exon 2 comprises amino acids #34-1593 of SEQ ID NO: 299, exon 3 comprises amino acids #1594-1605 of SEQ ID NO: 299, exon 4 comprises amino acids #1606-1617 of SEQ ID NO: 299, and exon 5 comprises amino acids #1618-1637 of SEQ ID NO: 299; (b) an amino terminal extension, comprising 4 genomic exons, wherein exon 1 comprises amino acids #1-3157 of SEQ ID NO: 310, exon 2 comprises amino acids #3158-3193 of SEQ ID NO: 310, exon 3 comprises amino acids #3194-9277 of SEQ ID NO: 310, and exon 4 comprises amino acids #9278-10,427 of SEQ ID NO: 310; (c) a multiple repeat domain, wherein each repeat unit comprises 5 genomic exons, wherein exon 1 comprises amino acids #1-42 in any of SEQ ID NOS: 164 through 194; exon 2 comprises amino acids #43-65 in any of SEQ ID NOS: 195 through 221; exon 3 comprises amino acids #66-123 in any of SEQ ID NOS: 222

through 249; exon 4 comprises amino acids #124-135 in any of SEQ ID NOS: 250 through 277; and exon 5 comprises amino acids #136-156 in any of SEQ ID NOS: 278 through 298; and (d) a carboxy terminal domain comprising a transmembrane anchor with a short cytoplasmic domain, and further comprising 9 genomic exons, wherein exon 1 comprises amino acids #1-11 of SEQ ID NO: 300; exon 2 comprises amino acids #12-33 of SEQ ID NO: 300; exon 3 comprises amino acids #34-82 of SEQ ID NO: 300; exon 4 comprises amino acids #83-133 of SEQ ID NO: 300; exon 5 comprises amino acids #134-156 of SEQ ID NO: 300; exon 6 comprises amino acids #157-212 of SEQ ID NO: 300; exon 7 comprises amino acids #213-225 of SEQ ID NO: 300; exon 8 comprises amino acids #226-253 of SEQ ID NO: 300; and exon 9 comprises amino acids #254-284 of SEQ ID NO: 300.

In another aspect of the present invention, the N-glycosylation sites of the amino terminal domain marked (x) in Figure 8B are encoded at positions #81, #271, #320, #624, #795, #834, #938, and #1,165 in SEQ ID NO: 299.

In another aspect of the present invention, the serine and threonine O-glycosylation pattern for the amino terminal domain is marked (o) in SEQ ID NO: 299 in Figure 8B.

In another aspect of the present invention, the N-glycosylation sites of the amino terminal extension marked (x) in Table 26 are encoded at positions #139, #434, #787, #930, #957, #1266, #1375, #1633, #1840, #1877, #1890, #2345, #2375, #2737, #3085, #3178, #3501, #4221, #4499, #4607, #4614, #4625, #5048, #5133, #5322, #5396, #5422, #5691, #5865, #6090, #6734, #6861, #6963, #8031, #8057, #8326, #8620, #8686, #8915, #9204, #9495, #9787, #10, 077, and #10, 175.

In another aspect, the serine and threonine O-glycosylation pattern for the amino terminal extension is marked (o) in Table 26.

In another aspect of the present invention, exon 2 in the repeat domain comprises at least 31 different copies; exon 2 comprises at least 27 different copies; exon 3 comprises at least 28 different copies; exon 4 comprises at least 28 different copies, and exon 5 comprises at least 21 different copies.

In another aspect of the present invention, the repeat domain comprises 156 amino acid repeat units which comprise epitope binding sites. The epitope binding sites are located in the C-enclosure at amino acids #59-79 (marked C-C) in SEQ ID NO: 150 in Figure 5.

In another aspect, the 156 amino acid repeat unit comprises O-glycosylation sites at positions #128, #129, #132, #133, #134, #135, #139, #145, #146, #148, #150, #151, and #156 in SEQ ID NO: 150 in Figure 5C. The 156 amino acid repeat unit further comprises N-glycosylation sites at positions #33 and #49 in SEQ ID NO: 150 in Figure 5C. The repeat unit also includes at least one conserved methionine (designated M) at position #24 in SEQ ID NO: 150 in Figure 5C.

In yet another aspect, the transmembrane domain of the carboxy terminal domain is located at positions #230-252 (underlined) in SEQ ID NO: 300 of Figure 9B. The cytoplasmic domain of the carboxy terminal domain comprises a highly basic sequence adjacent to the transmembrane at positions #256-260 in SEQ ID NO: 300 of Figure 9B, serine and threonine phosporylation sites at positions #254, #255, and #276 in SEQ ID NO: 300 in Figure 9B, and tyrosine phosphorylation sites at positions #264, #273, and #274 in SEQ ID NO: 300 of Figure 9B.

In another aspect of the present invention, an isolated nucleic acid of the CA125 gene is disclosed, which comprises a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequences set forth in SEQ ID NOS: 49, 67, 81, 83-145, 147, 150, and 152; (b) a nucleotide sequence having at least 70% sequence identity to any one of the sequences in (a); (c) a degenerate variant of any one of (a) to (b); and (d)a fragment of any one of (a) to (c).

In another aspect of the present invention, an isolated nucleic acid of the CA125 gene, comprising a sequence that encodes a polypeptide with the amino acid sequence selected from the group consisting of: (a) the amino acid sequences set forth in SEQ ID NOS: 11-47, 50-80, 82, 146, 148, 149, 151, and 153-158; (b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a); (c) a conservative variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

In yet another aspect, a vector comprising the nucleic acid of the CA125 gene is disclosed. The vector may be a cloning vector, a shuttle vector, or an expression vector. A cultured cell comprising the vector is also disclosed.

In yet another aspect, a method of expressing CA125 antigen in a cell is disclosed, comprising the steps of: (a) providing at least one nucleic acid comprising a nucleotide sequence selected from the group consisting of: (i) the nucleotide sequences set forth in SEQ ID NOS: 49, 67, 81, 83-145, 147, 150, and 152; (ii) a nucleotide sequence having at least 70% sequence

identity to any one of the sequences in (i); (iii) a degenerate variant of any one of (i) to (ii); and (iv) a fragment of any one of (i) to (iii); (b) providing cells comprising an mRNA encoding the CA125 antigen; and (c) introducing the nucleic acid into the cells, wherein the CA125 antigen is expressed in the cells.

In yet another aspect, a purified polypeptide of the CA125 gene, comprising an amino acid sequence selected from the group consisting of: (a) the amino acid sequences set forth in SEQ ID NOS: 11-48, 50, 68-80, 82, 146, 148, 149, 150, 151, and 153-158; (b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a); (c) a conservative variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

In another aspect, a purified antibody that selectively binds to an epitope in the receptor-binding domain of CA125 protein, wherein the epitope is within the amino acid sequence selected from the group consisting of: (a) the amino acid sequences set forth in SEQ ID NOS: 11-48, 50, 68-80, 146, 151, and 153-158; (b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a); (c) a conservative variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

A diagnostic for detecting and monitoring the presence of CA125 antigen is also disclosed, which comprises recombinant CA125 comprising at least one repeat unit of the CA125 repeat domain including epitope binding sites selected from the group consisting of amino acid sequences set forth in SEQ ID NOS: 11-48, 50, 68-80, 82, 146, 150, 151, 153-161, and 162 (amino acids #1,643-11,438).

A therapeutic vaccine to treat mammals with elevated CA125 antigen levels or at risk of developing a disease or disease recurrence associated with elevated CA125 antigen levels is also disclosed. The vaccine comprises recombinant CA125 repeat domains including epitope binding sites, wherein the repeat domains are selected from the group of amino acid sequences consisting of SEQ ID NOS: 11-48, 50, 68-80, 82, 146, 148, 149, 150, 151, 153-161, and 162 (amino acids #1,643-11,438), and amino acids #175-284 of SEQ ID NO: 300. Mammals include animals and humans.

In another aspect of the present invention, an antisense oligonucleotide is disclosed that inhibits the expression of CA 125 encloded by: (a) the nucleotide sequences set forth in SEQ ID NOS: 49, 67, 81, 83-145, 147, 150, and 152; (b) a nucleotide sequence having at least 70%

sequence identity to any one of the sequences in (a); (c) a degenerate variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

The preceeding and further aspects of the present invention will be apparent to those of ordinary skill in the art from the following description of the presently preferred embodiments of the invention, such description being merely illustrative of the present invention.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 illustrates the cyanogen bromide digested products of CA125 on Western blot probed with M11 and OC125 antibodies. Table 1 shows the amino acid sequence derived from the amino terminal end of the 40 kDa cyanogen bromide peptide along with internal sequences obtained after protease digestion of the 40 kDa fragment (SEQ ID NOS: 1-4). SEQ ID NO: 1 is the amino terminal sequence derived of the 40 kDa peptide and SEQ ID NOS: 2, 3, and 4 reflect internal amino acid sequences derived from peptides after protease digestion of the 40 kDa fragment. Table 1 further provides a translation of the EST (BE005912) with homologous sequences (SEQ ID NOS: 5 and 6) either boxed or underlined. Protease cleavage sites are indicated by arrows.

Figure 2A illustrates PCR amplification of products generated from primers utilizing the EST sequence referred to in Figure 1, the amino acid sequence obtained from the 40 kDa fragment and EST sequence AA# 640762. Lane 1-2: normal; 3: serous ovarian carcinoma; 4: serous ovarian carcinoma; 5: mucinous ovarian carcinoma; 6: β-tubulin control. The anticipated size band 400 b is present in lane 3 and less abundantly in lane 4.

Figure 2B illustrates the RT-PCR that was performed to determine the presence or absence of CA125 transcripts in primary culture cells of ovarian tumors. This expression was compared to tubulin expression as an internal control. Lanes 1, 3, 5, 7, and 9 represent the primary ovarian tumor cell lines. Lanes 2, 4, 6, and 8 represent peripheral blood mononuclear cell lines derived from the corresponding patients in lanes 1, 3, 5, and 7. Lane 10 represents fibroblasts from the patient tumor in lane 9. Lanes 11 and 12 are CaOV3 and a primary tumor specimen, respectively.

Figure 3 illustrates repeat sequences determined by sequencing cloned cDNA from the 400 b band in Figure 2B. Placing of repeat sequences in a contiguous fashion was accomplished by PCR amplification and sequencing of overlap areas between two repeat sequences. A sample of the complete repeat sequences is shown in SEQ ID NOS: 158, 159, 160, and 161, which was obtained in this manner and placed next to each other based on overlap sequences. The complete list of repeat sequences that was obtained is shown in Table 21 (SEQ ID NO: 162).

Figure 4 illustrates three Western immunoblot patterns: Panel A = probed with M11, Panel B = probed with OC125 and Panel C = probed with antibody ISOBM 9.2. Each panel represents *E. coli* extracts as follows: lane 1 = *E. coli* extract from bacteria with the plasmid PQE-30 only. Lane 2 = *E. coli* extract from bacteria with the plasmid PQE-30 which includes the CA125 repeat unit. Lane 3 = *E. coli* extract from bacteria with the plasmid PQE-30 which includes the TADG-14 protease unrelated to CA125. Panel D shows a Coomassie blue stain of a PAGE gel of *E. coli* extract derived from either PQE-30 alone or from bacteria infected with PQE-30 - CA125 repeat (recombinant CA125 repeat).

Figure 5 represents Western blots of the CA125 repeat sequence that were generated to determine the position of the M11 epitope within the recombinant CA125 repeat. The expressed protein was bound to Ni-NTA agarose beads. The protein was left undigested or digested with Asp-N or Lys-C. The protein remaining bound to the beads was loaded into lanes 1, 2, or 3 corresponding to undigested, Asp-N digested and Lys-C digested, respectively. The supernatants from the digestions were loaded in lanes 4, 5, and 6 corresponding to undigested, Asp-N digested and Lys-C digested, respectively. The blots were probed with either anti-His tag antibody (A) or M11 antibody (B). Panel C shows a typical repeat sequence corresponding to SEQ ID NO: 150 with each exon defined by arrows. All proteolytic aspartic acid and lysine sites are marked with overhead arrow or dashes. In the lower panel, the O-glycosylation sites in exons 4 and 5 are marked with O, the N-glycosylation sites are marked with X plus the amino acid number in the repeat (#12, 33, and 49) the conserved methionine is designated with M plus the amino acid number (M#24), and the cysteine enclosure which is also present in all repeats and encompasses 19 amino acids between the cysteines is marked with C-C (amino acids #59-79). The epitopes for M11 and OC125 are located in the latter part of the C-enclosure or downstream from the C-enclosure.

Figure 6 illustrates a Northern blot analysis of RNA derived from either normal ovary (N) or ovarian carcinoma (T) probed with a P^{32} cDNA repeat sequence of CA125. Total RNA samples (10μg) were size separated by electrophoresis on a formaldehyde 1.2% agarose gel. After blotting to Hybond N, the lanes were probed with P^{32} radiolabelled 400 bp repeat (see Figure 2). Lane 1 represents RNA from normal ovarian tissue, and lane 2 represents RNA from serous ovarian tumor tissue.

Figure 7A is a schematic diagram of a typical repeat unit for CA125 showing the N-glycosylation sites at the amino end and the totally conserved methionine (M). Also shown is the proposed cysteine enclosed loop with antibody binding sites for OC125 and M11. Also noted are the highly O-glycosylated residues at the carboxy end of the repeat.

Figure 7B represents the genomic structure and exon configuration of a 156 amino acid repeat sequence of CA125 (SEQ ID NO: 163), which comprises a standard repeat unit.

Figure 7C lists the individual known sequences for each exon, which have been determined as follows: Exon 1 – SEQ ID NOS: 164-194; Exon 2 – SEQ ID NOS: 195-221; Exon 3 – SEQ ID NOS: 222-249; Exon 4 – SEQ ID NOS: 250-277; and Exon 5 – SEQ ID NOS: 278-298.

Figure 8A shows the genomic structure of the amino terminal end of the CA125 gene. It also indicates the amino composition of each exon in the extracellular domain.

Figure 8B illustrates the amino acid composition of the amino terminal domain (SEQ ID NO: 299) with each potential O-glycosylation site marked with a superscript (o) and N-glycosylation sites marked with a superscript (x). T-TALK sequences are underlined.

Figure 9A illustrates the genomic exon structure of the carboxy-terminal domain of the CA125 gene. It includes a diagram showing the extracellular portion, the potential cleavage site, the transmembrane domain and the cytoplasmic tail.

Figure 9B illustrates the amino acid composition of the carboxy terminal domain (SEQ ID NO: 300) including the exon boundaries, O-glycosylation sites (o), and N-glycosylation sites (x). The proposed transmembrane domain is underlined.

Figure 10 illustrates the proposed structure of the CA125 molecule based on the open reading frame sequence described herein. As shown, the molecule is dominated by a major repeat domain in the extracellular space along with a highly glycosylated amino terminal repeat.

The molecule is anchored by a transmembrane domain and also includes a cytoplasmic tail with potential for phosphorylation.

Figure 11 is a diagram of the CA125 gene showing the originally cloned domains of both the genomic and amino acid sequences and the extension of the glycosylated amino terminal protein sequence.

Figure 12 is a diagram of the contig alignment from overlapping chromosome 19 cosmids.

Figure 13 illustrates the genomic exon structure of the CA125 gene amino terminal extension.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the present invention, conventional molecular biology, microbiology, and recombinant DNA techniques may be used that will be apparent to those skilled in the relevant art. Such techniques are explained fully in the literature (see, e.g., Maniatis, Fritsch & Sambrook, "Molecular Cloning: A Laboratory Manual (1982); "DNA Cloning: A Practical Approach," Volumes I and II (D. N. Glover ed. 1985); "Oligonucleotide Synthesis" (M. J. Gait ed. 1984); "Nucleic Acid Hybridization" (B. D. Hames & S. J. Higgins eds. (1985)); "Transcription and Translation" (B. D. Hames & S. J. Higgins eds. (1984)); "Animal Cell Culture" (R. I. Freshney, ed. (1986)); "Immobilized Cells And Enzymes" (IRL Press, (1986)); and B. Perbal, "A Practical Guide To Molecular Cloning" (1984)).

Therefore, if appearing herein, the following terms shall have the definitions set out below.

A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

A "DNA molecule" refers to the polymeric form of deoxyribonucleotides (adenine, guanine, thymine, or cytosine) in either single stranded form, or a double-stranded helix. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA

found, inter alia, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes.

As used herein, the term "gene" shall mean a region of DNA encoding a polypeptide chain.

"Messenger RNA" or "mRNA" shall mean an RNA molecule that encodes for one or more polypeptides.

"DNA polymerase" shall mean an enzyme which catalyzes the polymerization of deoxyribonucleotide triphosphates to make DNA chains using a DNA template.

"Reverse transcriptase" shall mean an enzyme which catalyzes the polymerization of deoxy- or ribonucleotide triphosphates to make DNA or RNA chains using an RNA or DNA template.

"Complementary DNA" or "cDNA" shall mean the DNA molecule synthesized by polymerization of deoxyribonucleotides by an enzyme with reverse transcriptase activity.

An "isolated nucleic acid" is a nucleic acid the structure of which is not identical to that of any naturally occurring nucleic acid or to that of any fragment of a naturally occurring genomic nucleic acid spanning more than three separate genes. The term therefore covers, for example, (a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule but is not flanked by both of the coding sequences that flank that part of the molecule in the genome of the organism in which it naturally occurs; (b) a nucleic acid incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion protein.

"Oligonucleotide", as used herein in referring to the probes or primers of the present invention, is defined as a molecule comprised of two or more deoxy- or ribonucleotides, preferably more than ten. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the oligonucleotide.

"DNA fragment" includes polynucleotides and/or oligonucleotides and refers to a plurality of joined nucleotide units formed from naturally-occurring bases and cyclofuranosyl groups joined by native phosphodiester bonds. This term effectively refers to naturally-occurring species or synthetic species formed from naturally-occurring subunits. "DNA fragment" also refers to purine and pyrimidine groups and moieties which function similarly but which have non naturally-occurring portions. Thus, DNA fragments may have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. They may also contain altered base units or other modifications, provided that biological activity is retained. DNA fragments may also include species which include at least some modified base forms. Thus, purines and pyrimidines other than those normally found in nature may be so employed. Similarly, modifications on the cyclofuranose portions of the nucleotide subunits may also occur as long as biological function is not eliminated by such modifications.

"Primer" shall refer to an oligonucleotide, whether occurring naturally or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH. The primer may be either single-stranded or double-stranded and must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, the source of primer and the method used. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 10-25 or more nucleotides, although it may contain fewer nucleotides.

The primers herein are selected to be "substantially" complementary to different strands of a particular target DNA sequence. This means that the primers must be sufficiently complementary to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the

remainder of the primer sequence being complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence or hybridize therewith and thereby form the template for the synthesis of the extension product.

As used herein, the term "hybridization" refers generally to a technique wherein denatured RNA or DNA is combined with complementary nucleic acid sequence which is either free in solution or bound to a solid phase. As recognized by one skilled in the art, complete complementarity between the two nucleic acid sequences is not a pre-requisite for hybridization to occur. The technique is ubiquitous in molecular genetics and its use centers around the identification of particular DNA or RNA sequences within complex mixtures of nucleic acids.

As used herein, "restriction endonucleases" and "restriction enzymes" shall refer to bacterial enzymes which cut double-stranded DNA at or near a specific nucleotide sequence.

"Purified polypeptide"refers to any peptide generated from CA125 either by proteolytic cleavage or chemical cleavage.

"Degenerate variant" refers to any amino acid variation in the repeat sequence, which fulfills the homology exon structure and conserved sequences and is recognized by the M11, OC125 and ISOBM series of antibodies.

"Fragment" refers to any part of the CA125 molecule identified in a purification scheme.

"Conservative variant antibody" shall mean any antibody that fulfills the criteria of M11, OC125 or any of the ISOBM antibody series.

MATERIALS AND METHODS

A. Tissue collection, RNA Isolation and cDNA Synthesis

Both normal and ovarian tumor tissues were utilized for cDNA preparation. Tissues were routinely collected and stored at -80°C according to a tissue collection protocol.

Total RNA isolation was performed according to the manufacturer's instructions using the TriZol Reagent purchased from GibcoBRL (Catalog #15596-018). In some

instances, mRNA was isolated using oligo dT affinity chromatography. The amount of RNA recovered was quantitated by UV spectrophotometry. First strand complementary DNA (cDNA) was synthesized using 5.0 μg of RNA and random hexamer primers according to the manufacturer's protocol utilizing a first strand synthesis kit obtained from Clontech (Catalog #K1402-1). The purity of the cDNA was evaluated by PCR using primers specific for the ß-tubulin gene. These primers span an intron such that the PCR products generated from pure cDNA can be distinguished from cDNA contaminated with genomic DNA.

B. Identification and Ordering of CA125 Repeat Units

It has been demonstrated that the 2-5 million dalton CA125 glycoprotein (with repeat domains) can be chemically segmented into glycopeptide fragments using cyanogen bromide. As shown in Figure 1, several of these fragments, in particular the 40 kDa and 60 kDa fragments, still bind to the to the two classical antibody groups defined by OC 125 and M11.

To convert CA125 into a consistent glycopeptide, the CA125 parent molecule was processed by cyanogen bromide digestion. This cleavage process resulted in two main fractions on commassie blue staining following polyacrylamide gel electrophoresis. An approximately 60 kDa band and a more dominant 40 kDa band were identified as shown in Figure 1. When a Western blot of these bands was probed with either OC125 or M11 antibodies (both of which define the CA125 molecule), these bands bound both antibodies. The 40 kDa band was significantly more prominent than the 60 kDa band. These data thus established the likelihood of these bands (most especially the 40 kDa band) as being an authentic cleavage peptide of the CA125 molecule, which retained the identifying characteristic of OC125 and M11 binding.

The 40 kDa and 60 kDa bands were excised from PVDF blots and submitted to amino terminal and internal peptide amino acid sequencing as described and practiced by Harvard Sequencing , (Harvard Microchemistry Facility and The Biological Laboratories, 16 Divinity Avenue, Cambridge, Massachusetts 02138). Sequencing was successful only for the 40 kDa band where both amino terminal sequences and some internal sequences were obtained as shown in Table 1 at SEQ ID NOS: 1-4. The 40 kDa fragment of the CA125 protein was

found to have homology to two translated EST sequences (GenBank Accession Nos. BE005912 and AA640762). Visual examination of these translated sequences revealed similar amino acid regions, indicating a possible repetitive domain. The nucleotide and amino acid sequences for EST Genbank Accession No. BE005912 (corresponding to SEQ ID NO: 5 and SEQ ID NO: 6, respectively) are illustrated in Table 1. Common sequences are boxed or underlined.

In an attempt to identify other individual members of this proposed repeat family, two oligonucleotide primers were synthesized based upon regions of homology in these EST sequences. Shown in Table 2A, the primer sequences correspond to SEQ ID NOS: 7 and 8 (sense primers) and SEQ ID NOS: 9 and 10 (antisense primers). Repeat sequences were amplified in accordance with the methods disclosed in the following references: Shigemasa K *et al.*, p21: A monitor of p53 dysfunction in ovarian neoplasia, *Int. J. Gynecol. Cancer* 7:296-303 (1997) and Shigemasa K *et al.*, p16 Overexpression: A potential early indicator of transformation in ovarian carcinoma, *J. Soc. Gynecol. Invest.* 4:95-102 (1997). Ovarian tumor cDNA obtained from a tumor cDNA bank was used.

Amplification was accomplished in a Thermal Cycler (Perkin-Elmer Cetus). The reaction mixture consisted of 1U Taq DNA Polymerase in storage buffer A (Promega), 1X Thermophilic DNA Polymerase 10X Mg free buffer (Promega), 300mM dNTPs, 2.5mM MgCl2, and 0.25mM each of the sense and antisense primers for the target gene. A 20 µl reaction included 1 µl of cDNA synthesized from 50ng of mRNA from serous tumor mRNA as the template. PCR reactions required an initial denaturation step at 94°C/1.5 min. followed by 35 cycles of 94°C/0.5 min., 48°C/0.5 min., 72°C/0.5 min. with a final extension at 72°C/7 min. Three bands were initially identified (»400 bp, »800 bp, and »1200 bp) and isolated. After size analysis by agarose gel electrophoresis, these bands as well as any other products of interest were then ligated into a T-vector plasmid (Promega) and transformed into competent DH5α strain of *E. coli* cells. After growth on selective media, individual colonies were cultured overnight at 37°C, and plasmid DNA was extracted using the QIAprep Spin Miniprep kit (Qiagen). Positive clones were identified by restriction digests

using *Apa* I and *Sac* I. Inserts were sequenced using an ABI automatic sequencer, Model 377, T7 primers, and a Big Dye Terminator Cycle Sequencing Kit (Applied Biosystems).

Obtained sequences were analyzed using the Pileup program of the Wisconsin Genetic's Computer Group (GCG). Repeat units were ordered using primers designed against two highly conserved regions within the nucleotide sequence of these identified repeat units. Shown in Table 2B, the sense and antisense primers (5'-GTCTCTATGTCAATGGTTTCACCC-3' / 5'-TAGCTGCTCTCTGTCCAGTCC-3' SEQ ID NOS: 301 and 302, respectively) faced away from one another within any one repeat creating an overlap sequence, thus enabling amplification across the junction of any two repeat units. PCR reactions, cloning, sequencing, and analysis were performed as described above.

C. Identification and Assembly of the CA125 Amino Terminal Domain

In search of open reading frames containing sequences in addition to CA125 repeat units, database searches were performed using the BLAST program available at the National Center for Biotechnology Information (www.ncbi.nlm.nih.gov/). Using a repeat unit as the query sequence, cosmid AC008734 was identified as having multiple repeat sequences throughout the unordered (35) contiguous pieces of DNA, also known as contigs. One of these contigs, #32, was found to have exons 1 and 2 of a repeat region at its 3' end. Contig#32 was also found to contain a large open reading frame (ORF) upstream of the repeat sequence. PCR was again used to verify the existence of this ORF and confirm its connection to the repeat sequence. The specific primers recognized the 3' end of this ORF (5'-CAGCAGAGACCAGCACGAGTACTC-3')(SEQ ID NO: 51) and sequence within the repeat (5'-TCCACTGCCATGGCTGAGCT-3')(SEQ ID NO: 52). The remainder of the amino-terminal domain was assembled from this contig in a similar manner. With each PCR confirmation, a new primer (see Table 10A) was designed against the assembled sequence and used in combination with a primer designed against another upstream potential ORF (Set 1: 5'-CCAGCACAGCTCTTCCCAGGAC-3' / 5'-GGAATGGCTGAGCTGACGTCTG-3'(SEQ ID NO: 53 and SEQ ID NO: 54); Set 2: 5'-CTTCCCAGGACAACCTCAAGG-3' / 5'-GCAGGATGAGTGAGCCACGTG-3'(SEQ ID NO: 55 and SEQ ID NO: 56); Set 3: 5'-GTCAGATCTGGTGACCTCACTG-3' / 5'-GAGGCACTGGAAAGCCCAGAG-3')(SEQ ID NO: 57 and SEQ ID NO: 58). Potential

adjoining sequence (contig #7 containing EST AU133673) was also identified using contig #32 sequence as query sequence in database searches. Confirmation primers were designed and used in a typical manner (5'-CTGATGGCATTATGGAACACATCAC-3' / 5'-CCCAGAACGAGAGACCAGTGAG-3')(SEQ ID NO: 59 and SEQ ID NO: 60).

In order to identify the 5' end of the CA125 sequence, 5' Rapid Amplification of cDNA Ends (FirstChoice™ RLM-RACE Kit, Ambion) was performed using tumor cDNA . The primary PCR reaction used a sense primer supplied by Ambion (5'-GCTGATGGCGATGAATGAACACTG-3') (SEQ ID NO: 61) and an anti-sense primer specific to confirmed contig #32 sequence (5'-CCCAGAACGAGAGACCAGTGAG-3')(SEQ ID NO: 62). The secondary PCR was then performed using nested primers, sense from Ambion (5'-CGCGGATCCGAACACTGCGTTTGCTGGCTTTGATG-3') (SEQ ID NO: 63) and the anti-sense was specific to confirmed contig #7 sequence (5'-CCTCTGTGTGCTGCTTCATTGGG-3')(SEQ ID NO: 64). The RACE PCR product (a band of approximately 300 bp) was cloned and sequenced as previously described.

D. Identification and Assembly of the CA125 Carboxy Terminal Domain

Database searches using confirmed repeat units as query also identified a cDNA sequence (GenBank AK024365) containing other repeat units, but also a potential carboxy terminal sequence. The contiguous nature of this sequence with assembled CA125 was confirmed using PCR (5'-GGACAAGGTCACCACACTCTAC-3' / 5'-GCAGATCCTCCAGGTCTAGGTGTG-3'), (SEQ ID NO: 303 and SEQ ID NO: 304, respectively) as well as contig and EST analysis.

E. Expression of 6xHis-tagged CA125 repeat in *E. coli*

The open reading frame of a CA125 repeat shown in Table 11 was amplified by PCR with the sense primer (5'-ACCGGATCCATGGGCCACACAGAGCCTGGCCC-3') (SEQ ID NO: 65) the antisense primer (5'-TGTAAGCTTAGGCAGGGAGGATGGAGTCC-3') (SEQ ID NO: 66) PCR was performed in a reaction mixture consisting of ovarian tumor cDNA derived from 50 ng of mRNA, 5 pmol each of sense and antisense primers for the CA125 repeat, 0.2 mmol of dNTPs, and 0.625 U of Taq polymerase in 1x buffer in a final volume of 25 ml. This mixture was subjected to 1 minute of denaturation at 95°C followed by 30 cycles of PCR consisting of the following: denaturation for 30 seconds at 95°C, 30 seconds of annealing at 62°C, and 1 minute of extension at 72°C with an additional 7 minutes of extension on the last cycle. The product was electrophoresed through a 2% agarose gel for separation. The PCR

product was purified and digested with the restriction enzymes *Bam HI* and *Hind III*. This digested PCR product was then ligated into the expression vector pQE-30, which had also been digested with *Bam HI* and *Hind III*. This clone would allow for expression of recombinant 6xHis-tagged CA125 repeat. Transformed *E. coli* (JM109) were grown to an OD600 of 1.5-2.0 at 37°C and then induced with IPTG (0.1 mM) for 4-6 hours at 25°C to produce recombinant protein. Whole *E. coli* lysate was electrophoresed through a 12% SDS polyacrylamide gel and Coomassie stained to detect highly expressed proteins.

F. Western Blot Analysis

Proteins were separated on a 12% SDS-PAGE gel and electroblotted at 100V for 40 minutes at 4°C to nitrocellulose membrane. Blots were blocked overnight in phosphate-buffered saline (PBS) pH 7.3 containing 5% non-fat milk. CA125 antibodies M11, OC125, or ISOBM 9.2 were incubated with the membrane at a dilution of 5μg/ml in 5% milk/PBS-T (PBS plus 0.1% TX-100) and incubated for 2 hours at room temperature. The blot was washed for 30 minutes with several changes of PBS and incubated with a 1:10,000 dilution of horseradish peroxidase (HRP) conjugated goat anti-mouse IgG antibody (Bio-Rad) for 1 hour at room temperature. Blots were washed for 30 minutes with several changes of PBS and incubated with a chemiluminescent substrate (ECL from Amersham Pharmacia Biotech) before a 10-second exposure to X-ray film for visualization.

Figure 4 illustrates three Western immunoblot patterns of the recombinant CA125 repeat purified from *E. coli* lysate (lane 2) compared to *E. coli* lysate with no recombinant protein (lane 1-negative control) and a recombinant protein TADG-14 which is unrelated to CA125 (lane 3). As shown, the M11 antibody, the OC125 antibody and the antibody ISOBM 9.2 (an OC125-like antibody) all recognized the CA125 recombinant repeat (lane 2), but did *not* recognize either the *E. coli* lysate (lane 1) or the unrelated TADG-14 recombinant (lane 3). These data confirm that the recombinant repeat encodes both independent epitopes for CA125, the OC125 epitope and the M11 epitope.

G. Northern Blot Analysis

Total RNA samples (approximately 10μg) were separated by electrophoresis through a 6.3% formaldehyde, 1.2% agarose gel in 0.02 M MOPS, 0.05 M sodium acetate (pH 7.0), and 0.001 M EDTA. The RNAs were then blotted to Hybond-N (Amersham) by capillary

action in 20x SSPE and fixed to the membrane by baking for 2 hours at 80°C. A PCR product representing one 400 bp repeat of the CA125 molecule was radiolabelled using the Prime-a-Gene Labeling System available from Promega (cat. #U1100). The blot was probed and stripped according to the ExpressHyb Hybridization Solution protocol available from Clontech (Catalog #8015-1).

RESULTS

In 1997, a system was described by a co-inventor of the present invention and others for purification of CA125 (primarily from patient ascites fluid), which when followed by cyanogen bromide digestion, resulted in peptide fragments of CA125 of 60 kDa and 40 kDa [O'Brien TJ *et al.*, More than 15 years of CA125: What is known about the antigen, its structure and its function, *Int J Biological Markers* 13(4)188-195 (1998)]. Both fragments were identifiable by commassie blue staining on polyacrylamide gels and by Western blot. Both fragments were shown to bind both OC125 and M11 antibodies, indicating both major classes of epitopes were preserved in the released peptides (Figure 1).

Protein sequencing of the 40 kDa band yielded both amino terminal sequences and some internal sequences generated by protease digestion (Table 1 – SEQ ID NOS: 1-4). Insufficient yields of the 60 kDa band resulted in unreliable sequence information. Unfortunately, efforts to amplify PCR products utilizing redundant primers designed to these sequences were not successful. In mid 2000, an EST (#BE005912) was entered into the GCG database, which contained homology to the 40 kDa band sequence as shown in Table 1 (SEQ ID NOS: 5 and 6). The translation of this EST indicated good homology to the amino terminal sequence of the 40 kDa repeat (e.g. PGSRKFKTTE) with only one amino acid difference (i.e. an asparagine is present instead of phenylalanine in the EST sequence). Also, some of the internal sequences are partially conserved (e.g. SEQ ID NO: 2 and to a lesser extent, SEQ ID NO: 3 and SEQ ID NO: 4). More importantly, all the internal sequences are preceded by a basic amino acid (Table 1, indicated by arrows) appropriate for proteolysis by the trypsin used to create the internal peptides from the 40 kDa cyanogen bromide repeat. Utilizing the combined sequences, those obtained by amino acid sequencing and those identified in the EST (#BE005912) and a second EST (#AA640762) identified in the database, sense primers were created as follows: 5'-GGA GAG GGT TCT GCA GGG TC-3' (SEQ ID NO: 7) representing amino acids ERVLQG and anti-sense

primer, 5' GTG AAT GGT ATC AGG AGA GG-3' (SEQ ID NO: 9) representing PLLIPF. Using PCR, the presence of transcripts was confirmed representing these sequences in ovarian tumors and their absence in normal ovary and either very low levels or no detectable levels in a mucinous tumor (Figure 2A). The existence of transcripts was further confirmed in cDNA derived from multiple primary ovarian carcinoma cell lines and the absence of transcripts in matched lymphocyte cultures from the same patient (Figure 2B).

After cloning and sequencing of the amplified 400 base pair PCR products, a series of sequences were identified, which had high homology to each other but which were clearly distinct repeat entities (Figure 3) (SEQ ID NOS: 158 through 161).

Examples of each category of repeats were sequenced, and the results are shown in Tables 3, 4, and 5. The sequences represent amplification and sequence data of PCR products obtained using oligonucleotide primers derived from an EST (Genbank Accession No. BE005912). Table 3 illustrates the amino acid sequence for a 400 bp repeat in the CA125 molecule, which is identified as SEQ ID NO: 11 through SEQ ID NO: 21. Table 4 illustrates the amino acid sequence for a 800 bp repeat in the CA125 molecule, which corresponds to SEQ ID NO: 22 through SEQ ID NO: 35. Table 5 illustrates the amino acid sequence for a 1200 bp repeat in the CA125 molecule, which is identified as SEQ ID NO: 36 through SEQ ID NO: 46. Assembly of these repeat sequences (which showed 75-80% homology to each other as determined by GCG Software (GCG = Genetics Computer Group) using the Pileup application) utilizing PCR amplification and sequencing of overlapping sequences allowed for the construction of a 9 repeat structure. The amino acid sequence for the 9 repeat is shown in Table 6 as SEQ ID NO: 47. The individual C-enclosures are highlighted in the table.

Using the assembled repeat sequence in Table 6 to search genebank databases, a cDNA sequence referred to as Genbank Accession No. AK024365 (entered on 9/29/00) was discovered. Table 7 shows the amino acid sequence for AK024365, which corresponds to SEQ ID NO: 48. AK024365 was found to overlap with two repeats of the assembled repeat sequence shown in Table 6. Individual C-enclosures are highlighted in Table 7.

The cDNA for AK024365 allowed alignment of four additional repeats as well as a downstream carboxy terminus sequence of the CA125 gene. Table 8 illustrates the complete

DNA sequence of 13 repeats contiguous with the carboxy terminus of the CA125 molecule, which corresponds to SEQ ID NO: 49. Table 9 illustrates the complete amino acid sequence of the 13 repeats and the carboxy terminus of the CA125 molecule, which corresponds to SEQ ID NO: 50. The carboxy terminus domain was further confirmed by the existence of two EST's (Genbank Accession Nos. AW150602 and AI923224) in the genebank database, both of which confirmed the stop-codon indicated (TGA) as well as the poly A signal sequence (AATAA) and the poly A tail (see Table 9). The presence of these repeats has been confirmed in serous ovarian tumors and their absence in normal ovarian tissue and mucinous tumors as expected (see Figure 2A). Also, the transcripts for these repeats have been shown to be present in tumor cell lines derived from ovarian tumors, but not in normal lymphocyte cell lines (Figure 2B). Moreover, Northern blot analysis of mRNA derived from normal or ovarian carcinoma and probed with a P^{32} labeled CA125 repeat sequence (as shown in Figure 6) confirmed the presence of an RNA transcript in excess of 20 kb in ovarian tumor extracts (see Figure 2B).

To date, 45 repeat sequences have been identified with high homology to each other. To order these repeat units, overlapping sequences were amplified using a sense primer (5' GTC TCT ATG TCA ATG GTT TCA CCC-3') (SEQ ID NO: 305) from an upstream repeat and an antisense primer from a downstream repeat sequence (antisense 5' TAG CTG CTC TCT GTC CAG TCC-3') (SEQ ID NO: 306). Attempts have been made to place these repeats in a contiguous fashion as shown in Figure 3. There is some potential redundancy. Further, there is evidence from overlapping sequences that some repeats exist in more than one location in the sequence giving a total of more than 60 repeats in the CA125 molecule (see Table 21 SEQ ID NO: 162).

Final confirmation of the relationship of the putative CA125 repeat domain to the known CA125 molecule was achieved by expressing a recombinant repeat domain in *E. coli*. In Figure 4, expression of a recombinant CA125 repeat domain is shown in lane 2 compared to the vector alone in lane 1, Panel D. A series of Western blots representing *E. coli* extracts of vector alone in lane 1; CA125 recombinant protein lane in 2 and recombinant TADG-14 (an unrelated recombinant protease), lane 3, were probed with the CA125 antibodies M11, Panel A; OC125,

Panel B; and ISOBM 9.2, Panel C. In all cases, CA125 antibodies recognized only the recombinant CA125 antigen (lane 2 of each panel).

To further characterize the epitope location of the CA125 antibodies, recombinant CA125 repeat was digested with the endoprotease Lys-C and separately with the protease Asp-N. In both cases, epitope recognition was destroyed. As shown in Figure 5, the initial cleavage site for ASP-N is at amino acid #76 (indicated by arrow in Figure 5C). This sequence (amino acids # 1-76), a 17 kDa band, was detected with anti-histidine antibodies (Figure 5A,Lane 3) and found to have no capacity to bind CA125 antibodies (Figure 5B, Lane 3). The upper bands in Figures 5A and 5B represent the undigested remaining portion of the CA125 recombinant repeat. From these data, one can reasonably conclude that epitopes are either located at the site of cleavage and are destroyed by Asp-N or are downstream from this site and also destroyed by cleavage. Likewise, cleavage with Lys-C would result in a peptide, which includes amino acids # 68-154 (Figure 5C) and again, no antibody binding was detected. In view of the foregoing, it seems likely that epitope binding resides in the cysteine loop region containing a possible disulfide bridge (amino acids # 59-79). Final confirmation of epitope sites are being examined by mutating individual amino acids.

To determine transcript size of the CA125 molecule, Northern blot analysis was performed on mRNA extracts from both normal and tumor tissues. In agreement with the notion that CA125 may be represented by an unusually large transcript due to its known mega dalton size in tumor sera, ascites fluid, and peritoneal fluid [Nustad K *et al.*, CA125 – epitopes and molecular size, *Int. J of Biolog.* Markers, 13(4)196-199 (1998)], a transcript was discovered which barely entered the gel from the holding well (Figure 6). CA125 mRNA was only present in the tumor RNA sample and while a precise designation of its true size remains difficult due to the lack of appropriate standards, its unusually large size would accommodate a protein core structure in excess of 11,000 amino acids.

Evidence demonstrates that the repeat domain of the CA125 molecule encompasses a minimum of 45 different 156 amino acid repeat units and possibly greater than 60 repeats, as individual repeats occur more than once in the sequence. This finding may well account for the extraordinary size of the observed transcript. The amino acid composition of the repeat units (Figure 7A, 7C, Table 21) indicates that the sequence is rich in serine,threonine, and proline typical of the high STP repeat regions of the mucin genes [Gum Jr., JR, Mucin genes and the

proteins they encode: Structure, diversity and regulation, *Am J Respir. Cell Mol. Biol.* 7:557-564 (1992)]. Results suggest that the downstream end of the repeat is heavily glycosylated.

Also noteworthy is a totally conserved methionine at position 24 of the repeat (Figure 7A, 7C). It is this methionine which allowed cyanogen bromide digestion of the CA125 molecule, resulting in the 40 kDa glycopeptide that was identified with OC125 and M11 antibodies in Western blots of the CNBr digested peptides. These data predict that the epitopes for the CA125 antibodies are located in the repeat sequence. By production of a recombinant product representing the repeat sequence, results have confirmed this to be true. A potential disulfide bond is noted, which would encompass a C-enclosure comprising 19 amino acids enclosed by two cysteines at positions #59 and #79. The cysteines are totally conserved, which suggest a biological role for the resulting putative C-enclosure in each repeat. As mentioned above, it is likely that the OC125 and M11 epitopes are located in the C-enclosure, indicating its relative availability for immune detection. This is probably due to the C-enclosure structure and the paucity of glycosylation in the immediate surrounding areas. Domain searches also suggest some homology in the repeat domain to an SEA domain commonly found in the mucin genes [Williams SJ *et al.*, MUC13, a novel human cell surface mucin expressed by epithelial and hemopoietic cells, *J of Biol. Chem* 276(21)18327-18336 (2001)] beginning at amino acid #1 and ending at #131 of each repeat. No biological function has been described for this domain.

Based on homology of the repeat sequences to chromosome 19q 13.2 (cosmid #AC008734) and confirmed by genomic amplification, it has been established that each repeat is comprised of 5 exons (covering approximately 1900 bases of genomic DNA): exon 1 comprises 42 amino acids (#1-42); exon 2 comprises 23 amino acids (#43-65); exon 3 comprises 58 amino acids (#66-123); exon 4 comprises 12 amino acids (#124-135); and exon 5 comprises 21amino acids (#136-156) (see Figure 7B). Homology pile-ups of individual exons have also been completed (see Figure 7C), which indicates that exon 1 has a minimum of 31different copies of the exon; exon 2 has 27 copies; exon 3 has 28 copies, exon 4 has 28 copies and exon 5 has 21 copies. If all exons were only found in a single configuration relative to each other, one could determine that a minimum number of repeats of 31 were present in the CA125 molecule. Using the exon 2 pile-up data as an example, it has been established as mentioned above that there are 27 individual exon 2 sequences. Using exon 2, which was sequenced fully in both the repeat units and the overlaps, results established that a minimum of 45 repeat units are present when

exon 2 is combined with unique other exon combinations. However, based on overlap sequence information, 60+ repeat units are likely present in the CA125 molecule (Table 21). This larger number of repeat units can be accounted for by the presence of the same repeat unit occurring in more than one location.

Currently, the repetitive units of the repeat domain of the CA125 molecule constitute the majority of its extracellular molecular structure. These sequences have been presented in a tandem fashion based on overlap sequencing data. Some sequences may be incorrectly placed and some repeat units may not as yet be identified (Table 21). More recently, an additional repeat was identified in CA125 as shown in Tables 22 and 23 (SEQ. ID NOS: 307 and 308). The exact position has not yet been identified. Also, there is a potential that alternate splicing and/or mutation could account for some of the repeat variants that are listed. Studies are being conducted to compare both normal tissue derived CA125 repeats to individual tumor derived CA125 repeats to determine if such variation is present. Currently, the known exon configurations would easily accommodate the greater than 60 repeat units as projected. It is, therefore, unlikely that alternate splicing is a major contributor to the repetitive sequences in CA125. It should also be noted that the genomic database for chromosome 19q 13.2 only includes about 10 repeat units, thus indicating a discrepancy between the data of the present invention (more than 60 repeats) and the genomic database. A recent evaluation of the methods used for selection and assembly for genomic sequence [Marshall E, DNA Sequencing: Genome teams adjust to shotgum marriage, *Science* 292:1982-1983 (2001)] reports that "more research is needed on repeat blocks of almost identical DNA sequence which are more common in the human genome. Existing assembly programs can't handle them well and often delete them." The CA125 repeat units located on chromosome 19 may well be victims of deletion in the genomic database, thus accounting for most CA125 repeat units absent from the current databases.

A. Sequence Confirmation and Assembly of the Amino Terminal Domain (Domain 1) of the CA125 Molecule

As previously mentioned, homology for repeat sequences was found in the chromosome 19 cosmid AC008734 of the GCG database. This cosmid at the time consisted of 35 unordered contigs. After searching the cosmid for repeat sequences, contig #32 was found to have exons 1 and 2 of a repeat unit at its 3' end. Contig #32 also had a large open reading frame upstream

from the two repeat units, which suggested that this contig contained sequences consistent with the amino terminal end of the CA125 molecule. A sense primer was synthesized to the upstream non-repeat part of contig #32 coupled with a specific primer from within the repeat region (see Methods). PCR amplification of ovarian tumor cDNA confirmed the contiguous positioning of these two domains. The PCR reaction yielded a band of approximately 980bp. The band was sequenced and found to connect the upstream open reading frame to the repeat region of CA125. From these data, more primer sets (see Methods) were synthesized and used in PCR reactions to piece together the entire open reading frame contained in contig #32. To find the 5' most end of the sequence, an EST (AU133673) was discovered, which linked contig #32 to contig #7 of the same cosmid. Specific primers were synthesized, (5'-CTGATGGCATTATGGAACACATCAC-3' (SEQ ID NO: 59) and 5'-CCCAGAACGAGAGACCAGTGAG-3' (SEQ ID NO: 60)), to the EST and contig #32. A PCR reaction was performed to confirm that part of the EST sequence was in fact contiguous with contig #32. Confirmation of this contiguous 5' prime sequencing strategy using overlapping sequences allowed the assembly of the 5' region (Domain 1) (Figure 8A). 5' RACE PCR was performed on tumor cDNA to confirm the amino terminal sequence to CA125. The test confirmed the presence of contig #7 sequence at the amino terminal end of CA125.

The amino terminal domain comprises five genomic exons covering approximately 13,250 bp. Exon 1, a small exon, (amino acids #1-33) is derived from contig #7 (Figure 8A). The remaining exons are all derived from contig #32: Exon 2 (amino acids #34-1593), an extraordinarily large exon, Exon 3 (amino acids #1594-1605), Exon 4 (amino acids #1606-1617) and Exon 5 (amino acids #1618-1637) (see Figure 8A).

Potential N-glycosylation sites marked (x) are encoded at positions #81, #271, #320, #624, #795, #834, #938, and #1,165 (see Figure 8B). O-glycosylation sites are extraordinarily abundant and essentially cover the amino terminal domain (Figure 8B). As shown by the O-glycosylation pattern, Domain 1 is highly enriched in both threonine and serine (Figure 8B).

With additional research, an extension of the glycosylated amino terminal sequence was identified and cloned. Table 24 (SEQ ID NO: 309) illustrates the DNA sequence of the CA125 amino terminal extension. Table 25 (SEQ ID NO: 310) illustrates the protein sequence for the amino terminal extension of the CA125 gene. It should be noted that the last four amino acids,

TDGI, in SEQ ID NO: 310 belong to exon 1 of the amino terminal domain. Table 26 illustrates the serine/threonine o-glycosylation pattern for the CA125 amino terminal extension.

B. Sequence Confirmation and Assembly of the CA125 Carboxy Terminal End (Domain 3)

A search of Genbank using the repeat sequences described above uncovered a cDNA sequence referred to as Genbank accession number AK024365. This sequence was found to have 2 repeat sequences, which overlapped 2 known repeat sequences of a series of 6 repeats. As a result, the cDNA allowed the alignment of all six carboxy terminal repeats along with a unique carboxy terminal sequence. The carboxy terminus was further confirmed by the existence of two other ESTs (Genbank accession numbers AW150602 and A1923224), both of which confirmed a stop codon as well as a poly-A signal sequence and a poly-A tail (see GCG database #AF414442). The sequence of the carboxy terminal domain was confirmed using primers designed to sequence just downstream of the repeat domain (sense primer 5' GGA CAA GGT CAC CAC ACT CTA C-3') (SEQ ID NO: 303) and an antisense primer (5'-GCA GAT CCT CCA GGT CTA GGT GTG-3') (SEQ ID NO: 304) designed to carboxy terminus (Figure 9A).

The carboxy terminal domain covers more than 14,000 genomic bp. By ligation, this domain comprises nine exons as shown in Figure 9A. The carboxy-terminus is defined by a 284 amino acid sequence downstream from the repeat domains (see Figure 9B). Both N-glycosylation sites marked (x) (#31, #64, #103, #140, #194, #200) and a small number of O-glycosylation sites marked (o) are predicted for the carboxy end of the molecule (Figures 9A, 9B). Of special note is a putative transmembrane domain at positions #230-#252 followed by a cytoplasmic domain, which is characterized by a highly basic sequence adjacent to the membrane (#256-#260) as well as several potential S/T phosphorylation sites (#254, #255, #276) and tyrosine phosphorylation sites (at # 264, #273, #274) (Figures 9A, 9B).

Assembly of the CA125 molecule as validated by PCR amplification of overlap sequence provides a picture of the whole molecule (see Figure 10 and Table 21). The complete nucleotide sequence is available in Genebank, Accession #AF414442 and the amino acid sequence as currently aligned is shown in Table 21.

DISCUSSION

The CA125 molecule comprises three major domains; an extracellular amino terminal domain (Domain 1), a large multiple repeat domain (Domain 2) and a carboxy terminal domain (Domain 3), which includes a transmembrane anchor with a short cytoplasmic domain (Figure 10). The amino terminal domain is assembled by combining five genomic exons, four very short amino terminal sequences and one extraordinarily large exon, which often typifies mucin extracellular glycosylated domains [Desseyn JL *et al.*, Human mucin gene MUC5B, the 10.7-kb large central exon encodes various alternate subdomains resulting in a super-repeat. Structural evidence for a 11p15.5 gene family, *J. Biol. Chem.* 272(6):3168-3178 (1997)]. This domain is dominated by its capacity for O-glycosylation and its resultant richness in serine and threonine residues. Overall, the potential for O-glycosylation essentially covers this domain and, as such, may allow the carbohydrate superstructure to influence ECM interaction at this end of the CA125 molecule (Figure 8). There is one short area (amino acids # 74-120) where little or no glycosylation is predicted, which could allow for protein-protein interaction in the extracellular matrix.

Efforts to purify CA125 over the years were obviously complicated by the presence of this amino terminal domain, which is unlikely to have any epitope sites recognized by the OC125 or M11 class antibodies. As the CA125 molecule is degraded *in vivo*, it is likely that this highly glycosylated amino terminal end will be found associated with varying numbers of repeat units. This could very well account for both the charge and size heterogeneity of the CA125 molecule so often identified from serum and ascites fluid. Also of note are two T-TALK sequences at amino acids # 45-58 (underlined in Figure 8B), which are unique to the CA125 molecule.

The extracellular repeat domain, which characterizes the CA125 molecule, also represents a major portion of the molecular structure. It is downstream from the amino terminal domain and presents itself in a much different manner to its extracellular matrix neighbors. These repeats are characterized by many features including a highly-conserved nature (Figure 3) and a uniformity in exon structure (Figure 7). But most consistently, a cysteine enclosed sequence may form a cysteine loop (Table 21). This structure may provide extraordinary potential for interaction with neighboring matrix molecules. Domain 2 encompasses the 156 amino acid repeat units of the CA125 molecule. The repeat domain constitutes the largest proportion of the CA125 molecule (Table 21 and Figure 10). Because it has been known for more than 15 years that antibodies bind in a multivalent fashion to CA125, it has been predicted

that the CA125 molecule would include multiple repeat domains capable of binding the OC125 and M11 class of sentinel antibodies which define this molecule [O'Brien *et al.*, New monoclonal antibodies identify the glycoprotein carrying the CA125 epitope, *Am J Obstet Gynecol.* 165:1857-1964 (1991); Nustad K *et al.*, Specificity and affinity of 26 monoclonal antibodies against the CA125 antigen: First report from the ISOBM TD-1 workshop, *Tumor Biology* 17:196-219 (1996); and Bast RC *et al.*, A radioimmunoassay using a monoclonal antibody to monitor the course of epithelial ovarian cancer, *N. Engl. J. Med.* 309:883-887 (1983)]. In the present invention, more than 60 repeat units have been identified, which are in tandem array in the extracellular portion of the CA125 molecule. Individual repeat units have been confirmed by sequencing and further identified by PCR amplification of the overlapping repeat sequences. Results confirm the contiguous placement of most repeats relative to its neighbor (Table 21).

Initial evidence suggests that this area is a potential site for antibody binding and also for ligand binding. The highly conserved methionine and several highly conserved sequences within the repeat domain also suggests a functional capacity for these repeat units. The extensive glycosylation of exons 4 & 5 of the repeat unit and the N-glycosylation potential in exon 1 and the 5' end of exon 2 might further point to a functional capacity for the latter part of exon 2 and exon 3 which includes the C-enclosure (see Figure 7). It should be apparent that the C-enclosure might be a prime target for protease activity and such cleavage may well explain the difficulty experienced by many investigators in obtaining an undigested CA125 parent molecule. Such activity might explain the diffuse pattern of antibody binding and the loss of antibody binding for molecules of less than 200,000 kDa. Proteolysis would destroy the epitopes and, therefore, only multiple repeats could be identified by blotting with CA125 antibodies. The repeat unit organization also suggests the potential for a multivalent interaction with extracellular entities.

The carboxy terminal domain of the CA125 molecule comprises an extracellular domain, which does not have any homology to other known domains. It encodes a typical transmembrane domain and a short cytoplasmic tail. It also contains a proteolytic cleavage site approximately 50 amino acids upstream from the transmembrane domain. This would allow for proteolytic cleavage and release of the CA125 molecule (Figure 9). As indicated by Fendrick, *et al.* [CA125 phosphorylation is associated with its secretion from the WISH human amnion cell line, *Tumor Biology* 18:278-289 (1997)], release of the CA125 molecule is preceded by

phosphorylation and sustained by inhibitors of phosphatases, especially inhibition of phosphatase 2B. The cytoplasmic tail which contains S/T phosphorylation sites next to the transmembrane domain and tyrosine phosphorylation sites downstream from there could accommodate such phosphorylation. A very distinguishable positively charged sequence is present upstream from the tyrosine, suggesting a signal transduction system involving negatively charged phosphate groups and positively charged lysine and arginine groups.

These features of the CA125 molecule suggest a signal transduction pathway involvement in the biological function of CA125 [Fendrick JL *et al.*, CA125 phosphorylation is associated with its secretion from the WISH human amnion cell line, *Tumor Biology* 18:278-289 (1997); and Konish I *et al.*, Epidermal growth factor enhances secretion of the ovarian tumor-associated cancer antigen CA125 from the human amnion WISH cell line, *J Soc. Gynecol. Invest.* 1:89-96 (1994)]. It also reinforces the prediction of phosphorylation prior to CA125 release from the membrane surface as previously proposed [Fendrick JL *et al.*, CA125 phosphorylation is associated with its secretion from the WISH human amnion cell line, *Tumor Biology* 18:278-289 (1997); and Konish I *et al.*, Epidermal growth factor enhances secretion of the ovarian tumor-associated cancer antigen CA125 from the human amnion WISH cell line, *J Soc. Gynecol. Invest.* 1:89-96 (1994)]. Furthermore, a putative proteolytic cleavage site on the extra-cellular side of the transmembrane domain is present at position #176-181.

How well does the CA125 structure described in the present invention compare to the previously known CA125 structure? O'Brien *et al.* reported that a number of questions needed to be addressed: 1) the multivalent nature of the molecule; 2) the heterogeneity of CA125; 3) the carbohydrate composition; 4) the secretory or membrane bound nature of the CA125 molecule; 5) the function of the CA125 molecule; and 6) the elusive CA125 gene [More than 15 years of CA125: What is known about the antigen, its structure and its function, *Int J Biological Markers* 13(4)188-195 (1998)]. Several of these questions have been addressed in the present invention including, of course, the gene and its protein core product. Perhaps, most interestingly is the question of whether an individual large transcript accounted for the whole CA125 molecule, or a number of smaller transcripts which represented subunits that specifically associated to produce the CA125 molecule. From the results produced by way of the present invention, it is now apparent that the transcript of CA125 is large - similar to some of the mucin gene transcripts e.g. MUC 5B [see Verma M *et al.*, Mucin genes: Structure, expression and regulation,

Glycoconjugate J. 11:172-179 (1994); and Gendler SJ *et al.*, Epithelial mucin genes, *Annu. Rev. Physiol.* 57:607-634 (1995)]. The protein core extracellular domains all have a high capacity for O-glycosylation and, therefore, probably accounts for the heterogeneity of charge and size encountered in the isolation of CA125. The data also confirm the O-glycosylation inhibition data, indicating CA125 to be rich in O-glycosylation [Lloyd KO *et al.*, Synthesis and secretion of the ovarian cancer antigen CA125 by the human cancer cell line NIH: OVCAR-3, *Tumor Biology* 22, 77-82 (2001); Lloyd KO *et al.*, Isolation and characterization of ovarian cancer antigen CA125 using a new monoclonal antibody (VK-8): Identification as a mucin-type molecule, *Int. J. Cancer*, 71:842-850 (1997); and Fendrick JL *et al.*, Characterization of CA125 synthesized by the human epithelial amnion WISH cell line, *Tumor Biology* 14:310-318 (1993)].

The repeat domain which includes more than 60 repeat units accounts for the multivalent nature of the epitopes present, as each repeat unit likely contains epitope binding sites for both OC125-like antibodies and M11-like antibodies. The presence of a transmembrane domain and cleavage site confirms the membrane association of CA125, and reinforces the data which indicates a dependence of CA125 release on proteolysis. Also, the release of CA125 from the cell surface may well depend on cytoplasmic phosphorylation and be the result of EGF signaling [Nustad K *et al.*, Specificity and affinity of 26 monoclonal antibodies against the CA125 antigen: First report from the ISOBM TD-1 workshop, *Tumor Biology* 17:196-219 (1996)]. As for the question of inherent capacity of CA125 for proteolytic activity, this does not appear to be the case. However, it is likely that the associated proteins isolated along with CA125 (e.g. the 50 kDa protein which has no antibody binding ability) may have proteolytic activity. In any case, proteolysis of an extracellular cleavage site is the most likely mechanism of CA125 release. Such cleavage would be responsive to cytoplasmic signaling and mediated by an associated extracellular protease activity.

In summary, the large number of tandem repeats of the CA125 molecule, which dominate its molecular structure and contain the likely epitope binding sites of the CA125 molecule, was unexpected. Also, one cannot as yet account for the proteolytic activity, which has plagued the isolation and characterization of this molecule for many years. While no protease domain per se is constituitively part of the CA125 molecule, there is a high likelihood of a direct association by an extracellular protease with the ligand binding domains of the CA125 molecule. Finally, what is the role of the dominant repeat domain of this extracellular structure? Based on the expression

data of CA125 on epithelial surfaces and in glandular ducts, it is reasonable to conclude that the unique structure of these repeat units with their cysteine loops plays a role both as glandular anti-invasive molecules (bacterial entrapment) and/or a role in anti-adhesion (maintaining patency) between epithelial surfaces and in ductal linings.

Recently, Yin and Lloyd described the partial cloning of the CA125 antigen using a completely different approach to that described in the present invention [Yin TWT *et al.*, Molecular cloning of the CA125 ovarian cancer antigen. Identification as a new mucin (MUC16), *J Biol. Chem.* 276:27371-27375 (2001)]. Utilizing a polyclonal antibody to CA125 to screen an expression library of the ovarian tumor cell line OVCAR-3, these researchers identified a 5965 bp clone containing a stop codon and a poly A tail, which included nine partially conserved tandem repeats followed by a potential transmembrane region with a cytoplasmic tail. The 5965 bp sequence is almost completely homologous to the carboxy terminus region shown in Table 21. Although differing in a few bases, the sequences are homologous. As mentioned above, the cytoplasmic tail has the potential for phosphorylation and a transmembrane domain would anchor this part of the CA125 molecule to the surface of the epithelial or tumor cell. In the extracellular matrix, a relatively short transition domain connects the transmembrane anchor to a series of tandem repeats - in the case of Yin and Lloyd, nine.

By contrast, the major extracellular part of the molecule of the present invention as shown is upstream from the sequence described by Yin and includes a large series of tandem repeats. These results, of course, provide a different picture of the CA125 molecule, which suggest that CA125 is dominated by the series of extracellular repeats. Also included is a major amino terminal domain (~1638 amino acids) for the CA125 molecule, which it is believed accounts for a great deal of the O-glycosylation known to be an important structural component of CA125.

In conclusion, a CA125 molecule is disclosed which requires a transcript of more than 35,000 bases and occupies approximately 150,000 bp on chromosome 19q 13.2. It is dominated by a large series of extracellular repeat units (156 amino acids), which offer the potential for molecular interactions especially through a highly conserved unique cysteine loop. The repeat units also include the epitopes now well-described and classified for both the major class of CA125 antibodies (i.e., the OC125 and the M11 groups). The CA125 molecule is anchored at its carboxy terminal through a transmembrane domain and a short cytoplasmic tail. CA125 also

contains a highly glycosylated amino terminal domain, which includes a large extracellular exon typical of some mucins. Given the massive repeat domain presence of both epithelial surfaces and ovarian tumor cell surfaces, it might be anticipated that CA125 may play a major role in determining the extracellular environment surrounding epithelial and tumor cells.

Advantages and Uses of the CA125 Recombinant Products

1) Current assays to CA125 utilize as standards either CA125 produced from cultured cell lines or from patient ascites fluid. Neither source is defined with regard to the quality or purity of the CA125 molecule. Therefore arbitrary units are used to describe patient levels of CA125. Because cut-off values are important in the treatment of patients with elevated CA125 and because many different assay systems are used clinically to measure CA125, it is relevant and indeed necessary to define a standard for all CA125 assays. Recombinant CA125 containing epitope binding sites could fulfill this need for standardization. Furthermore, new and more specific assays may be developed utilizing recombinant products for antibody production.

2) Vaccines: Adequate data now exists [see Wagner U *et al.,* Immunological consolidation of ovarian carcinoma recurrences with monoclonal anti-idiotype antibody ACA125: Immune responses and survival in palliative treatment, *Clin. Cancer Res.* 7:1112-1115 (2001)], which suggest and support the idea that CA125 could be used as a therapeutic vaccine to treat patients with ovarian carcinoma. Heretofore, in order to induce cellular and humoral immunity in humans to CA125, murine antibodies specific for CA125 were utilized in anticipation of patient production of anti-ideotypic antibodies, thus indirectly allowing the induction of an immune response to the CA125 molecule. With the availability of recombinant CA125, especially domains which encompass epitope binding sites for known murine antibodies and domains directly anchoring CA125 on the tumor cell, it will be feasible to more directly stimulate patients' immune systems to CA125 and as a result, extend the life of ovarian carcinoma patients as demonstrated by Wagner et al.

Several approaches can be utilized to achieve such a therapeutic response in the immune system by: 1) directly immunizing the patient with recombinant antigen containing the CA125 epitopes or other domains; 2) harvesting dendritic cells from the patient; 3)

expanding these cells in *in vitro* culture; 4) activating the dendritic cells with the recombinant CA125 epitope domain or other domains or with peptides derived from these domains [see Santin AD *et al.,* Induction of ovarian tumor-specific CD8+ cytotoxic T lymphocytes by acid-eluted peptide-pulsed autologous dendritic cells, *Obstetrics & Gynecology* 96(3):422-430 (2000)]; and then 5) returning these immune stem cells to the patient to achieve an immune response to CA125. This procedure can also be accomplished using specific peptides which are compatible with histocompatibility antigens of the patient. Such peptides compatible with the HLA-A2 binding motifs common in the population are indicated in Figure 12.

3) Therapeutic Targets: Molecules, which are expressed on the surface of tumor cells as CA125 is, offer potential targets for immune stimulation, drug delivery, biological modifier delivery or any agent which can be specifically delivered to ultimately kill the tumor cells. CA125 offers such potential as a target: 1) Antibodies to CA125 epitopes or newly described potential epitopes: Most especially humanized or human antibodies to CA125 which could directly activate the patients' immune system to attack and kill tumor cells. Antibodies could be used to deliver all drug or toxic agents including radioactive agents to mediate direct killing of tumor cells. 2) Natural ligands: Under normal circumstances, molecules are bound to the CA125 molecule e.g. a 50 k dalton protein which does not contain CA125 epitopes co-purifies with CA125. Such a molecule, which might have a natural binding affinity for domains on the CA125 molecule, could also be utilized to deliver therapeutic agents to tumor cells.

4) Anti-sense therapy: CA125 expression may provide a survival or metastatic advantage to ovarian tumor cells as such antisense oligonucleotide derived from the CA125 sequence could be used to down-regulate the expression of CA125. Antisense therapy could be used in association with a tumor cell delivery system such as described above.

5) Small Molecules: Recombinant domains of CA125 also offer the potential to identify small molecules which bind to individual domains of the molecule. Small molecules either from combinatorial chemical libraries or small peptides can also be used as delivery agents or as biological modifiers.

All references referred to herein are hereby incorporated by reference in their entirety.

It should be understood that various changes and modifications to the presently preferred embodiments described herein will be apparent to those skilled in the art. Such changes and modifications can be made without departing from the spirit and scope of the present invention and without diminishing its attendant advantages.

TABLE 1

Comparison of the Amino Acid Terminal Sequences and Several Internal Sequences for the 40kD Band for CA125 glycoprotein (SEQ ID NO: 1 through SEQ ID NO: 4) to the Nucleotide and Amino Acid Sequences for EST Genbank Accession No. AA640762
(SEQ ID NO: 5 and SEQ ID NO: 6, respectively)

40kDa Nterm – QHPGSRKFKTTEQ (SEQ ID NO: 1)

Peak 68 – FLTVERVLQGL (SEQ ID NO: 2)

Peak 65 – DTYVGPLY (SEQ ID NO: 3)

Peak 30 – DGAANGVD (SEQ ID NO: 4)

(SEQ ID NO: 5 and SEQ ID NO: 6)

```
1   CGTCGACCTGGCTCTAGAAAGTTTAACACCACGGAGAGAGTCCTTCAGGGTCTGCTCAGG
    R  R  P  G  S  R  K  F  N  T  T  E  R  V  L  Q  G  L  L  R

61  CCTGTGTTCAAGAACACCAGTGTTGGCCCTCTGTACTCTGGCTGCAGACTGACCTTGCTC
    P  V  F  K  N  T  S  V  G  P  L  Y  S  G  C  R  L  T  L  L

121 AGGCCCAAGAAGGATGGGGCAGCCACCAAAGTGGATGCCATCTGCACCTACCGCCCTGAT
    R  P  K  K  D  G  A  A  T  K  V  D  A  I  C  T  Y  R  P  D

181 CCCAAAAGCCCTGGACTGGACAGAGAGCAGCTATACTGGGAGCTGAGCCAGGGTGATGCA
    P  K  S  P  G  L  D  R  E  Q  L  Y  W  E  L  S  Q  G  D  A
```

TABLE 2A

Nucleotide and Amino Acid Sequences for Sense Primer 5' 3' (SEQ ID NO: 7 and SEQ ID NO: 8 respectively) and Antisense Primer 5' 3' (SEQ ID NO: 9 and SEQ ID NO: 10 respectively) based upon Regions of Homology for EST Genbank Accession Nos. BE005912 and AA640762)

GGA GAG GGT TCT GCA GGG TC	(SEQ ID NO: 7)
E R V L Q G	(SEQ ID NO: 8)
GTG AAT GGT ATC AGG AGA GG	(SEQ ID NO: 9)
P L L I P F	(SEQ ID NO: 10)

TABLE 2B

Sense and Anti-Sense Primers Used for Ordering Repeat Units (SEQ ID NO: 301 and SEQ ID NO: 302, respectively)

5'-GTCTCTATGTCAATGGTTTCACCC-3'	(SEQ ID NO: 301)
5'-TAGCTGCTCTCTGTCCAGTCC-3'	(SEQ ID NO: 302)

TABLE 3

Amino Acid Sequence for a 400 bp Repeat in the CA125 Molecule
(SEQ ID NO: 11 thru SEQ ID NO: 21)

	1				50	
12	ERVLQGLLRS	LFKSTSVGPL	YSGCRLTLLR	PEKDGTATGV	DAICTHHPDP	(SEQ ID NO: 11)
34	ERVLQGLLMP	LFKNTSVSSL	YSGCRLTLLR	PEKDGAATRA	DAVCTHRPDP	(SEQ ID NO: 12)
32	ERVLQGLLGP	IFKNTSVGPL	YSGCRLTSLR	SEKDGAATGV	DAICIHRLDP	(SEQ ID NO: 13)
46	ERVLQGLLGP	MFKNTSVGLL	YSGCRLTLLR	PEKNGAATGM	DAICSHRLDP	(SEQ ID NO: 14)
33	ERVLQGLLGP	LFKNSSVGPL	YSGCRLISLR	SEKDGAATGV	DAICTHHLNP	(SEQ ID NO: 15)
15	ERVLQGLLRP	LFKSTSAGPL	YSGCRLTLLR	PEKHGAATGV	DAICTLRLDP	(SEQ ID NO: 16)
35	ERVLQGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKRGAATGV	DTICTHRLDP	(SEQ ID NO: 17)
111	ERVLQGLLTP	LFKNTSVGPL	YSGCRLTLLR	PEKQEAATGV	DTICTHRVDP	(SEQ ID NO: 18)
42	ERVLQGLLKP	LFKNTSVGPL	YSGCRLTLLR	PEKHEAATGV	DTICTHRLDP	(SEQ ID NO: 19)
116	ERVLQGLLSP	IFKNSSVGPL	YSGCRLTSLR	PEKDGAATGM	DAVCLYHPNP	(SEQ ID NO: 20)
23	ERVLQGLLRP	LFKNTSIGPL	YSSCRLTLLR	PEKDKAATRV	DAICTHHPDP	(SEQ ID NO: 21)

	51				100
12	KSPRLDREQL	YWELSQLTHN	ITELGPYALD	NDSLFVNGFT	HRSSVSTTST
34	KSPGLDRERL	YWKLSQLTHG	ITELGPYTLD	RHSLYVNGFT	HQSSMTTTRT
32	KSPGLNREQL	YWELSKLTND	IEELGPYTLD	RNSLYVNGFT	HQSSVSTTST
46	KSPGLNREQL	YWELSQLTHG	IKELGPYTLD	RNSLYVNGFT	HRSSVAPTST
33	QSPGLDREQL	YWQLSQMTNG	IKELGPYTLD	RNSLYVNGFT	HRSSGLTTST
15	TGPGLDRERL	YWELSQLTNS	VTELGPYTLD	RDSLYVNGFT	HRSSVPTTSI
35	LNPGLDREQL	YWELSKLTRG	IIELGPYTLD	RDSLYVNGFT	HRSSVPTTSI
111	IGPGLDRERL	YWELSQLTNS	ITELGPYTLD	RDSLYVDGFN	PWSSVPTTST
42	LNPGLDREQL	YWELSKLTRG	IIELGPYLLD	RGSLYVNGFT	HRNFVPITST
116	KRPGLDREQL	YWELSQLTHN	ITELGPYSLD	RDSLYVNGFT	HQNSVPTTST
23	QSPGLNREQL	YWELSQLTHG	ITELGPYTLD	RDSLYVDGFT	HWSPIPTTST

	101				150
12	PGTPTVYLGA	SKTPASIFGP	S..AASPLLI	PFT~~~~~~~	~~~~~~~~~~
34	PDTSTMHLAT	SRTPASLSGP	T..TASPLLI	PF~~~~~~~~	~~~~~~~~~~
32	PGTSTVDLRT	SGTPSSLSSP	TIMAAGPLLI	PF~~~~~~~~	~~~~~~~~~~
46	PGTSTVDLGT	SGTPSSLPSP	T..TAVPLLI	PF~~~~~~~~	~~~~~~~~~~
33	PWTSTVDLGT	SGTPSPVPSP	T..TAGPFLI	PF~~~~~~~~	~~~~~~~~~~
15	PGTSAVHLET	SGTPASLPGH	T..APGPLLI	PF~~~~~~~~	~~~~~~~~~~
35	PGTSAVHLET	SGTPASLPGH	I..VPGPLLI	PF~~~~~~~~	~~~~~~~~~~
111	PGTSTVHLAT	SGTPSPLPGH	T..APVPLLI	PFT~~~~~~~	~~~~~~~~~~
42	PGTSTVHLGT	SETPSSLPRP	I..VPGPLLV	PFT~~~~~~~	~~~~~~~~~~
116	PGTSTVYWAT	TGTPSSFPGH	T..EPGPLLI	PF~~~~~~~~	~~~~~~~~~~
23	PGTSIVNLGT	SGIPPSLPET	T..ATGPLLI	PFT~~~~~~~	~~~~~~~~~~

TABLE 3-continued

Amino Acid Sequence for a 400 bp Repeat in the CA125 Molecule
(SEQ ID NO: 11 thru SEQ ID NO: 21)

	151	170
12	~~~~~~~~~~	~~~~~~~~~~
34	~~~~~~~~~~	~~~~~~~~~~
32	~~~~~~~~~~	~~~~~~~~~~
46	~~~~~~~~~~	~~~~~~~~~~
33	~~~~~~~~~~	~~~~~~~~~~
15	~~~~~~~~~~	~~~~~~~~~~
35	~~~~~~~~~~	~~~~~~~~~~
111	~~~~~~~~~~	~~~~~~~~~~
42	~~~~~~~~~~	~~~~~~~~~~
116	~~~~~~~~~~	~~~~~~~~~~
23	~~~~~~~~~~	~~~~~~~~~~

TABLE 4

Amino Acid Sequence for a 800 bp Repeat in the CA125 Molecule
(SEQ ID NO: 22 thru SEQ ID NO: 35)

	1				50	
79	ERVLQGLLKP	LFRNSSLEYL	YSGCRLASLR	PEKDSSAMAV	DAICTHRPDP	(SEQ ID NO: 22)
811	ERVLQGLLKP	LFRNSSLEYL	YSGCRLASLR	PEKDSSAMAV	DAICTHRPDP	(SEQ ID NO: 23)
21	ERVLQGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKRGAATGV	DTICTHRLDP	(SEQ ID NO: 24)
89	ERVLQGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKRGAATGV	DTICTHRLDP	(SEQ ID NO: 25)
85	ERVLQGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKRGAATGV	DTICTHRLDP	(SEQ ID NO: 26)
712	ERVLQGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKRGAATGV	DTICTHRLDP	(SEQ ID NO: 27)
86	ERVLQGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKHGAATGV	DAICTLRLDP	(SEQ ID NO: 28)
87	ERVLQGLLTP	LFKNTSVGPL	YSGCRLTLLR	PEKQEAATGV	DTICTHRVDP	(SEQ ID NO: 29)
810	ERVLQGLLRP	LFKNTSIGPL	YSSCRLTLLR	PEKDKAATRV	DAICTHHPDP	(SEQ ID NO: 30)
83	ERVLQGLLRP	VFKNTSVGPL	YSGCRLTLLR	PKKDGAATKV	DAICTYRPDP	(SEQ ID NO: 31)
81	ERVLQGLLGP	MFKNTSVGLL	YSGCRLTLLR	PKKDGAATKV	DAICTYRPDP	(SEQ ID NO: 32)
44	ERVLQGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKDGAATGM	DAVCLYHPNP	(SEQ ID NO: 33)
812	ERVLQGLLSP	ISKNSSVGPL	YSGCRLTSLR	PEKDGAATGM	DAVCLYHPNP	(SEQ ID NO: 34)
76	ERVLQGLLSP	IFKNSSVGSL	YSGCRLTLLR	PEKDGAATRV	DAVCTHRPDP	(SEQ ID NO: 35)

	51				100
79	EDLGLDRERL	YWELSNLTNG	IQELGPYTLD	RNSLYVNGFT	HRSSMPTTST
811	EDLGLDRERL	YWELSNLTNG	IQELGPYTLD	RNSLYVNGFT	HRSSGLTTST
21	LNPGLDREQL	YWELSKLTRG	IIELGPYLLD	RGSLYVNGFT	HRTSVPTTST
89	LNPGLDREQL	YWELSKLTRG	IIELGPYLLD	RGSLYVNGFT	HRNFVPITST
85	LNPGLDREQL	YWELSKLTRG	IIELGPYLLD	RGSLYVNGFS	RQSSMTTTRT
712	LNPGLDREQL	YWELSKLTRG	IIELGPYLLD	RDSLYVNGFT	HRSSVPTTSI
86	TGPGLDRERL	YWELSQLTNS	VTELGPYTLD	RDSLYVNGFT	HRSSVPTTSI
87	IGPGLDRERL	YWELSQLTNS	ITELGPYTLD	RDSLYVNGFN	PWSSVPTTST
810	QSPGLNREQL	YWELSQLTHG	ITELGPYTLD	RDSLYVDGFT	HWSPIPTTST
83	KSPGLDREQL	YWELSQLTHS	ITELGPYTLD	RDSLYVNGFT	QRSSVPTTSI
81	KSPGLDREQL	YWELSQLTHS	ITELGPYTLD	RDSLYVNGFT	QRSSVPTTSI
44	KRPGLDREQL	YCELSQLTHD	ITELGPYSLD	RDSLYVNGFT	HQNSVPTTST
812	KRPGLDREQL	YWELSQLTHN	ITELGPYSLD	RDSLYVNGFT	HQNSVPTTST
76	KSPGLDRERL	YWKLSQLTHG	ITELGPYTLD	RHSLYVNGFT	HQSSMTTTRT

	101				150
79	PGTSTVDVGT	SGTPSSSPSP	TTAGPLLMPF	TLNFTITNLQ	YEEDMRRTGS
811	PWTSTVDLGT	SGTPSPVPSP	TTAGPLLIPF	TLNFTITNLQ	YEENMGHPGS
21	PGTSTVDLGT	SGTPFSLPSP	ATAGPLLVLF	TLNFTITNLK	YEEDMHRPGS
89	PGTSTVHLGT	SETPSSLPRP	IVPGPLLIPF	TINFTITNLR	YEENMHHPGS
85	PDTSTMHLAT	SRTPASLSGP	TTASPLLIPF	TLNFTITNLQ	YEENMGHPGS
712	PGTSAVHLET	FGTPASLHGH	TAPGPVLVPF	TLNFTITNLQ	YEEDMRHPGS
86	PGTSAVHLET	SGTPASLPGH	TAPGPLLVPF	TLNFTITNLQ	YEEDMRHPGS
87	PGTSTVHLAT	SGTPSSLPGH	TAPVPLLIPF	TLNFTITNLH	YEENMQHPGS
810	PGTSIVNLGT	SGIPPSLPET	TATGPLLIPF	TPNFTITNLQ	YEEDMRRTGS
83	PGTPTVDLGT	SGTPVSKPGP	SAASPLLVPF	TLNFTITNLQ	YEEDMHRPGS
81	PGTPTVDLGT	SGTPVSKPGP	SAASPLLIPF	TINFTITNLR	YEENMGHPGS
44	PGTSTVYWAT	TGTPSSFPGH	TEPGPLLIPF	TFNFTITNLH	YEENMQHPGS
812	PGTSTVYWAT	TGTPSSFPGH	TEPGPLLIPF	TVNFTITNLR	YEENMHHPGS
76	PDTSTMHLAT	SRTPASLSGP	TTASPLLVLF	TINFTITNQR	YEENMHHPGS

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TABLE 4-continued

Amino Acid Sequence for a 800 bp Repeat in the CA125 Molecule
(SEQ ID NO: 22 thru SEQ ID NO: 35)

```
     151                                                  200
 79  RKFNTMERVL QGLLSPIFKN SSVGPLYSGC RLTSLRPEKD GAATGMDAVC
811  RKFNIMERVL QGLLMPLFKN TSVSSLYSGC RLTLLRPEKD GAATRVDAVC
 21  RKFNTTERVL QTLLGPMFKN TSVGLLYSGC RLTLLRSEKD GAATGVDAIC

 89  RKFNIMERVL QGLLGPLFKN SSVGPLYSGC RLISLRSEKD GAATGVDAIC
 85  RKFNIMERVL QGLLNPIFKN SSVGPLYSGC RLTSLKPEKD GAATGMDAVC
712  RKFNTTERVL QGLLKPLFKS TSVGPLYSGC RLTLLRPEKR GAATGVDTIC
 86  RKFNTTERVL QGLLKPLFKS TSVGPLYSGC RLTLLRPEKR GAATGVDTIC
 87  RKFNTTERVL QGLLKPLFKS TSVGPLYSGC RLTLLRPEKH GAATGVDAIC
810  RKFNTMERVL QGLLSPIFKN SSVGPLYSGC RLTSLRPEKD GAATGMDAVC
 83  RKFNATERVL QGLLSPIFKN SSVGPLYSGC RLTSLRPEKD GAATGMDAVC
 81  RKFNIMERVL QGLLKPLFKN TSVGPLYSGC RLTLLRPKKD GAATGVDAIC
 44  RKFNTTERVL QGLLKPLFKN TSVGPLYSGC RLTLLRPEKH EAATGVDTIC
812  RKFNTTERVL QGLLRPVFKN TSVGPLYSGC RLTLLRPKKD GAATKVDAIC
 76  RKFNTTERVL QGLLRPVFKN TSVGPLYSGC RLTLLRPKKD GAATKVDAIC

     201                                                  250
 79  LYHPNPKRPG LDREQLYWEL SQLTHNITEL GPYSLDRDSL YVNGFTHQNS
811  TQRPDPKSPG LDRERLYWKL SQLTHGITEL GPYTLDRHSL YVNGLTHQSS
 21  THRLDPKSPG VDREQLYWEL SQLTNGIKEL GPYTLDRNSL YVNGFTHWIP
 89  THHLNPQSPG LDREQLYWQL SQMTNGIKEL GPYTLDRNSL YVNGFTHRSS
 85  LYHPNPKRPG LDREQLYWEL SQLTHGIKEL GPYTLDRNSL YVNGFTHRSS
712  THRLDPLNPG LDREQLYWEL SKLTRGIIEL GPYLLDRGSL YVNGFTHRNF
 86  THRLDPLNPG LDREQLYWEL SKLTRGIIEL GPYLLDRGSL YVNGFTHRNF
 87  THRLDPKSPG VDREQLYWEL SQLTNGIKEL GPYTLDRNSL YVNGFTHWIP
810  LYHPNPKRPG LDREQLY~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~
 83  LYHPNPKRPG LDREQLYWEL SQLTHNITEL GPYSLDRDSL YVNGFTHQSS
 81  THRLDPKSPG LNREQLYWEL SKLTNDIEEL GPYTLDRNSL YVNGFTHQSS
 44  THRVDPIGPG LDRERLYWEL SQLTNSIHEL GPYTLDRDSL YVNGFNPRSS
812  TYRPDPKSPG LDREQLYWEL SKLTNDIEEL GPYTLDRNSL YVNGFTHQSS
 76  TYRPDPKSPG LDREQLYWEL SQLTHSITEL GPYTQDRDSL YVNGFTHRSS

     251                                      288
 79  VPTTSTPGTS TVYWATTGTP SSFPGHT..E PGPL~~~~
811  MTTTRTPDTS TMHLATSRTP ASLSGPT..T ASPLLIPF
 21  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~
 89  GLTTSTPWTS TVDLGTSGTP SPVPSPT..T AGPLLIPF
 85  VAPTSTPGTS TVDLGTSGTP SSLPSPT..T AVPLLIPF
712  VPITSTPGTS TVHLGTSETP SSLPRPI..V PGPLLIPF
 86  VPITSTPGTS TVHLGTSETP SSLPRPI..V PGPLLIPF
 87  VPTSSTPGTS TVDLG.SGTP SSLPSPT..T AGPL~~~~
810  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~
 83  MTTTRTPDTS TMHLATSRTP ASLSGPT..T ASPLLIPF
 81  VSTTSTPGTS TVDLRTSGTP SSLSSPTIMA AGPLLIPF
 44  VPTTSTPGTS TVHLATSGTP SSLPGHT..A PVPLLI~~
812  VSTTSTPGTS TVDLRTSGTP SSLSSPTIMA AGPLLIPF
 76  VPTTSIPGTS AVHLETSGTP ASLP~~~~~~ ~~~~~~~~
```

TABLE 5

Amino Acid Sequence for a 1200 bp Repeat in the CA125 Molecule
(SEQ ID NO: 36 thru SEQ ID NO: 46)

	1				50	
910	ERVLQGLLGP	MFKNTSVGLL	YSGCRLTLLR	PEKRGAATGV	DTICTHRLDP	(SEQ ID NO: 36)
99	ERVLHGLLTP	LFKNTRVGPL	YSGCRLTLLR	PEKQEAATGV	DTICTHRVDP	(SEQ ID NO: 37)
112	~~~~~~~~~~	~~~~~~~GPL	YSGCRLTSLR	PEKDGAATGM	DAVCLYHPNP	(SEQ ID NO: 38)
95	ERVLQGPLSP	IFKNSSVGPL	YSGCRLTSLR	PEKDGAATGM	DAVCLYHPNP	(SEQ ID NO: 39)
71	~~~~~~~~~~	~~~~TSVGPL	YSGCRLTLLR	SEKDGAATGV	DAIYTHRLDP	(SEQ ID NO: 40)
78	~~~~~~~~~~	~~~~~~~~~~	~~~~~~TLLR	PKKDGVATGV	DAICTHRLDP	(SEQ ID NO: 41)
115	ERVLQGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKDGVATRV	DAICTHRPDP	(SEQ ID NO: 42)
91	ERVLQGLLKP	LFRNSSLEYL	YSGCRLASLR	PEKDSSAMAV	DAICTHRPDP	(SEQ ID NO: 43)
92	ERVLQGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKRGAATGV	DTICTHRLDP	(SEQ ID NO: 44)
113	ERVLQGLLGP	MFKNTSVGLL	YSGCRLTLLR	PEKNGAATGM	DAICSHRLDP	(SEQ ID NO: 45)
711	ERVLQGLLKP	LFKSTSVGPL	YSGCRLTLLR	PEKHGAATGV	DAICTLRLDP	(SEQ ID NO: 46)

	51				100
910	LNPGLDREQL	YWELSKLTRG	IIELGPYLLD	RGSLYVNGFT	HRNFVPITST
99	IGPGLDRERL	YWELSQLTNS	ITELGPYTLD	RDSLYVNGFN	PWSSVPTTST
112	KRPGLDREQL	YWELSQLTHN	ITELGPYSLD	RDSLYVNGFT	HQNSVPTTST
95	KRPGLDREQL	YWELSQLTHN	ITELGPYSLD	RDSLYVNGFT	HQNSVPTTST
71	KSPGVDREQL	YWELSQLTNG	IKELGPYTLD	RNSLYVNGFT	HQTSAPNTST
78	KSPGLNREQL	YWELSKLTND	IEELGPYTLD	RNSLYVNGFT	HQSSVSTTST
115	KIPGLDRQQL	YWELSQLTHS	ITELGPYTLD	RDSLYVNGFT	QRSSVPTTST
91	EDLGLDRERL	YWELSNLTNG	IQELGPYTLD	RNSLYVNGFT	HRSSMPTTST
92	LNPGLDREQL	YWELSKLTRG	IIELGPYLLD	RGSLYVNGFT	HRNFVPITST
113	KSPGLNREQL	YWELSQLTHG	IKELGPYTLD	RNSLYVNGFT	HRSSVAPTST
711	TGPGLDRERL	YWELSQLTNS	VTELGPYTLD	RDSLYVNGFT	HRSSVPTTSI

	101				150
910	PGTSTVHLGT	SETPSSLPRP	IV..PGPLLV	PFTLNFTITN	LQYEEAMRHP
99	PGTSTVHLAT	SGTPSSLPGH	TA..PVPLLI	PFTLNFTITN	LHYEENMQHP
112	PGTSTVYWAT	TGTPSSFPGH	T..EPGPLLI	PFTLNFTITN	LQYEENMGHP
95	PGTSTVYWAT	TGTPSSFPGH	T..EPGPLLI	PFTLNFTITN	LQYEENMGHP
71	PGTSTVDLGT	SGTPSSLPSP	T..SAGPLLI	PFTINFTITN	LRYEENMHHP
78	PGTSTVDLRT	SGTPSSLSSP	TIMAAGPLLI	PFTINFTITN	LRYEENMHHP
115	PGTFTVQPET	SETPSSLPGP	T..ATGPVLL	PFTLNFTIIN	LQYEEDMHRP
91	PGTSTVDVGT	SGTPSSSPSP	T..TAGPLLM	PFTLNFTITN	LQYEEDMRRT
92	PGTSTVHLGT	SETPSSLPRP	IV..PGPLLI	PFTLNFTITN	LQYEENMGHP
113	PGTSTVDLGT	SGTPSSLPSP	T..TAVPLLI	PFTLNFTITN	LKYEEDMHCP
711	PGTSAVHLET	SGTPASLPGH	T..APGPLLI	PFTLNFTITN	LHYEENMQHP

	151				200
910	GSRKFNTTER	VLQGLLRPLF	KNTSVSSLYS	GCRLTLLRPE	KDGAATRVDA
99	GSRKFNTTER	VLQGLLKPLF	KNTSVGPLYS	GCRLTLFKPE	KHEAATGVDA
112	GSRKFNITES	VLQGLLTPLF	KNSSVGPLYS	GCRLISLRSE	KDGAATGVDA
95	GSRKFNITER	VLQGLLNPIF	KNSSVGPLYS	GCRLTSLRPE	KDGAATGMDA
71	GSRKFNTMER	VLQGLLKPLF	KSTSVGPLYS	GCRLTLLRPE	KDGVATRVDA
78	GSRKFNTMER	VLQGLLMPLF	KNTSVSSLYS	GCRLTLLRPE	KDGAATRVDA
115	GSRKFNTTER	VLQGLLMPLF	KNTSVGPLYS	GCRLTLLRPE	KQEAATGVDT
91	GSRKFNTMES	VLQGLLKPLF	KNTSVGPLYS	GCRLTLLRPK	KDGAATGVDA
92	GSRKFNITER	VLQGLLKPLF	RNSSLEYLYS	GCRLTSLRPE	KDSSTMAVDA

TABLE 5-continued

Amino Acid Sequence for a 1200 bp Repeat in the CA125 Molecule
(SEQ ID NO: 36 thru SEQ ID NO: 46)

```
113  GSRKFNTTER VLQSLFGPMF KNTSVGPLYS GCRLTLFRSE KDGAATGVDA
711  GSRKFNTMER VLQGCLVPCS RNTNVGLLYS GCRLTLLXXX XXXXXXXXXX

     201                                                 250
910  ACTYRPDPKS PGLDREQLYW ELSQLTHSIT ELGPYTLDRV SLYVNGFNPR
 99  ICTLRLDPTG PGLDRERLYW ELSQLTNSVT ELGPYTLDRD SLYVNGFTHR
112  ICTHHLNPQS PGLDREQLYW QLSQMTNGIK ELGPYTLDRD SLYVNGFTHR
 95  VCLYHPNPKR PGLDREQLYC ELSQLTHNIT ELGPYSLDRD SLYVNGFTHQ
 71  ICTHRPDPKI PGLDRQQLYW ELSQLTHSIT ELGPYTLDRD SLYVNGFTQR
 78  VCTHRPDPKS PGLDRERLYW KLSQLTHGIT ELGPYTLDRN SLYVNGFTHR
115  ICTHRLDPSE PGLDREQLYW ELSQLTNSIT ELGPYTLDRD SLYVNGFTHS
 91  ICTHRLDPKS PGLNREQLYW ELSKLTNDIE EVGPYTLDRN SLYVNGFTHR
 92  ICTHRPDPED LGLDRERLYW ELSNLTNGIQ ELGPYTLDRN SLYVNGFTHR
113  ICTHRLDPKS PGVDREQLYW ELSQLTNGIK ELGPYTLDRN SLYVNGFTHQ
711  XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXGPYTLDRN SLYVNGFTHR

     251                                                 300
910  SSV.PTTSTP GTSTVHLATS GTPSSLPGHT APVPLLIPFT LNFTITNLQY
 99  SSV.PTTSIP GTSAVHLETS GTPASLPGHT APGPLLIPFT LNFTITNLQY
112  SL.GLTTSTP WTSTVDLGTS GTPSPVPSPT TAGPLLIPFT LNFTITNLQY
 95  NS.VPTTSTP GTSTVYWATT GTPSSFPGHT EPGPLLIPFT LNFTITNLQY
 71  SSV.PTTSTP GTFTVQPETS ETPSSLPGPT ATGPVLLPFT LNFTIINLQY
 78  SSM.PTTSTP GTSTVDVGTS GTPSSSPSPT TAGPLLMPFT LNFTITNLQY
115  GVLCPPPSIL GIFTVQPETF ETPSSLPGPT ATGPVLLPFT LNFTIINLQY
 91  SFVAP.TSTL GTSTVDLGTS GTPSSLPSPT TGVPLLIPFT LNFTITNLQY
 92  SFM.PTTSTL GTSTVDVGTS GTPSSSPSPT TAGPLLMPFT LNFTITNLQY
113  TS.APNTSTP GTSTVDLGTS GTPSSLPSPT SAGPLLVPFT LNFTITNLQY
711  SSVAP.TSTP GTSTVDLGTS GTPSSLPSPT TV.PLLVPFT LNFTITNLQY

     301                                                 350
910  EEDMRHPGSR KFNTMERVLQ GLLRPLFKNT SIGPLYSSCR LTLLRPEKDK
 99  EEDMRRTGSR KFNTMERVLQ GLLKPLFKST SVGPLYSGCR LTLLRPEKRG
112  EENMGHPGSR KFNIMERVLQ GLLRPVFKNT SVGPLYSGCR LTLLRPKKDG
 95  EEDMRRTGSR KFNTMERVLQ GLLKPLFKST SVGPLYSGCR LTLLRPEKHG
 71  EEDMHRPGSR KFNTTERVLQ GLLKPLFKST SVGPLYSGCR LTLLRPEKHG
 78  EEDMRRTGSR KFNTMERVLQ GLLKPLFKST SVGPLYSGCR LTLLRPEKHG
115  EEDMHRPGSR KFNTTERVLQ GLLMPLFKNT SVGPLYSGCR LTLLRPEKQE
 91  EENMGHPGSR KFNIMERVLQ GLLMPLFKNT SVSSLYSGCR LTLLRPEKDG
 92  EEDMRRTGSR KFNTMESVLQ GLLKPLFKNT SVGPLYSGCR LTLLRPKKDG
113  EEDMRRTGSR KFNTMESVLQ GLLKPLFKNT SVGPLYSGCR LTLLRPEKDG
711  GEDMRHPGSR KFNTTERVLQ GLLGPLFKNS SVGPLYSGCR LISLRSEKDG

     351                                                 400
910  AATRVDAICT HHPDPQSPGL NREQLYWELS QLTHGITEL~ ~~~~~~~~~~
 99  AATGVDTICT HRLDPLNPGL DREQLYWELS KLTRGIIELG PYLLDRGSLY
112  AATKVDAICT YRPDPKSPGL DREQLYWELS QLTHSITELG PYTLDRDSLY
 95  AATGVDAICT LRLDPTGPGL DRERLYWELS QLTNSVTELG PYTLDRDSLY
 71  AATGVDAICT LRLDPTGPGL DRERLYWELS QLTNSITELG PYTLDRDSLY
 78  AATGVDAICT LRLDPTGPGL DRERLYWELS QLTNSVTELG PYTLDRDSLY
```

TABLE 5-continued

Amino Acid Sequence for a 1200 bp Repeat in the CA125 Molecule
(SEQ ID NO: 36 thru SEQ ID NO: 46)

```
115  AATGVDTICT HRVDPIGPGL DRERLYWELS QLTNSITELG PYTLDRDSLY
 91  AATRVVAVCT HRPDPKSPGL DRERLYWKLS QLTHGITELG PYTLDRHSLY
 92  AATGVDAICT HRLDPKSPGL NREQLYWELS KLTNDIEELG PYTLDRNSLY
113  AATGVDAICT HRLDPKSPGL NREQLYWELS KL~~~~~~~~ ~~~~~~~~~~
711  AATGVDAICT HHLNPQSPGL DREQLYWQLS QVTNGIKELG PYTLDRNSLY

     401                                                 447

910  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~
 99  VNGFTHRNFV PITSTPGTST VHLGTSEIHP SLPRPI..VP GPL~~~~
112  VNGFTQRSSV PTTSIPGTPT VDLGTSGTPV SKPGPS..AA SP~~~~~
 95  VNGFTHRSSV PTTSIPGTSA VHLETSGTPA SLPGHT..AP GPLL~~~
 71  VNGFNPWSSV PTTSTPGTST VHLATSGTPS SLPGHT..AP VPL~~~~
 78  VNGFTHRSSV PTTSIPGTSA VHLETSGTPA SLPGHT..AP GPLLIPF
115  VNGFNPWSSV PTTSTPGTST VHLATSGTPS SLPGHT..AP VPLLIPF
 91  VNGFTHQSSM TTTRTPDTST MHLATSRTPA SLSGPT..TA SPLLIPF
 92  VNGFTHQSSV STTSTPGTST VDPRTSGTPS SLSSPTIMAA GPLLI~~
113  ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~~~~ ~~~~~~~
711  VNGFTHRSSG LTTSTPWTST VDLGTSGTPS PVPSPT..TA GPLLI~~
```

TABLE 6

Amino Acid Sequence for a 9 Repeat Structure in the CA125 Molecule
(SEQ ID NO: 47)

ERVLQGLLKP LFRNSSLEYL YSGCRLASLR PEKDSSAMAV DAICTHRPDP
EDLGLDRERL YWELSNLTNG IQELGPYTLD RNSLYVNGFT HRSSMPTTST
PGTSTVDVGT SGTPSSSPSP TTAGPLLMPF TLNFTITNLQ YEEDMRRTGS
RKFNTMERVL QGPLSPIFKN SSVGPLYSGC RLTSLRPEKD GAATGM DAV
CLYHPNPKRP GLDREQLYWE LSQLTHNITE LGPYSLDRDS LYVNGFTHQN
SVPTTSTPGT STVYWATTGT PSSFPGHTEP GPLLIPFTLN FTITNLQYEE
NMGHPGSRKF NITERVLQGL LNPIFKNSSV GPLYSGCRLT SLRPEKDGAA
TGMDAVCLYH PNPKRPGLDR EQLYCELSQL THNITELGPY SLDRDSLYVN
GFTHQNSVPT TSTPGTSTVY WATTGTPSSF PGHTEPGPLL IPFTLNFTIT
NLQYEEDMRR TGSRKFNTME RVLQGLLKPL FKSTSVGPLY SGCRLTLLRP
EKHGAATGVD AICTLRLDPT GPGLDRERLY WELSQLTNSV TELGPYTLDR
DSLYVNGFTH RSSVPTTSIP GTSAVHLETS GTPASLPGHT APGPLLVPFT
LNFTITNLQY EEDMRHPGSR KFNTTERVLQ GLLKPLFKST SVGPLYSGCR
LTLLRPEKRG AATGVDTICT HRLDPLNPGL DREQLYWELS KLTRGIIELG
PYLLDRGSLY VNGFTHRNFV PITSTPGTST VHLGTSETPS SLPRPIVPGP
LLIPFTLNFT ITNLQYEENM GHPGSRKFNI TERVLQGLLK PLFRNSSLEY
LYSGCRLASL RPEKDSSAMA VDAICTHRPD PEDLGLDRER LYWELSNLTN
GIQELGPYTL DRNSLYVNGF THRSSMPTTS TPGTSTVDVG TSGTPSSSPS
PTTAGPLLMP FTLNFTITNL QYEEDMRRTG SRKFNTMESV LQGLLKPLFK
NTSVGPLYSG CRLTLLRPKK DGAATGVDAI CTHRLDPKSP GLNREQLYWE
LSKLTNDIEE VGPYTLDRNS LYVNGFTHRS FVAPTSTLGT STVDLGTSGT
PSSLPSPTTG VPLLIPFTLN FTITNLQYEE NMGHPGSRKF NIMERVLQGL
LSPIFKNSSV GSLYSGCRLT LLRPEKDGAA TRVDAVCTHR PDPKSPGLDR
ERLYWKLSQL THGIIELGPY TLDRHSFYVN GFTHQSSMTT TRTPDTSTMH
LATSRTPASL SGPTTASPLL VLFTINFTIT NQRYEENMHH PGSRKFNTTE
RVLQGLLRPV FKNTSVGPLY SGCRLTLLRP KKDGAATKVD AICTYRPDPK
SPGLDREQLY WELSQLTHSI TELGPYTQDR DSLYVNGFTH RSSVPTTSIP
GTSAVHLETS GTPASLP

TABLE 7

cDNA Genbank Accession # AK024365 Encompasses Repeat Sequences (Repeats 1 & 2) Homologous to Two Repeats Shown in Table 6
(SEQ ID NO: 48)

MPLFKNTSVS SLYSGCRLTL LRPEKDGAAT RVDAVCTHRP DPKSPGLDRE
RLYWKLSQLT HGIIELGPYT LDRHSFYVNG FTHQSSMTTT RTPDTSTMHL
ATSRTPASLS GPTTASPLLV LFTINFTITN QRYEENMHHP GSRKFNTTER
VLQGLLRPVF KNTSVGPLYS GCRLTLLRPK KDGAATKVDA ICTYRPDPKS
PGLDREQLYW ELSQLTHSIT ELGPYTQDRD SLYVNGFTHR SSVPTTSIPG
TSAVHLETSG TPASLPGPSA ASPLLVLFTL NFTITNLRYE ENMQHPGSRK
FNTTERVLQG LLRSLFKSTS VGPLYSGCRL TLLRPEKDGT ATGVDAICTH
HPDPKSPRLD REQLYWELSQ LTHNITELGH YALDNDSLFV NGFTHRSSVS
TTSTPGTPTV YLGASKTPAS IFGPSAASHL LILFTLNFTI TNLRYEENMW
PGSRKFNTTE RVLQGLLRPL FKNTSVGPLY SGSRLTLLRP EKDGEATGVD
AICTHRPDPT GPGLDREQLY LELSQLTHSI TELGPYTLDR DSLYVNGFTH
RSSVPTTSTG VVSEEPFTLN FTINNLRYMA DMGQPGSLKF NITDNVMKHL
LSPLFQRSSL GARYTGCRVI ALRSVKNGAE TRVDLLCTYL QPLSGPGLPI
KQVFHELSQQ THGITRLGPY SLDKDSLYLN GYNEPGLDEP PTTPKPATTF
LPPLSEATTA MGYHLKTLTL NFTISNLQYS PDMGKGSATF NSTEGVLQHL
LRPLFQKSSM GPFYLGCQLI SLRPEKDGAA TGVDTTCTYH PDPVGPGLDI
QQLYWELSQL THGVTQLGFY VLDRDSLFIN GYAPQNLSIR GEYQINFHIV
NWNLSNPDPT SSEYITLLRD IQDKVTTLYK GSQLHDTFRF CLVTNLTMDS
VLVTVKALFS SNLDPSLVEQ VFLDKTLNAS FHWLGSTYQL VDIHVTEMES
SVYQPTSSSS TQHFYLNFTI TNLPYSQDKA QPGTTNYQRN KRNIEDALNQ
LFRNSSIKSY FSDCQVSTFR SVPNRHHTGV DSLCNFSPLA RRVDRVAIYE
EFLRMTRNGT QLQNFTLDRS SVLVDGYSPN RNEPLTGNSD LPFWAVILIG
LAGLLGLITC LICGVLVTTR RRKKEGEYNV QQQCPGYYQS HLDLEDLQ

TABLE 8

Complete DNA Sequence for 13 Repeats including the Carboxy Terminus of CA125 (SEQ ID NO: 49)

```
   1  GAGAGGGTTC TGCAGGGTCT GCTCAAACCC TTGTTCAGGA ATAGCAGTCT
  51  GGAATACCTC TATTCAGGCT GCAGACTAGC CTCACTCAGG CCAGAGAAGG
 101  ATAGCTCAGC CATGGCAGTG GATGCCATCT GCACACATCG CCCTGACCCT
 151  GAAGACCTCG GACTGGACAG AGAGCGACTG TACTGGGAGC TGAGCAATCT
 201  GACAAATGGC ATCCAGGAGC TGGGCCCCTA CACCCTGGAC CGGAACAGTC
 251  TCTATGTCAA TGGTTTCACC CATCGAAGCT CTATGCCCAC CACCAGCACT
 301  CCTGGGACCT CCACAGTGGA TGTGGGAACC TCAGGGACTC CATCCTCCAG
 351  CCCCAGCCCC ACGACTGCTG GCCCTCTCCT GATGCCGTTC ACCCTCAACT
 401  TCACCATCAC CAACCTGCAG TACGAGGAGG ACATGCGTCG CACTGGCTCC
 451  AGGAAGTTCA ACACCATGGA GAGGGTTCTG CAGGGTCCGC TTAGTCCCAT
 501  ATTCAAGAAC TCCAGTGTTG GCCCTCTGTA CTCTGGCTGC AGACTGACCT
 551  CTCTCAGGCC CGAGAAGGAT GGGGCAGCAA CTGGAATGGA TGCTGTCTGC
 601  CTCTACCACC CTAATCCCAA AAGACCTGGG CTGGACAGAG AGCAGCTGTA
 651  CTGGGAGCTA AGCCAGCTGA CCCACAACAT CACTGAGCTG GGCCCCTACA
 701  GCCTGGACAG GGACAGTCTC TATGTCAATG GTTTCACCCA TCAGAACTCT
 751  GTGCCCACCA CCAGTACTCC TGGGACCTCC ACAGTGTACT GGGCAACCAC
 801  TGGGACTCCA TCCTCCTTCC CCGGCCACAC AGAGCCTGGC CCTCTCCTGA
 851  TACCATTCAC GCTCAACTTC ACCATCACTA ACCTACAGTA TGAGGAGAAC
 901  ATGGGTCACC CTGGCTCCAG GAAGTTCAAC ATCACGGAGA GGGTTCTGCA
 951  GGGTCTGCTT AATCCCATTT TCAAGAACTC CAGTGTTGGC CCTCTGTACT
1001  CTGGCTGCAG ACTGACCTCT CTCAGGCCCG AGAAGGATGG GGCAGCAACT
1051  GGAATGGATG CTGTCTGCCT CTACCACCCT AATCCCAAAA GACCTGGGCT
1101  GGACAGAGAG CAGCTGTACT GCGAGCTAAG CCAGCTGACC CACAACATCA
1151  CTGAGCTGGG CCCCTACAGC TTGGACAGGG ACAGTCTTTA TGTCAATGGT
```

TABLE 8-continued

Complete DNA Sequence for 13 Repeats including the Carboxy Terminus of CA125 (SEQ ID NO: 49)

1201 TTCACCCATC AGAACTCTGT GCCCACCACC AGTACTCCTG GGACCTCCAC

1251 AGTGTACTGG GCAACCACTG GGACTCCATC CTCCTTCCCC GGCCACACAG

1301 AGCCTGGCCC TCTCCTGATA CCATTCACCC TCAACTTCAC CATCACCAAC

1351 CTGCAGTACG AGGAGGACAT GCGTCGCACT GGCTCCAGGA AGTTCAACAC

1401 CATGGAGAGG GTTCTGCAGG GTCTGCTCAA GCCCTTGTTC AAGAGCACCA

1451 GCGTTGGCCC TCTGTACTCT GGCTGCAGAC TGACCTTGCT CAGACCTGAG

1501 AAACATGGGG CAGCCACTGG AGTGGACGCC ATCTGCACCC TCCGCCTTGA

1551 TCCCACTGGT CCTGGACTGG ACAGAGAGCG GCTATACTGG GAGCTGAGCC

1601 AGCTGACCAA CAGCGTTACA GAGCTGGGCC CCTACACCCT GGACAGGGAC

1651 AGTCTCTATG TCAATGGCTT CACCCATCGG AGCTCTGTGC CAACCACCAG

1701 TATTCCTGGG ACCTCTGCAG TGCACCTGGA AACCTCTGGG ACTCCAGCCT

1751 CCCTCCCTGG CCACACAGCC CCTGGCCCTC TCCTGGTGCC ATTCACCCTC

1801 AACTTCACTA TCACCAACCT GCAGTATGAG GAGGACATGC GTCACCCTGG

1851 TTCCAGGAAG TTCAACACCA CGGAGAGAGT CCTGCAGGGT CTGCTCAAGC

1901 CCTTGTTCAA GAGCACCAGT GTTGGCCCTC TGTACTCTGG CTGCAGACTG

1951 ACCTTGCTCA GGCCTGAAAA ACGTGGGGCA GCCACCGGCG TGGACACCAT

2001 CTGCACTCAC CGCCTTGACC CTCTAAACCC TGGACTGGAC AGAGAGCAGC

2051 TATACTGGGA GCTGAGCAAA CTGACCCGTG GCATCATCGA GCTGGGCCCC

2101 TACCTCCTGG ACAGAGGCAG TCTCTATGTC AATGGTTTCA CCCATCGGAA

2151 CTTTGTGCCC ATCACCAGCA CTCCTGGGAC CTCCACAGTA CACCTAGGAA

2201 CCTCTGAAAC TCCATCCTCC CTACCTAGAC CCATAGTGCC TGGCCCTCTC

2251 CTGATACCAT TCACACTCAA CTTCACCATC ACTAACCTAC AGTATGAGGA

2301 GAACATGGGT CACCCTGGCT CCAGGAAGTT CAACATCACG GAGAGGGTTC

2351 TGCAGGGTCT GCTCAAACCC TTGTTCAGGA ATAGCAGTCT GGAATACCTC

TABLE 8-continued

Complete DNA Sequence for 13 Repeats including the Carboxy Terminus of CA125 (SEQ ID NO: 49)

2401 TATTCAGGCT GCAGACTAAC CTCACTCAGG CCAGAGAAGG ATAGCTCAAC

2451 CATGGCAGTG GATGCCATCT GCACACATCG CCCTGACCCT GAAGACCTCG

2501 GACTGGACAG AGAGCGACTG TACTGGGAGC TGAGCAATCT GACAAATGGC

2551 ATCCAGGAGC TGGGCCCCTA CACCCTGGAC CGGAACAGTC TCTATGTCAA

2601 TGGTTTCACC CATCGAAGCT CTATGCCCAC CACCAGCACT CCTGGGACCT

2651 CCACAGTGGA TGTGGGAACC TCAGGGACTC CATCCTCCAG CCCCAGCCCC

2701 ACGACTGCTG GCCCTCTCCT GATGCCGTTC ACCCTCAACT TCACCATCAC

2751 CAACCTGCAG TACGAGGAGG ACATGCGTCG CACTGGCTCC AGGAAGTTCA

2801 ACACCATGGA GAGTGTCCTG CAGGGTCTGC TCAAGCCCTT GTTCAAGAAC

2851 ACCAGTGTTG GCCCTCTGTA CTCTGGCTGC AGATTGACCT TGCTCAGGCC

2901 CAAGAAAGAT GGGGCAGCCA CTGGAGTGGA TGCCATCTGC ACCCACCGCC

2951 TTGACCCCAA AAGCCCTGGA CTCAACAGGG AGCAGCTGTA CTGGGAGTTA

3001 AGCAAACTGA CCAATGACAT TGAAGAGGTG GGCCCCTACA CCTTGGACAG

3051 GAACAGTCTC TATGTCAATG GTTTCACCCA TCGGAGCTTT GTGGCCCCCA

3101 CCAGCACTCT TGGGACCTCC ACAGTGGACC TTGGGACCTC AGGGACTCCA

3151 TCCTCCCTCC CCAGCCCCAC AACAGGTGTT CCTCTCCTGA TACCATTCAC

3201 ACTCAACTTC ACCATCACTA ACCTACAGTA TGAGGAGAAC ATGGGTCACC

3251 CTGGCTCCAG GAAGTTCAAC ATCATGGAGA GGGTTCTGCA GGGTCTGCTT

3301 ATGCCCTTGT TCAAGAACAC CAGTGTCAGC TCTCTGTACT CTGGTTGCAG

3351 ACTGACCTTG CTCAGGCCTG AGAAGGATGG GGCAGCCACC AGAGTGGTTG

3401 CTGTCTGCAC CCATCGTCCT GACCCCAAAA GCCCTGGACT GGACAGAGAG

3451 CGGCTGTACT GGAAGCTGAG CCAGCTGACC CACGGCATCA CTGAGCTGGG

3501 CCCCTACACC CTGGACAGGC ACAGTCTCTA TGTCAATGGT TTCACCCATC

3551 AGAGCTCTAT GACGACCACC AGAACTCCTG ATACCTCCAC AATGCACCTG

TABLE 8-continued

Complete DNA Sequence for 13 Repeats including the Carboxy Terminus of CA125 (SEQ ID NO: 49)

3601 GCAACCTCGA GAACTCCAGC CTCCCTGTCT GGACCTACGA CCGCCAGCCC

3651 TCTCCTGATA CCATTCACAA TTAACTTCAC CATCACTAAC CTGCGGTATG

3701 AGGAGAACAT GCATCACCCT GGCTCTAGAA AGTTTAACAC CACGGAGAGA

3751 GTCCTTCAGG GTCTGCTCAG GCCTGTGTTC AAGAACACCA GTGTTGGCCC

3801 TCTGTACTCT GGCTGCAGAC TGACCTTGCT CAGGCCCAAG AAGGATGGGG

3851 CAGCCACCAA AGTGGATGCC ATCTGCACCT ACCGCCCTGA TCCCAAAAGC

3901 CCTGGACTGG ACAGAGAGCA GCTATACTGG GAGCTGAGCC AGCTAACCCA

3951 CAGCATCACT GAGCTGGGCC CCTACACCCT GGACAGGGAC AGTCTCTATG

4001 TCAATGGTTT CACACAGCGG AGCTCTGTGC CCACCACTAG CATTCCTGGG

4051 ACCCCCACAG TGGACCTGGG AACATCTGGG ACTCCAGTTT CTAAACCTGG

4101 TCCCTCGGCT GCCAGCCCTC TCCTGGTGCT ATTCACTCTC AACTTCACCA

4151 TCACCAACCT GCGGTATGAG GAGAACATGC AGCACCCTGG CTCCAGGAAG

4201 TTCAACACCA CGGAGAGGGT CCTTCAGGGC CTGCTCAGGT CCCTGTTCAA

4251 GAGCACCAGT GTTGGCCCTC TGTACTCTGG CTGCAGACTG ACTTTGCTCA

4301 GGCCTGAAAA GGATGGGACA GCCACTGGAG TGGATGCCAT CTGCACCCAC

4351 CACCCTGACC CCAAAAGCCC TAGGCTGGAC AGAGAGCAGC TGTATTGGGA

4401 GCTGAGCCAG CTGACCCACA ATATCACTGA GCTGGGCCAC TATGCCCTGG

4451 ACAACGACAG CCTCTTTGTC AATGGTTTCA CTCATCGGAG CTCTGTGTCC

4501 ACCACCAGCA CTCCTGGGAC CCCCACAGTG TATCTGGGAG CATCTAAGAC

4551 TCCAGCCTCG ATATTTGGCC CTTCAGCTGC CAGCCATCTC CTGATACTAT

4601 TCACCCTCAA CTTCACCATC ACTAACCTGC GGTATGAGGA GAACATGTGG

4651 CCTGGCTCCA GGAAGTTCAA CACTACAGAG AGGGTCCTTC AGGGCCTGCT

4701 AAGGCCCTTG TTCAAGAACA CCAGTGTTGG CCCTCTGTAC TCTGGCTCCA

4751 GGCTGACCTT GCTCAGGCCA GAGAAAGATG GGGAAGCCAC CGGAGTGGAT

TABLE 8-continued

Complete DNA Sequence for 13 Repeats including the Carboxy Terminus of CA125 (SEQ ID NO: 49)

4801 GCCATCTGCA CCCACCGCCC TGACCCCACA GGCCCTGGGC TGGACAGAGA

4851 GCAGCTGTAT TTGGAGCTGA GCCAGCTGAC CCACAGCATC ACTGAGCTGG

4901 GCCCCTACAC ACTGGACAGG GACAGTCTCT ATGTCAATGG TTTCACCCAT

4951 CGGAGCTCTG TACCCACCAC CAGCACCGGG GTGGTCAGCG AGGAGCCATT

5001 CACACTGAAC TTCACCATCA ACAACCTGCG CTACATGGCG GACATGGGCC

5051 AACCCGGCTC CCTCAAGTTC AACATCACAG ACAACGTCAT GAAGCACCTG

5101 CTCAGTCCTT TGTTCCAGAG GAGCAGCCTG GGTGCACGGT ACACAGGCTG

5151 CAGGGTCATC GCACTAAGGT CTGTGAAGAA CGGTGCTGAG ACACGGGTGG

5201 ACCTCCTCTG CACCTACCTG CAGCCCCTCA GCGGCCCAGG TCTGCCTATC

5251 AAGCAGGTGT TCCATGAGCT GAGCCAGCAG ACCCATGGCA TCACCCGGCT

5301 GGGCCCCTAC TCTCTGGACA AAGACAGCCT CTACCTTAAC GGTTACAATG

5351 AACCTGGTCT AGATGAGCCT CCTACAACTC CCAAGCCAGC CACCACATTC

5401 CTGCCTCCTC TGTCAGAAGC CACAACAGCC ATGGGGTACC ACCTGAAGAC

5451 CCTCACACTC AACTTCACCA TCTCCAATCT CCAGTATTCA CCAGATATGG

5501 GCAAGGGCTC AGCTACATTC AACTCCACCG AGGGGGTCCT TCAGCACCTG

5551 CTCAGACCCT TGTTCCAGAA GAGCAGCATG GGCCCCTTCT ACTTGGGTTG

5601 CCAACTGATC TCCCTCAGGC CTGAGAAGGA TGGGGCAGCC ACTGGTGTGG

5651 ACACCACCTG CACCTACCAC CCTGACCCTG TGGGCCCCGG GCTGGACATA

5701 CAGCAGCTTT ACTGGGAGCT GAGTCAGCTG ACCCATGGTG TCACCCAACT

5751 GGGCTTCTAT GTCCTGGACA GGGATAGCCT CTTCATCAAT GGCTATGCAC

5801 CCCAGAATTT ATCAATCCGG GGCGAGTACC AGATAAATTT CCACATTGTC

5851 AACTGGAACC TCAGTAATCC AGACCCCACA TCCTCAGAGT ACATCACCCT

5901 GCTGAGGGAC ATCCAGGACA AGGTCACCAC ACTCTACAAA GGCAGTCAAC

5951 TACATGACAC ATTCCGCTTC TGCCTGGTCA CCAACTTGAC GATGGACTCC

TABLE 8-continued

Complete DNA Sequence for 13 Repeats including the Carboxy Terminus of CA125 (SEQ ID NO: 49)

6001 GTGTTGGTCA CTGTCAAGGC ATTGTTCTCC TCCAATTTGG ACCCCAGCCT

6051 GGTGGAGCAA GTCTTTCTAG ATAAGACCCT GAATGCCTCA TTCCATTGGC

6101 TGGGCTCCAC CTACCAGTTG GTGGACATCC ATGTGACAGA AATGGAGTCA

6151 TCAGTTTATC AACCAACAAG CAGCTCCAGC ACCCAGCACT TCTACCCGAA

6201 TTTCACCATC ACCAACCTAC CATATTCCCA GGACAAAGCC CAGCCAGGCA

6251 CCACCAATTA CCAGAGGAAC AAAAGGAATA TTGAGGATGC GCTCAACCAA

6301 CTCTTCCGAA ACAGCAGCAT CAAGAGTTAT TTTTCTGACT GTCAAGTTTC

6351 AACATTCAGG TCTGTCCCCA ACAGGCACCA CACCGGGGTG GACTCCCTGT

6401 GTAACTTCTC GCCACTGGCT CGGAGAGTAG ACAGAGTTGC CATCTATGAG

6451 GAATTTCTGC GGATGACCCG GAATGGTACC CAGCTGCAGA ACTTCACCCT

6501 GGACAGGAGC AGTGTCCTTG TGGATGGGTA TTCTCCCAAC AGAAATGAGC

6551 CCTTAACTGG GAATTCTGAC CTTCCCTTCT GGGCTGTCAT CTTCATCGGC

6601 TTGGCAGGAC TCCTGGGACT CATCACATGC CTGATCTGCG GTGTCCTGGT

6651 GACCACCCGC CGGCGGAAGA AGGAAGGAGA ATACAACGTC CAGCAACAGT

6701 GCCCAGGCTA CTACCAGTCA CACCTAGACC TGGAGGATCT GCAATGACTG

6751 GAACTTGCCG GTGCCTGGGG TGCCTTTCCC CCAGCCAGGG TCCAAAGAAG

6801 CTTGGCTGGG GCAGAAATAA ACCATATTGG TCG

TABLE 9

Complete Amino Acid Sequence for 13 Repeats Contiguous with the Carboxy Terminus of CA125 (SEQ ID NO: 50)

1
ERVLQGLLKP LFRNSSLEYL YSGCRLASLR PEKDSSAMAV DAICTHRPDP

EDLGLDRERL YWELSNLTNG IQELGPYTLD RNSLYVNGFT HRSSMPTTST

PGTSTVDVGT SGTPSSSPSP TTAGPLLMPF TLNFTITNLQ YEEDMRRTGS

2
RKFNTMERVL QGPLSPIFKN SSVGPLYSGC RLTSLRPEKD GAATGMDAVC

LYHPNPKRPG LDREQLYWEL SQLTHNITEL GPYSLDRDSL YVNGFTHQNS

VPTTSTPGTS TVYWATTGTP SSFPGHTEPG PLLIPFTLNF TITNLQYEEN

3
MGHPGSRKFN ITERVLQGLL NPIFKNSSVG PLYSGCRLTS LRPEKDGAAT

GMDAVCLYHP NPKRPGLDRE QLYCELSQLT HNITELGPYS LDRDSLYVNG

FTHQNSVPTT STPGTSTVYW ATTGTPSSFP GHTEPGPLLI PFTLNFTITN

4
LQYEEDMRRT GSRKFNTMER VLQGLLKPLF KSTSVGPLYS GCRLTLLRPE

KHGAATGVDA ICTLRLDPTG PGLDRERLYW ELSQLTNSVT ELGPYTLDRD

SLYVNGFTHR SSVPTTSIPG TSAVHLETSG TPASLPGHTA PGPLLVPFTL

NFTITNLQYE EDMRHPGSRK FNTTERVLQG LLKPLFKSTS VGPLYSGCRL

5
TLLRPEKRGA ATGVDTICTH RLDPLNPGLD REQLYWELSK LTRGIIELGP

YLLDRGSLYV NGFTHRNFVP ITSTPGTSTV HLGTSETPSS LPRPIVPGPL

LIPFTLNFTI TNLQYEENMG HPGSRKFNIT ERVLQGLLKP LFRNSSLEYL

6
YSGCRLASLR PEKDSSAMAV DAICTHRPDP EDLGLDRERL YWELSNLTNG

IQELGPYTLD RNSLYVNGFT HRSSMPTTST PGTSTVDVGT SGTPSSSPSP

TTAGPLLMPF TLNFTITNLQ YEEDMRRTGS RKFNTMESVL QGLLKPLFKN

7
TSVGPLYSGC RLTLLRPKKD GAATGVDAIC THRLDPKSPG LNREQLYWEL

SKLTNDIEEV GPYTLDRNSL YVNGFTHRSF VAPTSTLGTS TVDLGTSGTP

SSLPSPTTGV PLLIPFTLNF TITNLQYEEN MGHPGSRKFN IMERVLQGLL

8
SPIFKNSSVG SLYSGCRLTL LRPEKDGAAT RVDAVCTHRP DPKSPGLDRE

RLYWKLSQLT HGIIELGPYT LDRHSFYVNG FTHQSSMTTT RTPDTSTMHL

ATSRTPASLS GPTTASPLLV LFTINFTITN QRYEENMHHP GSRKFNTTER

TABLE 9-continued

Complete Amino Acid Sequence for 13 Repeats Contiguous with the Carboxy Terminus of CA125 (SEQ ID NO: 50)

9

VLQGLLRPVF KNTSVGPLYS GCRLTLLRPK KDGAATKVDA ICTYRPDPKS

PGLDREQLYW ELSQLTHSIT ELGPYTQDRD SLYVNGFTHR SSVPTTSIPG

TSAVHLETSG TPASLPGPSA ASPLLVLFTL NFTITNLRYE ENMQHPGSRK

10

FNTTERVLQG LLRSLFKSTS VGPLYSGCRL TLLRPEKDGT ATGVDAICTH

HPDPKSPRLD REQLYWELSQ LTHNITELGH YALDNDSLFV NGFTHRSSVS

TTSTPGTPTV YLGASKTPAS IFGPSAASHL LILFTLNFTI TNLRYEENMW

11

PGSRKFNTTE RVLQGLLRPL FKNTSVGPLY SGSRLTLLRP EKDGEATGVD

AICTHRPDPT GPGLDREQLY LELSQLTHSI TELGPYTLDR DSLYVNGFTH

RSSVPTTSTG VVSEEPFTLN FTINNLRYMA DMGQPGSLKF NITDNVMKHL

12

LSPLFQRSSL GARYTGCRVI ALRSVKNGAE TRVDLLCTYL QPLSGPGLPI

KQVFHELSQQ THGITRLGPY SLDKDSLYLN GYNEPGLDEP PTTPKPATTF

LPPLSEATTA MGYHLKTLTL NFTISNLQYS PDMGKGSATF NSTEGVLQHL

13

LRPLFQKSSM GPFYLGCQLI SLRPEKDGAA TGVDTTCTYH PDPVGPGLDI

QQLYWELSQL THGVTQLGFY VLDRDSLFIN GYAPQNLSIR GEYQINFHIV

NWNLSNPDPT SSEYITLLRD IQDKVTTLYK GSQLHDTFRF CLVTNLTMDS

VLVTVKALFS SNLDPSLVEQ VFLDKTLNAS FHWLGSTYQL VDIHVTEMES

SVYQPTSSSS TQHFYLNFTI TNLPYSQDKA QPGTTNYQRN KRNIEDALNQ

LFRNSSIKSY FSDCQVSTFR SVPNRHHTGV DSLCNFSPLA RRVDRVAIYE

EFLRMTRNGT QLQNFTLDRS SVLVDGYSPN RNEPLTGNSD LPFWAVILIG

LAGLLGLITC LICGVLVTTR RRKKEGEYNV QQQCPGYYQS HLDLEDLQ

TABLE 10A

5′ Primer Sequence for End of the Open Reading Frame for Contig #32 of Chromosome 19 Cosmid AC008734 (SEQ ID NO: 51), Primer Sequence from within the Repeat Region (SEQ ID NO: 52, 3 Primer Sets Synthesized to Piece Together Entire Open Reading Frame in Contig #32 (SEQ ID NOS: 53 thru 58), Primers to Cosmid No. AC008734 for Contig #32 (SEQ ID NOS: 59 and 60), Sense Primer Sequence (supplied by Ambion) (SEQ ID NO: 61), Anti-Sense Primer Sequence for CA125 (SEQ ID NO: 62), and 5′Sense Primer Sequence (from Ambion) (SEQ ID NO: 63) and Anti-Sense Primer Specific to CA125 (SEQ ID NO: 64)

(SEQ ID NO: 51) (5'-CAGCAGAGACCAGCACGAGTACTC-3')

(SEQ ID NO: 52) (5'-TCCACTGCCATGGCTGAGCT-3')

Primer Sets

(SEQ ID NO: 53) (Set 1) 5'-CCAGCACAGCTCTTCCCAGGAC-3'
(SEQ ID NO: 54) 5'-GGAATGGCTGAGCTGACGTCTG-3')

(SEQ ID NO: 55) (Set 2) 5'-CTTCCCAGGACAACCTCAAGG-3'
(SEQ ID NO: 56 5'-GCAGGATGAGTGAGCCACGTG-3'

(SEQ ID NO: 57) (Set 3) 5'-GTCAGATCTGGTGACCTCACTG-3'
(SEQ ID NO: 58) 5'-GAGGCACTGGAAAGCCCAGAG-3'

(SEQ ID NO: 59) 5'-CTGATGGCATTATGGAACACATCAC-3'
(SEQ ID NO: 60) 5'-CCCAGAACGAGAGACCAGTGAG-3'

(SEQ ID NO: 61) 5'-GCTGATGGCGATGAATGAACACTG-3'

(SEQ ID NO: 62) 5'-CCCAGAACGAGAGACCAGTGAG-3'

(SEQ ID NO: 63) 5'-CGCGGATCCGAACACTGCGTTTGCTGGCTTTGATG-3'
(SEQ ID NO: 64) 5'-CCTCTGTGTGCTGCTTCATTGGG-3'

TABLE 10B

Sense and Anti-Sense Primers Used to Order the CA125 Carboxy Terminal Domain
(SEQ. ID NO: 303 and SEQ ID NO: 304, respectively)

(SEQ ID NO: 303) 5'-GGACAAGGTCACCACACTCTAC-3'
(SEQ ID NO: 304) 5'-GCAGATCCTCCAGGTCTAGGTGTG-3'

TABLE 10C

Sense and Anti-Sense Primers Used to Amplify Overlapping Sequences
in the Repeat Domain
(SEQ ID NO: 305 and SEQ ID NO: 306, respectively)

(SEQ ID NO: 305) 5' GTC TCT ATG TCA ATG GTT TCA CCC-3'
(SEQ ID NO: 306) 5'-TAG CTG CTC TCT GTC CAG TCC-3'

TABLE 11

5' Sense Primer 1 Sequence and 3' Antisense Primer 2 (SEQ ID NO: 65 and SEQ ID NO: 66, respectively), and Nucleotide and Amino Acid Sequences of the CA125 Repeat Expressed in *E. coli* (SEQ ID NO: 67 and SEQ ID NO: 68, respectively)

(SEQ ID NO: 65) 5'-ACCGGATCCATGGGCCACACAGAGCCTGGCCC-3'

(SEQ ID NO: 66) 5'-TGTAAGCTTAGGCAGGGAGGATGGAGTCC -3'

(SEQ ID NO: 67)

```
   1  ATGAGAGGAT CGCATCACCA TCACCATCAC GGATCCATGG GCCACACAGA
                                                        ↑
  51  GCCTGGCCCT CTCCTGATAC CATTCACTTT CAACTTTACC ATCACCAACC
 101  TGCATTATGA GGAAAACATG CAACACCCTG GTTCCAGGAA GTTCAACACC
 151  ACGGAGAGGG TTCTGCAGGG TCTGCTCAAG CCCTTGTTCA AGAACACCAG
 201  TGTTGGCCCT CTGTACTCTG GCTGCAGACT GACCTTGCTC AGACCTGAGA
 251  AGCATGAGGC AGCCACTGGA GTGGACACCA TCTGTACCCA CCGCGTTGAT
 301  CCCATCGGAC CTGGACTGGA CAGAGAGCGG CTATACTGGG AGCTGAGCCA
 351  GCTGACCAAC AGCATCACAG AGCTGGGACC CTACACCCTG GACAGGGACA
 401  GTCTCTATGT CAATGGCTTC AACCCTCGGA GCTCTGTGCC AACCACCAGC
 451  ACTCCTGGGA CCTCCACAGT GCACCTGGCA ACCTCTGGGA CTCCATCCTC
 501  CCTGCCT
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(SEQ ID NO: 68)

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M R G S H H H H H H G S M G H T E P G P L L I P F T F N F T I T N L
H Y E E N M Q H P G S R K F N T T E R V L Q G L L K P L F K N T S V
G P L Y S G C R L T L L R P E K H E A A T G V D T I C T H R V D P I
G P G L D R E R L Y W E L S Q L T N S I T E L G P Y T L D R D S L Y
V N G F N P R S S V P T T S T P G T S T V H L A T S G T P S S L P
```

TABLE 12

Additional Multiple Repeat Amino Acid Sequences
(SEQ ID NO: 69 thru SEQ ID NO: 80)

(SEQ ID NO: 69)

ERVLQGLLGP MFKNTSVGLL YSGCRLTLLR PKKDGAATKV DAICTYRPDP
KSPGLDREQL YWELSQLTHS ITELGPYTLD RDSLYVNGFT QRSSVPTTSI
PGTPTVDLGT SGTPVSKPGP SAASPLLIPF TINFTITNLR YEENMGHPGS
RKFNIMERVL QGLLKPLFKN TSVGPLYSGC RLTLLRPKKD GAATGVDAIC
THRLDPKSPG LNREQLYWEL SKLTNDIEEL GPYTLDRNSL YVNGFTHQSS
VSTTSTPGTS TVDLRTSGTP SSLSSPTIMA AGPLLIPFTI NFTITNLRYE
ENMHHPGSRK FNTMERVLQG LLMPLFKNTS VSSLYSGCRL TLLRPEKDGA
ATRVDAVCTH RPDPKSPGLD RERLYWKLSQ LTHGITELGP YTLDRNSLYV
NGFTHRSSMP TTSTPGTSTV DVGTSGTPSS SPSPTTAGPL LMPFTLNFTI
TNLQYEEDMR RTGSRKFNTM ERVLQGLLKP LFKSTSVGPL YSGCRLTLLR
PEKHGAATGV DAICTLRLDP TGPGLDRERL YWELSQLTNS VTELGPYTLD
RDSLYVNGFT HRSSVPTTSI PGTSAVHLET SGTPASLPGH TAPGPLLIPF
TLNFTITNLH YEENMQHPGS RKFNTMERVL QGCLVPCSRN TNVGLLYSGC
RLTLLRXEKX XAATXVDXXC XXXXDPXXPG LDREXLYWEL SXLTXXIXEL
GPYTLDRNSL YVNGFTHRSS VAPTSTPGTS TVDLGTSGTP SSLPSPTTVP
LLVPFTLNFT ITNLQYGEDM RHPGSRKFNT TERVLQGLLG PLFKNSSVGP
LYSGCRLISL RSEKDGAATG VDAICTHHLN PQSPGLDREQ LYWQLSQVTN
GIKELGPYTL DRNSLYVNGF THRSSGLTTS TPWTSTVDLG TSGTPSPVPS
PTTAGPLLI

TABLE 12-continued

Additional Multiple Repeat Amino Acid Sequences
(SEQ ID NO: 69 through SEQ ID NO: 80)

(SEQ ID NO: 70)

QGLLGPMFKN TSVGLLYSGC RLTLLRPEKR GAATGVDTIC THRLDPLNPG
LDREQLYWEL SKLTRGIIEL GPYLLDRGSL YVNGFTHRNF VPITSTPGTS
TVHLGTSETP SSLPRPIVPG PLLVPFTLNF TITNLQYEEA MRHPGSRKFN
TTERVLQGLL RPLFKNTSVS SLYSGCRLTL LRPEKDGAAT RVDAACTYRP
DPKSPGLDRE QLYWELSQLT HSITELGPYT LDRVSLYVNG FNPRSSVPTT
STPGTSTVHL ATSGTPSSLP GHTAPVPLLI PFTLNFTITN LQYEEDMRHP
GSRKFNTMER VLQGLLRPLF KNTSIGPLYS SCRLTLLRPE KDKAATRVDA
ICTHHPDPQS PGLNREQLYW ELSQLTHGIT ELGPYTLDRD SLYVDGFTHW
SPIPTTSTPG TSIVNLGTSG IPPSLPETTA TGPLLIPFTP NFTITNLQYE
EDMRRTGSRK FNTMERVLQG LLSPIFKNSS VGPLYSGCRL TSLRPEKDGA
ATGMDAVCLY HPNPKRPGLD REQLY

(SEQ ID NO:71)

ERVLQGLLKP LFKSTSVGPL YSGCRLTLLR PEKDGVATRV DAICTHRPDP
KIPGLDRQQL YWELSQLTHS ITELGPYTLD RDSLYVNGFT QRSSVPTTST
PGTFTVQPET SETPSSLPGP TATGPVLLPF TLNFTIINLQ YEEDMHRPGS
RKFNTTERVL QGLLMPLFKN TSVGPLYSGC RLTLLRPEKQ EAATGVDTIC
THRLDPSEPG LDREQLYWEL SQLTNSITEL GPYTLDRDSL YVNGFTHSGV
LCPPPSILGI FTVQPETFET PSSLPGPTAT GPVLLPFTLN FTIINLQYEE
DMHRPGSRKF NTTERVLQGL LTPLFKNTSV GPLYSGCRLT LLRPEKQEAA
TGVDTICTHR VDPIGPGLDR ERLYWELSQL TNSITELGPY TLDRDSLYVN
GFNPWSSVPT TSTPGTSTVH LATSGTPSSL PGHTAPVPLL IPFTLNFTIT

TABLE 12-continued

Additional Multiple Repeat Amino Acid Sequences
(SEQ ID NO: 69 through SEQ ID NO: 80)

NLHYEENMQH PGSRKFNTTE RVLQGLLKPL FKSTSVGPLY SGCRLTLLRP

EKHGAATGVD AICTHRLDPK SPGVDREQLY WELSQLTNGI KELGPYTLDR

NSLYVNGFTH WIPVPTSSTP GTSTVDLGSG TPSSLPSPTT AGPL

(SEQ ID NO: 72)

TSVGPLYSGC RLTLLRSEKD GAATGVDAIY THRLDPKSPG VDREQLYWEL

SQLTNGIKEL GPYTLDRNSL YVNGFTHQTS APNTSTPGTS TVDLGTSGTP

SSLPSPTSAG PLLIPFTINF TITNLRYEEN MHHPGSRKFN TMERVLQGLL

KPLFKSTSVG PLYSGCRLTL LRPEKDGVAT RVDAICTHRP DPKIPGLDRQ

QLYWELSQLT HSITELGPYT LDRDSLYVNG FTQRSSVPTT STPGTFTVQP

ETSETPSSLP GPTATGPVLL PFTLNFTIIN LQYEEDMHRP GSRKFNTTER

VLQGLLKPLF KSTSVGPLYS GCRLTLLRPE KHGAATGVDA ICTLRLDPTG

PGLDRERLYW ELSQLTNSIT ELGPYTLDRD SLYVNGFNPW SSVPTTSTPG

TSTVHLATSG TPSSLPGHTA PVPL

(SEQ ID NO:73)

ERVLQGLLKP LFKSTSVGPL YSGCRLTLLR PEKRGAATGV DTICTHRLDP

LNPGLDREQL YWELSKLTRG IIELGPYLLD RDSLYVNGFT HRSSVPTTSI

PGTSAVHLET SGTPASLPGH TAPGPLLVPF TLNFTITNLQ YEEDMRHPGS

RKFNTTERVL QGLLKPLFKS TSVGPLYSGC RLTLLRPEKR GAATGVDTIC

THRLDPLNPG LDREQLYWEL SKLTRGIIEL GPYLLDRGSL YVNGFTHRNF

VPITSTPGTS TVHLGTSETP SSLPRPIVPG PLLIPF

TABLE 12-continued

Additional Multiple Repeat Amino Acid Sequences
(SEQ ID NO: 69 through SEQ ID NO: 80)

(SEQ ID NO: 74)

ERVLQGLLRP VFKNTSVGPL YSGCRLTLLR PKKDGAATKV DAICTYRPDP

KSPGLDREQL YWELSQLTHS ITELGPYTLD RDSLYVNGFT QRSSVPTTSI

PGTPTVDLGT SGTPVSKPGP SAASPLLVPF TLNFTITNLQ YEEDMHRPGS

RKFNATERVL QGLLSPIFKN SSVGPLYSGC RLTSLRPEKD GAATGMDAVC

LYHPNPKRPG LDREQLYWEL SQLTHNITEL GPYSLDRDSL YVNGFTHQSS

MTTTRTPDTS TMHLATSRTP ASLSGPTTAS PLLIPF

(SEQ ID NO: 75)

ERVLQGLLKP LFKSTSVGPL YSGCRLTLLR PEKRGAATGV DTICTHRLDP

LNPGLDREQL YWELSKLTRG IIELGPYLLD RGSLYVNGFS RQSSMTTTRT

PDTSTMHLAT SRTPASLSGP TTASPLLIPF TLNFTITNLQ YEENMGHPGS

RKFNIMERVL QGLLNPIFKN SSVGPLYSGC RLTSLKPEKD GAATGMDAVC

LYHPNPKRPG LDREQLYWEL SQLTHGIKEL GPYTLDRNSL YVNGFTHRSS

VAPTSTPGTS TVDLGTSGTP SSLPSPTTAV PLLIPF

(SEQ ID NO: 76)

ERVLQGLLKP LFRNSSLEYL YSGCRLASLR PEKDSSAMAV DAICTHRPDP

EDLGLDRERL YWELSNLTNG IQELGPYTLD RNSLYVNGFT HRSSGLTTST

PWTSTVDLGT SGTPSPVPSP TTAGPLLIPF TLNFTITNLQ YEENMGHPGS

RKFNIMERVL QGLLMPLFKN TSVSSLYSGC RLTLLRPEKD GAATRVDAVC

TQRPDPKSPG LDRERLYWKL SQLTHGITEL GPYTLDRHSL YVNGLTHQSS

MTTTRTPDTS TMHLATSRTP ASLSGPTTAS PLLIPF

TABLE 12-continued

Additional Multiple Repeat Amino Acid Sequences
(SEQ ID NO: 69 through SEQ ID NO: 80)

(SEQ ID NO: 77)

ERVLQGLLSP ISKNSSVGPL YSGCRLTSLR PEKDGAATGM DAVCLYHPNP

KRPGLDREQL YWELSQLTHN ITELGPYSLD RDSLYVNGFT HQNSVPTTST

PGTSTVYWAT TGTPSSFPGH TEPGPLLIPF TVNFTITNLR YEENMHHPGS

RKFNTTERVL QGLLRPVFKN TSVGPLYSGC RLTLLRPKKD GAATKVDAIC

TYRPDPKSPG LDREQLYWEL SKLTNDIEEL GPYTLDRNSL YVNGFTHQSS

VSTTSTPGTS TVDLRTSGTP SSLSSPTIMA AGPLLIPF

(SEQ ID NO: 78)

ERVLHGLLTP LFKNTRVGPL YSGCRLTLLR PEKQEAATGV DTICTHRVDP

IGPGLDRERL YWELSQLTNS ITELGPYTLD RDSLYVNGFN PWSSVPTTST

PGTSTVHLAT SGTPSSLPGH TAPVPLLIPF TLNFTITNLH YEENMQHPGS

RKFNTTERVL QGLLKPLFKN TSVGPLYSGC RLTLFKPEKH EAATGVDAIC

TLRLDPTGPG LDRQLYWELS QLTNSVTELG PYTLDRDSLY VNGFTHRSSV

PTTSIPGTSA VHLETSGTPA SLPGHTAPGP LLIPFTLNFT ITNLQYEEDM

RRTGSRKFNT MERVLQGLLK PLFKSTSVGP LYSGCRLTLL RPEKRGAATG

VDTICTHRLD PLNPGLDREQ LYWELSKLTR GIIELGPYLL DRGSLYVNGF

THRNFVPITS TPGTSTVHLG TSETPSSLPR PIVPGPLLIP FTINFTITNL

RYEENMHHPG SRKFNIMERV LQGLLGPLFK NSSVGPLYSG CRLISLRSEK

DGAATGVDAI CTHHLNPQSP GLDREQLYWQ LSQMTNGIKE LGPYTLDRNS

LYVNGFTHRS SGLTTSTPWT STVDLGTSGT PSPVPSPTTA GPLLIPF

TABLE 12-continued

Additional Multiple Repeat Amino Acid Sequences
(SEQ ID NO: 69 through SEQ ID NO: 80)

(SEQ ID NO: 79)

GPLYSGCRLT SLRPEKDGAA TGMDAVCLYH PNPKRPGLDR EQLYWELSQL
THNITELGPY SLDRDSLYVN GFTHQNSVPT TSTPGTSTVY WATTGTPSSF
PGHTEPGPLL IPFTLNFTIT NLQYEENMGH PGSRKFNITE SVLQGLLTPL
FKNSSVGPLY SGCRLISLRS EKDGAATGVD AICTHHLNPQ SPGLDREQLY
WQLSQMTNGI KELGPYTLDR DSLYVNGFTH RSLGLTTSTP WTSTVDLGTS
GTPSPVPSPT TAGPLLIPFT LNFTITNLQY EENMGHPGSR KFNIMERVLQ
GLLRPVFKNT SVGPLYSGCR LTLLRPKKDG AATKVDAICT YRPDPKSPGL
DREQLYWELS QLTHSITELG PYTLDRDSLY VNGFTQRSSV PTTSIPGTPT
VDLGTSGTPV SKPGPSAASP

(SEQ ID NO: 80)

QLYWELSKLT NDIEELGPYT LDRNSLYVNG FTHQSSVSTT STPGTSTVDL
RTSGTPSSLS SPTIMAAGPL LIPFTLNFTI TNLQYEENMG HPGSRKFNIM
ERVLQGLLGP MFKNTSVGLL YSGCRLTLLR PEKNGAATGM DAICSHRLDP
KSPGLNREQL YWELSQLTHG IKELGPYTLD RNSLYVNGFT HRSSVAPTST
PGTSTVDLGT SGTPSSLPSP TTAVPLLIPF TLNFTITNLK YEEDMHCPGS
RKFNTTERVL QSLFGPMFKN TSVGPLYSGC RLTLLRSEKD GAATGVDAIC
THRLDPKSLG VDREQLYWEL SQLTNGIKEL GPYTLDRNSL YVNGFTHQTS
APNTSTPGTS TVDLGTSGTP SSLPSPTSAG PLLVPFTLNF TITNLQYEED
MRRTGSRKFN TMESVLQGLL KPLFKNTSVG PLYSGCRLTL LRPEKDGAAT
GVDAICTHRL DPKSPGLNRE QLYWELSKL

TABLE 13

Amino Terminal Nucleotide Sequence
(SEQ ID NO: 81)

```
   1  CAGAGAGCGT TGAGCTGGGA ACAGTGACAA GTGCTTATCA AGTTCCTTCA
  51  CTCTCAACAC GGTTGACAAG AACTGATGGC ATTATGGAAC ACATCACAAA
 101  AATACCCAAT GAAGCAGCAC ACAGAGGTAC CATAAGACCA GTCAAAGGCC
 151  CTCAGACATC CACTTCGCCT GCCAGTCCTA AAGGACTACA CACAGGAGGG
 201  ACAAAAAGAA TGGAGACCAC CACCACAGCT TTGAAGACCA CCACCACAGC
 251  TTTGAAGACC ACTTCCAGAG CCACCTTGAC CACCAGTGTC TATACTCCCA
 301  CTTTGGGAAC ACTGACTCCC CTCAATGCAT CAAGGCAAAT GGCCAGCACA
 351  ATCCTCACAG AAATGATGAT CACAACCCCA TATGTTTTCC CTGATGTTCC
 401  AGAAACGACA TCCTCATTGG CTACCAGCCT GGGAGCAGAA ACCAGCACAG
 451  CTCTTCCCAG GACAACCCCA TCTGTTCTCA ATAGAGAATC AGAGACCACA
 501  GCCTCACTGG TCTCTCGTTC TGGGGCAGAG AGAAGTCCGG TTATTCAAAC
 551  TCTAGATGTT TCTTCTAGTG AGCCAGATAC AACAGCTTCA TGGGTTATCC
 601  ATCCTGCAGA GACCATCCCA ACTGTTTCCA AGACAACCCC CAATTTTTTC
 651  CACAGTGAAT TAGACACTGT ATCTTCCACA GCCACCAGTC ATGGGGCAGA
 701  CGTCAGCTCA GCCATTCCAA CAAATATCTC ACCTAGTGAA CTAGATGCAC
 751  TGACCCCACT GGTCACTATT TCGGGGACAG ATACTAGTAC AACATTCCCA
 801  ACACTGACTA AGTCCCCACA TGAAACAGAG ACAAGAACCA CATGGCTCAC
 851  TCATCCTGCA GAGACCAGCT CAACTATTCC CAGAACAATC CCCAATTTTT
 901  CTCATCATGA ATCAGATGCC ACACCTTCAA TAGCCACCAG TCCTGGGGCA
 951  GAAACCAGTT CAGCTATTCC AATTATGACT GTCTCACCTG GTGCAGAAGA
```

TABLE 13-continued

Amino Terminal Nucleotide Sequence
(SEQ ID NO: 81)

1001 TCTGGTGACC TCACAGGTCA CTAGTTCTGG GACAGACAGA AATATGACTA

1051 TTCCAACTTT GACTCTTTCT CCTGGTGAAC CAAAGACGAT AGCCTCATTA

1101 GTCACCCATC CTGAAGCACA GACAAGTTCG GCCATTCCAA CTTCAACTAT

1151 CTCGCCTGCT GTATCACGGT TGGTGACCTC AATGGTCACC AGTTTGGCGG

1201 CAAAGACAAG TACAACTAAT CGAGCTCTGA CAAACTCCCC TGGTGAACCA

1251 GCTACAACAG TTTCATTGGT CACGCATCCT GCACAGACCA GCCCAACAGT

1301 TCCCTGGACA ACTTCCATTT TTTTCCATAG TAAATCAGAC ACCACACCTT

1351 CAATGACCAC CAGTCATGGG GCAGAATCCA GTTCAGCTGT TCCAACTCCA

1401 ACTGTTTCAA CTGAGGTACC AGGAGTAGTG ACCCCTTTGG TCACCAGTTC

1451 TAGGGCAGTG ATCAGTACAA CTATTCCAAT TCTGACTCTT TCTCCTGGTG

1501 AACCAGAGAC CACACCTTCA ATGGCCACCA GTCATGGGGA AGAAGCCAGT

1551 TCTGCTATTC CAACTCCAAC TGTTTCACCT GGGGTACCAG GAGTGGTGAC

1601 CTCTCTGGTC ACTAGTTCTA GGGCAGTGAC TAGTACAACT ATTCCAATTC

1651 TGACTTTTTC TCTTGGTGAA CCAGAGACCA CACCTTCAAT GGCCACCAGT

1701 CATGGGACAG AAGCTGGCTC AGCTGTTCCA ACTGTTTTAC CTGAGGTACC

1751 AGGAATGGTG ACCTCTCTGG TTGCTAGTTC TAGGGCAGTA ACCAGTACAA

1801 CTCTTCCAAC TCTGACTCTT TCTCCTGGTG AACCAGAGAC CACACCTTCA

1851 ATGGCCACCA GTCATGGGGC AGAAGCCAGC TCAACTGTTC CAACTGTTTC

1901 ACCTGAGGTA CCAGGAGTGG TGACCTCTCT GGTCACTAGT TCTAGTGGAG

1951 TAAACAGTAC AAGTATTCCA ACTCTGATTC TTTCTCCTGG TGAACTAGAA

TABLE 13-continued

Amino Terminal Nucleotide Sequence (SEQ ID NO: 81)	
2001	ACCACACCTT CAATGGCCAC CAGTCATGGG GCAGAAGCCA GCTCAGCTGT
2051	TCCAACTCCA ACTGTTTCAC CTGGGGTATC AGGAGTGGTG ACCCCTCTGG
2101	TCACTAGTTC CAGGGCAGTG ACCAGTACAA CTATTCCAAT TCTAACTCTT
2151	TCTTCTAGTG AGCCAGAGAC CACACCTTCA ATGGCCACCA GTCATGGGGT
2201	AGAAGCCAGC TCAGCTGTTC TAACTGTTTC ACCTGAGGTA CCAGGAATGG
2251	TGACCTCTCT GGTCACTAGT TCTAGAGCAG TAACCAGTAC AACTATTCCA
2301	ACTCTGACTA TTTCTTCTGA TGAACCAGAG ACCACAACTT CATTGGTCAC
2351	CCATTCTGAG GCAAAGATGA TTTCAGCCAT TCCAACTTTA GCTGTCTCCC
2401	CTACTGTACA AGGGCTGGTG ACTTCACTGG TCACTAGTTC TGGGTCAGAG
2451	ACCAGTGCGT TTTCAAATCT AACTGTTGCC TCAAGTCAAC CAGAGACCAT
2501	AGACTCATGG GTCGCTCATC CTGGGACAGA AGCAAGTTCT GTTGTTCCAA
2551	CTTTGACTGT CTCCACTGGT GAGCCGTTTA CAAATATCTC ATTGGTCACC
2601	CATCCTGCAG AGAGTAGCTC AACTCTTCCC AGGACAACCT CAAGGTTTTC
2651	CCACAGTGAA TTAGACACTA TGCCTTCTAC AGTCACCAGT CCTGAGGCAG
2701	AATCCAGCTC AGCCATTTCA ACTACTATTT CACCTGGTAT ACCAGGTGTG
2751	CTGACATCAC TGGTCACTAG CTCTGGGAGA GACATCAGTG CAACTTTTCC
2801	AACAGTGCCT GAGTCCCCAC ATGAATCAGA GGCAACAGCC TCATGGGTTA
2851	CTCATCCTGC AGTCACCAGC ACAACAGTTC CCAGGACAAC CCCTAATTAT
2901	TCTCATAGTG AACCAGACAC CACACCATCA ATAGCCACCA GTCCTGGGGC
2951	AGAAGCCACT TCAGATTTTC CAACAATAAC TGTCTCACCT GATGTACCAG

TABLE 13-continued

Amino Terminal Nucleotide Sequence
(SEQ ID NO: 81)

3001 ATATGGTAAC CTCACAGGTC ACTAGTTCTG GGACAGACAC CAGTATAACT

3051 ATTCCAACTC TGACTCTTTC TTCTGGTGAG CCAGAGACCA CAACCTCATT

3101 TATCACCTAT TCTGAGACAC ACACAAGTTC AGCCATTCCA ACTCTCCCTG

3151 TCTCCCCTGG TGCATCAAAG ATGCTGACCT CACTGGTCAT CAGTTCTGGG

3201 ACAGACAGCA CTACAACTTT CCCAACACTG ACGGAGACCC CATATGAACC

3251 AGAGACAACA GCCATACAGC TCATTCATCC TGCAGAGACC AACACAATGG

3301 TTCCCAAGAC AACTCCCAAG TTTTCCCATA GTAAGTCAGA CACCACACTC

3351 CCAGTAGCCA TCACCAGTCC TGGGCCAGAA GCCAGTTCAG CTGTTTCAAC

3401 GACAACTATC TCACCTGATA TGTCAGATCT GGTGACCTCA CTGGTCCCTA

3451 GTTCTGGGAC AGACACCAGT ACAACCTTCC CAACATTGAG TGAGACCCCA

3501 TATGAACCAG AGACTACAGT CACGTGGCTC ACTCATCCTG CAGAAACCAG

3551 CACAACGGTT TCTGGGACAA TTCCCAACTT TTCCCATAGG GGATCAGACA

3601 CTGCACCCTC AATGGTCACC AGTCCTGGAG TAGACACGAG GTCAGGTGTT

3651 CCAACTACAA CCATCCCACC CAGTATACCA GGGGTAGTGA CCTCACAGGT

3701 CACTAGTTCT GCAACAGACA CTAGTACAGC TATTCCAACT TTGACTCCTT

3751 CTCCTGGTGA ACCAGAGACC ACAGCCTCAT CAGCTACCCA TCCTGGGACA

3801 CAGACTGGCT TCACTGTTCC AATTCGGACT GTTCCCTCTA GTGAGCCAGA

3851 TACAATGGCT TCCTGGGTCA CTCATCCTCC ACAGACCAGC ACACCTGTTT

3901 CCAGAACAAC CTCCAGTTTT TCCCATAGTA GTCCAGATGC CACACCTGTA

3951 ATGGCCACCA GTCCTAGGAC AGAAGCCAGT TCAGCTGTAC TGACAACAAT

TABLE 13-continued

Amino Terminal Nucleotide Sequence (SEQ ID NO: 81)	
4001	CTCACCTGGT GCACCAGAGA TGGTGACTTC ACAGATCACT AGTTCTGGGG
4051	CAGCAACCAG TACAACTGTT CCAACTTTGA CTCATTCTCC TGGTATGCCA
4101	GAGACCACAG CCTTATTGAG CACCCATCCC AGAACAGGGA CAAGTAAAAC
4151	ATTTCCTGCT TCAACTGTGT TTCCTCAAGT ATCAGAGACC ACAGCCTCAC
4201	TCACCATTAG ACCTGGTGCA GAGACTAGCA CAGCTCTCCC AACTCAGACA
4251	ACATCCTCTC TCTTCACCCT ACTTGTAACT GGAACCAGCA GAGTTGATCT
4301	AAGTCCAACT GCTTCACCTG GTGTTTCTGC AAAAACAGCC CCACTTTCCA
4351	CCCATCCAGG GACAGAGACC AGCACAATGA TTCCAACTTC AACTCTTTCC
4401	CTTGGTTTAC TAGAGACTAC AGGCTTACTG GCCACCAGCT CTTCAGCAGA
4451	GACCAGCACG AGTACTCTAA CTCTGACTGT TTCCCCTGCT GTCTCTGGGC
4501	TTTCCAGTGC CTCTATAACA ACTGATAAGC CCCAAACTGT GACCTCCTGG
4551	AACACAGAAA CCTCACCATC TGTAACTTCA GTTGGACCCC CAGAATTTTC
4601	CAGGACTGTC ACAGGCACCA CTATGACCTT GATACCATCA GAGATGCCAA
4651	CACCACCTAA AACCAGTCAT GGAGAAGGAG TGAGTCCAAC CACTATCTTG
4701	AGAACTACAA TGGTTGAAGC CACTAATTTA GCTACCACAG GTTCCAGTCC
4751	CACTGTGGCC AAGACAACAA CCACCTTCAA TACACTGGCT GGAAGCCTCT
4801	TTACTCCTCT GACCACACCT GGGATGTCCA CCTTGGCCTC TGAGAGTGTG
4851	ACCTCAAGAA CAAGTTATAA CCATCGGTCC TGGATCTCCA CCACCAGCAG
4901	TTATAACCGT CGGTACTGGA CCCCTGCCAC CAGCACTCCA GTGACTTCTA
4951	CATTCTCCCC AGGGATTTCC ACATCCTCCA TCCCCAGCTC CACAGCAGCC

TABLE 13-continued

Amino Terminal Nucleotide Sequence (SEQ ID NO: 81)					
5001	ACAGTCCCAT	TCATGGTGCC	ATTCACCCTC	AACTTCACCA	TCACCAACCT
5051	GCAGTACGAG	GAGGACATGC	GGCACCCTGG	TTCCAGGAAG	TTCAACGCCA
5101	CAGAGAGAGA	ACTGCAGGGT	CTGCTCAAAC	CCTTGTTCAG	GAATAGCAGT
5151	CTGGAATACC	TCTATTCAGG	CTGCAGACTA	GCCTCACTCA	GGCCAGAGAA
5201	GGATAGCTCA	GCCATGGCAG	TGGATGCCAT	CTGCACACAT	CGCCCTGACC
5251	CTGAAGACCT	CGGACTGGAC	AGAGAGCGAC	TGTACTGGGA	GCTGAGCAAT
5301	CTGACAAATG	GCATCCAGGA	GCTGGGCCCC	TACACCCTGG	ACCGGAACAG
5351	TCTCTATGTC	AATGGTTTCA	CCCATCGAAG	CTCTATGCCC	ACCACCAGCA
5401	CTCCTGGGAC	CTCCACAGTG	GATGTGGGAA	CCTCAGGGAC	TCCATCCTCC
5451	AGCCCCAGCC	CCACG			

TABLE 14

Amino Terminal Protein Sequence
(SEQ ID NO: 82)

```
  1  ESVLEGTVTS AYQVPSLSTR LTRTDGIMEH ITKIPNEAAH RGTIRPVKGP
 51  QTSTSPASPK GLHTGGTKRM ETTTTALKTT TTALKTTSRA TLTTSVYTPT
101  LGTLTPLNAS RQMASTILTE MMITTPYVFP DVPETTSSLA TSLGAETSTA
151  LPRTTPSVLN RESETTASLV SRSGAERSPV IQTLDVSSSE PDTTASWVIH
201  PAETIPTVSK TTPNFFHSEL DTVSSTATSH GADVSSAIPT NISPSELDAL
251  TPLVTISGTD TSTTFPTLTK SPHETETRTT WLTHPAETSS TIPRTIPNFS
301  HHESDATPSI ATSPGAETSS AIPIMTVSPG AEDLVTSQVT SSGTDRNMTI
351  PTLTLSPGEP KTIASLVTHP EAQTSSAIPT STISPAVSRL VTSMVTSLAA
401  KTSTTNRALT NSPGEPATTV SLVTHPAQTS PTVPWTTSIF FHSKSDTTPS
451  MTTSHGAESS SAVPTPTVST EVPGVVTPLV TSSRAVISTT IPILTLSPGE
501  PETTPSMATS HGEEASSAIP TPTVSPGVPG VVTSLVTSSR AVTSTTIPIL
551  TFSLGEPETT PSMATSHGTE AGSAVPTVLP EVPGMVTSLV ASSRAVTSTT
601  LPTLTLSPGE PETTPSMATS HGAEASSTVP TVSPEVPGVV TSLVTSSSGV
651  NSTSIPTLIL SPGELETTPS MATSHGAEAS SAVPTPTVSP GVSGVVTPLV
701  TSSRAVTSTT IPILTLSSSE PETTPSMATS HGVEASSAVL TVSPEVPGMV
751  TSLVTSSRAV TSTTIPTLTI SSDEPETTTS LVTHSEAKMI SAIPTLAVSP
801  TVQGLVTSLV TSSGSETSAF SNLTVASSQP ETIDSWVAHP GTEASSVVPT
851  LTVSTGEPFT NISLVTHPAE SSSTLPRTTS RFSHSELDTM PSTVTSPEAE
901  SSSAISTTIS PGIPGVLTSL VTSSGRDISA TFPTVPESPH ESEATASWVT
```

TABLE 14-continued

Amino Terminal Protein Sequence
(SEQ ID NO: 82)

951 HPAVTSTTVP RTTPNYSHSE PDTTPSIATS PGAEATSDFP TITVSPDVPD

1001 MVTSQVTSSG TDTSITIPTL TLSSGEPETT TSFITYSETH TSSAIPTLPV

1051 SPGASKMLTS LVISSGTDST TTFPTLTETP YEPETTAIQL IHPAETNTMV

1101 PRTTPKFSHS KSDTTLPVAI TSPGPEASSA VSTTTISPDM SDLVTSLVPS

1151 SGTDTSTTFP TLSETPYEPE TTATWLTHPA ETSTTVSGTI PNFSHRGSDT

1201 APSMVTSPGV DTRSGVPTTT IPPSIPGVVT SQVTSSATDT STAIPTLTPS

1251 PGEPETTASS ATHPGTQTGF TVPIRTVPSS EPDTMASWVT HPPQTSTPVS

1301 RTTSSFSHSS PDATPVMATS PRTEASSAVL TTISPGAPEM VTSQITSSGA

1351 ATSTTVPTLT HSPGMPETTA LLSTHPRTET SKTFPASTVF PQVSETTASL

1401 TIRPGAETST ALPTQTTSSL FTLLVTGTSR VDLSPTASPG VSAKTAPLST

1451 HPGTETSTMI PTSTLSLGLL ETTGLLATSS SAETSTSTLT LTVSPAVSGL

1501 SSASITTDKP QTVTSWNTET SPSVTSVGPP EFSRTVTGTT MTLIPSEMPT

1551 PPKTSHGEGV SPTTILRTTM VEATNLATTG SSPTVAKTTT TFNTLAGSLF

1601 TPLTTPGMST LASESVTSRT SYNHRSWIST TSSYNRRYWT PATSTPVTST
*

1651 FSPGISTSSI PSSTAATVPF MVPFTLNFTI TNLQYEEDMR HPGSRKFNAT

1701 ERELQGLLKP LFRNSSLEYL YSGCRLASLR PEKDSSAMAV DAICTHRPDP

1751 EDLGLDRERL YWELSNLTNG IQELGPYTLD RNSLYVNGFT HRSSMPTTST

1801 PGTSTVDVGT SGTPSSSPSP T

TABLE 15

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

(SEQ ID NO: 83)

1 GCCACAGTCC CATTCATGGT GCCATTCACC CTCAACTTCA CCATCACCAA

51 CCTGCAGTAC GAGGAGGACA TGCGGCACCC TGGTTCCAGG AAGTTCAACG

101 CCACAGAGAG AGAACTGCAG GGTCTGCTCA AACCCTTGTT CAGGAATAGC

151 AGTCTGGAAT ACCTCTATTC AGGCTGCAGA CTAGCCTCAC TCAGGCCAGA

201 GAAGGATAGC TCAGCCATGG CAGTGGATGC CATCTGCATA CATCGCCCTG

251 ACCCTGAAGA CCTCGGACTG GACAGAGAGC GACTGTACTG GGAGCTGAGC

301 AATCTGACAA ATGGCATCCA GGAGCTGGGC CCCTACACCC TGGACCGGAA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCG AAGCTCTATG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGGATGTGG GAACCTCAGG GACTCCATCC

451 TCCAGCCCCA GCCCCACG

(SEQ ID NO: 84)

1 GCTGCTGGCC CTCTCCTGAT GCCGTTCACC CTCAACTTCA CCATCACCAA

51 CCTGCAGTAC GAGGAGGACA TGCGTCGCAC TGGCTCCAGG AAGTTCAACA

101 CCATGGAGAG TGTCCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAACACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA TTGACCTTGC TCAGGCCCAA

201 GAAAGATGGG GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGCCTTG

251 ACCCCAAAAG CCCTGGACTC AACAGGGAGC AGCTGTACTG GGAGCTAAGC

301 AAACTGACCA ATGACATTGA AGAGCTGGGC CCCTACACCC TGGACAGGAA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GAGCTCTGTG TCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGGATCTCA GAACCTCAGG GACTCCATCC

TABLE 15- continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

451 TCCCTCTCCA GCCCCACAAT TATG

(SEQ ID NO: 85)

1 GCTGCTGGCC CTCTCCTGGT ACCATTCACC CTCAACTTCA CCATCACCAA

51 CCTGCAGTAT GGGGAGGACA TGGGTCACCC TGGCTCCAGG AAGTTCAACA

101 CCACAGAGAG GGTCCTGCAG GGTCTGCTTG GTCCCATATT CAAGAACACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGTCTGA

201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCATC CATCATCTTG

251 ACCCCAAAAG CCCTGGACTC AACAGAGAGC GGCTGTACTG GGAGCTGAGC

301 CAACTGACCA ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACAGGAA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GACCTCTGTG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGGACCTTG GAACCTCAGG GACTCCATTC

451 TCCCTCCCAA GCCCCGCA

(SEQ ID NO: 86)

1 ACTGCTGGCC CTCTCCTGGT GCTGTTCACC CTCAACTTCA CCATCACCAA

51 CCTGAAGTAT GAGGAGGACA TGCATCGCCC TGGCTCCAGG AAGTTCAACA

101 CCACTGAGAG GGTCCTGCAG ACTCTGCTTG GTCCTATGTT CAAGAACACC

151 AGTGTTGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTCCGA

201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTCTTG

251 ACCCCAAAAG CCCTGGACTG GACAGAGAGC AGCTATACTG GGAGCTGAGC

301 CAGCTGACCA ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACAGGAA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

351 CAGTCTCTAT GTCAATGGTT TCACCCATTG GATCCCTGTG CCCACCAGCA

401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGTCAGGGAC TCCATCCTCC

451 CTCCCCAGCC CCACA

(SEQ ID NO: 87)

1 GCTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA

51 CCTGCAGTAC GAGGAGGACA TGCATCACCC AGGCTCCAGG AAGTTCAACA

101 CCACGGAGCG GGTCCTGCAG GGTCTGCTTG GTCCCATGTT CAAGAACACC

151 AGTGTCGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTCCGA

201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTCTTG

251 ACCCCAAAAG CCCTGGAGTG GACAGGGAGC AGCTATACTG GGAGCTGAGC

301 CAGCTGACCA ATGGCATCAA AGAGCTGGGT CCCTACACCC TGGACAGAAA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GACCTCTGCG CCCAACACCA

401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGACCTCAGG GACTCCATCC

451 TCCCTCCCCA GCCCTACA

(SEQ ID NO: 88)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNTNTT CAAGAACACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTCCGA

201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTCTTG

251 ACCCCAAAAG CCCTGGAGTG GACAGGGAGC AGCTATACTG GGAGCTGAGC

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TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

301 CAGCTGACCA ATGGCATCAA AGAGCTGGGT CCCTACACCC TGGACAGAAA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GACCTCTGCG CCCAACACCA

401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGACCTCAGG GACTCCATCC

451 TCCCTCCCCA GCCCTACA

(SEQ ID NO: 89)

1 TCTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA

51 CCTGCAGTAC GAGGAGGACA TGCATCACCC AGGCTCCAGG AAGTTCAACA

101 CCACGGAGCG GGTCCTGCAG GGTCTGCTTG GTCCCATGTT CAAGAACACC

151 AGTGTCGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA

201 GAAGAATGGG GCAGCCACTG GAATGGATGC CATCTGCAGC CACCGTCTTG

251 ACCCCAAAAG CCCTGGACTC AACAGAGAGC AGCTGTACTG GGAGCTGAGC

301 CAGCTGACCC ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACAGGAA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GAGCTCTGTG GCCCCCACCA

401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGACCTCAGG GACTCCATCC

451 TCCCTCCCCA GCCCCACA

(SEQ ID NO: 90)

1 ACAGCTGTTC CTCTCCTGGT GCCGTTCACC CTCAACTTTA CCATCACCAA

51 TCTGCAGTAT GGGGAGGACA TGCGTCACCC TGGCTCCAGG AAGTTCAACA

101 CCACAGAGAG GGTCCTGCAG GGTCTGCTTG GTCCCTTGTT CAAGAACTCC

151 AGTGTCGGCC CTCTGTACTC TGGCTGCAGA CTGATCTCTC TCAGGTCTGA

201 GAAGGATGGG GCAGCCACTG GAGTGGATGC CATCTGCACC CACCACCTTA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

```
251  ACCCTCAAAG CCCTGGACTG GACAGGGAGC AGCTGTACTG GCAGCTGAGC
301  CAGATGACCA ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACCGGAA
351  CAGTCTCTAC GTCAATGGTT TCACCCATCG GAGCTCTGGG CTCACCACCA
401  GCACTCCTTG GACTTCCACA GTTGACCTTG GAACCTCAGG GACTCCATCC
451  CCCGTCCCCA GCCCCACA
```

(SEQ ID NO: 91)

```
  1  ACTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA
 51  CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGATCTAGG AAGTTCAACA
101  CCACAGAGAG GGTCCTGCAG GGTCTGCTTA GTCCCATTTT CAAGAACTCC
151  AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGCCCGA
201  GAAGGATGGG GCAGCAACTG GAATGGATGC TGTCTGCCTC TACCACCCTA
251  ATCCCAAAAG ACCTGGACTG GACAGAGAGC AGCTGTACTG GGAGCTAAGC
301  CAGCTGACCC ACAACATCAC TGAGCTGGGC CCCTACAGCC TGGACAGGGA
351  CAGTCTCTAT GTCAATGGTT TCACCCATCA GAACTCTGTG CCCACCACCA
401  GTACTCCTGG GACCTCCACA GTGTACTGGG CAACCACTGG GACTCCATCC
451  TCCTTCCCCG GCCACACA
```

(SEQ ID NO: 92)

```
  1  GAGCCTGGCC CTCTCCTGAT ACCATTCACT TTCAACTTTA CCATCACCAA
 51  CCTGCATTAT GAGGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA
101  CCACGGAGAG GGTTCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAACACC
151  AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGCCCGA
```

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

201 GAAGGATGGG GCAGCAACTG GAATGGATGC TGTCTGCCTC TACCACCCTA

251 ATCCCAAAAG ACCTGGGCTG GACAGAGAGC AGCTGTACTG GGAGCTAAGC

301 CAGCTGACCC ACAACATCAC TGAGCTGGGC CCCTACAGCC TGGACAGGGA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GAACTCTGTG CCCACCACCA

401 GTACTCCTGG GACCTCCACA GTGTACTGGG CAACCACTGG GACTCCATCC

451 TCCTTCCCCG GCCACACA

(SEQ ID NO: 93)

1 GAGCCTGGCC CTCTCCTGAT ACCATTCACT TTCAACTTTA CCATCACCAA

51 CCTGCATTAT GAGGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA

101 CCACGGAGAG GGTTCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAACACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA

201 GAAGCATGAG GCAGCCACTG GAGTGGACAC CATCTGTACC CACCGCGTTG

251 ATCCCATCGG ACCTGGACTG GACAGGGAGC GGCTATACTG GGAGCTGAGC

301 CAGCTGACCA ACAGCATTAC CGAACTGGGA CCCTACACCC TGGACAGGGA

351 CAGTCTCTAT GTCAATGGCT TCAACCCTCG GAGCTCTGTG CCAACCACCA

401 GCACTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC

451 TCCCTGCCTG GCCACACA

(SEQ ID NO: 94)

1 GCCCCTGTCC CTCTCTTGAT ACCATTCACC CTCAACTTTA CCATCACCAA

51 CCTGCATTAT GAGGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA

101 CCACGGAGAG GGTTCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAACACC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA

201 GAAGCATGAG GCAGCCACTG GAGTGGACAC CATCTGTACC CACCGCGTTG

251 ATCCCATCGG ACCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC

451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 95)

1 TCTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA

51 CCTGCAGTAC GAGGAGGACA TGCATCACCC AGGCTCCAGG AAGTTCAACA

101 CCACGGAGCG GGTCCTGCAG GGTCTGCTTG GTCCCATGTT CAAGAACACC

151 AGTGTCGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA

201 GAAGAATGGG GCAGCCACTG GAATGGATGC CATCTGCAGC CACCGTCTTG

251 ACCCCAAAAG CCCTGGACTC GACAGAGAGC AGCTGTACTG GGAGCTGAGC

301 CAGCTGACCC ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACAGGAA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GAGCTCTGTG GCCCCCACCA

401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGACCTCAGG GACTCCATCC

451 TCCCTCCCCA GCCCCACA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

(SEQ ID NO: 96)

```
   1  ACAGCTGTTC CTCTCCTGGT GCCGTTCACC CTCAACTTTA CCATCACCAA
  51  TCTGCAGTAT GGGGAGGACA TGCGTCACCC TGGCTCCAGG AAGTTCAACA
 101  CCACAGAGAG GGTCCTGCAG GGTCTGCTTG GTCCCTTGTT CAAGAACTCC
 151  AGTGTCGGCC CTCTGTACTC TGGCTGCAGA CTGATCTCTC TCAGGTCTGA
 201  GAAGGATGGG GCAGCCACTG GAGTGGATGC CATCTGCACC CACCACCTTA
 251  ACCCTCAAAG CCCTGGACTG GACAGGGAGC AGCTGTACTG GCAGCTGAGC
 301  CAGATGACCA ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACCGGAA
 351  CAGTCTCTAC GTCAATGGTT TCACCCATCG GAGCTCTGGG CTCACCACCA
 401  GCACTCCTTG GACTTCCACA GTTGACCTTG GAACCTCAGG GACTCCATCC
 451  CCCGTCCCCA GCCCCACA
```

(SEQ ID NO: 97)

```
   1  ACTGCTGGCC CTCTCCTGGT GCCATTCACC CTAAACTTCA CCATCACCAA
  51  CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGATCTAGG AAGTTCAACG
 101  CCACAGAGAG GGTCCTGCAG GGTCTGCTTA GTCCCATATT CAAGAACTCC
 151  AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGCCCGA
 201  GAAGGATGGG GCAGCAACTG GAATGGATGC TGTCTGCCTC TACCACCCTA
 251  ATCCCAAAAG ACCTGGACTG GACAGAGAGC AGCTGTACTG GGAGCTAAGC
 301  CAGCTGACCC ACAACATCAC TGAGCTGGGC CCCTACAGCC TGGACAGGGA
 351  CAGTCTCTAT GTCAATGGTT TCACCCATCA GAGCTCTATG ACGACCACCA
```

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

401 GAACTCCTGA TACCTCCACA ATGCACCTGG CAACCTCGAG AACTCCAGCC

451 TCCCTGTCTG GACCTACG

(SEQ ID NO: 98)

1 ACCGCCAGCC CTCTCCTGGT GCTATTCACA ATCAACTGCA CCATCACCAA

51 CCTGCAGTAC GAGGAGGACA TGCGTCGCAC TGGCTCCAGG AAGTTCAACA

101 CCATGGAGAG TGTCCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAACACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA TTGACCTTGC TCAGGCCCAA

201 GAAAGATGGG GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGCCTTG

251 ACCCCAAAAG CCCTGGACTC AACAGGGAGC AGCTGTACTG GGAGCTAAGC

301 AAACTGACCA ATGACATTGA AGAGCTGGGC CCCTACACCC TGGACAGGAA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GAGCTCTGTG TCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGGATCTCA GAACCTCAGG GACTCCATCC

451 TCCCTCTCCA GCCCCACAAT TATG

(SEQ ID NO: 99)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

101 CCACNGAGAG GGTCCTACAG GGTCTGCTCA GGCCCTTGTT CAAGAACACC

151 AGTGTCAGCT CTCTGTACTC TGGTTGCAGA CTGACCTTGC TCAGGCCTGA

201 GAAGGATGGG GCAGCCACCA GAGTGGATGC TGCCTGCACC TACCGCCCTG

251 ATCCCAAAAG CCCTGGACTG GACAGAGAGC AACTATACTG GGAGCTGAGC

301 CAGCTAACCC ACAGCATCAC TGAGCTGGGA CCCTACACCC TGGACAGGGT

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru 145)

351 CAGTCTCTAT GTCAATGGCT TCAACCCTCG GAGCTCTGTG CCAACCACCA

401 GCACTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC

451 TCCCTGCCTG GCCACACA

(SEQ ID NO: 100)

1 GCCCCTGTCC CTCTCTTGAT ACCATTCACC CTCAACTTTA CCATCACCAA

51 CCTGCATTAT GAAGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA

101 CCACGGAGAG GGTTCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC

151 AGCGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA

201 GAAACATGGG GCAGCCACTG GAGTGGACGC CATCTGCACC CTCCGCCTTG

251 ATCCCACTGG TCCTGGACTG GACAGAGAGC GGCTATACTG GGAGCTGAGC

301 CAGCTGACCA ACAGCGTTAC AGAGCTGGGC CCCTACACCC TGGACAGGGA

351 CAGTCTCTAT GTCAATGGCT TCACCCAGCG GAGCTCTGTG CCAACCACCA

401 GTATTCCTGG GACCTCTGCA GTGCACCTGG AAACCTCTGG GACTCCAGCC

451 TCCCTCCCTG GCCACACA

(SEQ ID NO: 101)

1 GCCCCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CTATCACCAA

51 CCTGCAGTAT GAGGTGGACA TGCGTCACCC TGGTTCCAGG AAGTTCAACA

101 CCACGGAGAG AGTCCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA

201 AAAACGTGGG GCAGCCACCG GCGTGGACAC CATCTGCACT CACCGCCTTG

251 ACCCTCTAAA CCCTGGACTG GACAGAGAGC AGCTATACTG GGAGCTGAGC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

301 AAACTGACCC GTGGCATCAT CGAGCTGGGC CCCTACCTCC TGGACAGAGG

351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GAACTTTGTG CCCATCACCA

401 GCACTCCTGG GACCTCCACA GTACACCTAG GAACCTCTGA AACTCCATCC

451 TCCCTACCTA GACCCATA

(SEQ ID NO: 102)

1 GTGCCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA

51 CTTGCAGTAT GAGGAGGCCA TGCGACACCC TGGCTCCAGG AAGTTCAATA

101 CCACGGAGAG GGTCCTACAG GGTCTGCTCA GGCCCTTGTT CAAGAATACC

151 AGTATCGGCC CTCTGTACTC CAGCTGCAGA CTGACCTTGC TCAGGCCAGA

201 GAAGGACAAG GCAGCCACCA GAGTGGATGC CATCTGTACC CACCACCCTG

251 ACCCTCAAAG CCCTGGACTG AACAGAGAGC AGCTGTACTG GGAGCTGAGC

301 CAGCTGACCC ACGGCATCAC TGAGCTGGGC CCCTACACCC TGGACAGGGA

351 CAGTCTCTAT GTCGATGGTT TCACTCATTG GAGCCCCATA CCGACCACCA

401 GCACTCCTGG GACCTCCATA GTGAACCTGG GAACCTCTGG GATCCCACCT

451 TCCCTCCCTG AAACTACA

(SEQ ID NO: 103)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

101 CCACNGAGAG GGTTCTGCAG GGTCTGCTCA AACCCTTGTT CAGGAATAGC

151 AGTCTGGAAT ACCTCTATTC AGGCTGCAGA CTAGCCTCAC TCAGGCCAGA

201 GAAGGATAGC TCAGCCATGG CAGTGGATGC CATCTGCACA CATCGCCCTG

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru 145)

251 ACCCTGAAGA CCTCGGACTG GACAGAGAGC GACTGTACTG GGAGCTGAGC

301 AATCTGACAA ATGGCATCCA GGAGCTGGGC CCCTACACCC TGGACCGGAA

351 CAGTCTCTAC GTCAATGGTT TCACCCATCG GAGCTCTGGG CTCACCACCA

401 GCACTCCTTG GACTTCCACA GTTGACCTTG GAACCTCAGG GACTCCATCC

451 CCCGTCCCCA GCCCCACA

(SEQ ID NO: 104)

1 ACTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA

51 CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGTTCCAGG AGGTTCAACA

101 CCACGGAGAG GGTTCTGCAG GGTCTGCTCA CGCCCTTGTT CAAGAACACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA

201 GAAGCAAGAG GCAGCCACTG GAGTGGACAC CATCTGTACC CACCGCGTTG

251 ATCCCATCGG ACCTGGACTG GACAGAGAGC GGCTATACTG GGAGCTGAGC

301 CAGCTGACCA ACAGCATCAC AGAGCTGGGA CCCTACACCC TGGATAGGGA

351 CAGTCTCTAT GTCAATGGCT TCAACCCTTG GAGCTCTGTG CCAACCACCA

401 GCACTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC

451 TCCCTGCCTG GCCACACA

(SEQ ID NO: 105)

1 GCCCCTGTCC CTCTCTTGAT ACCATTCACC CTCAACTTTA CCATCACCGA

51 CCTGCATTAT GAAGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA

101 CCACGGAGAG GGTTCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC

151 AGCGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

201 GAAACATGGG GCAGCCACTG GAGTGGACGC CATCTGCACC CTCCGCCTTG

251 ATCCCACTGG TCCTGGACTG GACAGAGAGC GGCTATACTG GGAGCTGAGC

301 CAGCTGACCA ACAGCGTTAC AGAGCTGGGC CCCTACACCC TGGACAGGGA

351 CAGTCTCTAT GTCAATGGCT TCACCCATCG GAGCTCTGTG CCAACCACCA

401 GTATTCCTGG GACCTCTGCA GTGCACCTGG AAACCTCTGG GACTCCAGCC

451 TCCCTCCCTG GCCACACA

(SEQ ID NO: 106)

1 GCCCCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CTATCACCAA

51 CCTGCAGTAT GAGGAGGACA TGCGTCACCC TGGTTCCAGG AAGTTCAGCA

101 CCACGGAGAG AGTCCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAACACC

151 AGTGTCAGCT CTCTGTACTC TGGTTGCAGA CTGACCTTGC TCAGGCCTGA

201 GAAGGATGGG GCAGCCACCA GAGTGGATGC TGTCTGCACC CATCGTCCTG

251 ACCCCAAAAG CCCTGGACTG GACAGAGAGC GGCTGTACTG GAAGCTGAGC

301 CAGCTGACCC ACGGCATCAC TGAGCTGGGC CCCTACACCC TGGACAGGCA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GAGCTCTATG ACGACCACCA

401 GAACTCCTGA TACCTCCACA ATGCACCTGG CAACCTCGAG AACTCCAGCC

451 TCCCTGTCTG GACCTACG

(SEQ ID NO: 107)

1 ACCGCCAGCC CTCTCCTGGT GCTATTCACA ATTAACTTCA CCATCACTAA

51 CCTGCGGTAT GAGGAGAACA TGCATCACCC TGGCTCTAGA AAGTTTAACA

101 CCACGGAGAG AGTCCTTCAG GGTCTGCTCA GGCCTGTGTT CAAGAACACC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCACGC TCAGGCCCAA

201 GAAGGATGGG GCAGCCACCA AAGTGGATGC CATCTGCACC TACCGCCCTG

251 ATCCCAAAAG CCCTGGACTG GACAGAGAGC AGCTATACTG GGAGCTGAGC

301 CAGCTAACCC ACAGCATCAC TGAGCTGGGC CCCTACACCC AGGACAGGGA

351 CAGTCTCTAT GTCAATGGCT TCACCCATCG GAGCTCTGTG CCAACCACCA

401 GTATTCCTGG GACCTCTGCA GTGCACCTGG AAACCTCTGG GACTCCAGCC

451 TCCCTCCCTG GCCACACA

(SEQ ID NO: 108)

1 GCCCCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CTATCACCAA

51 CCTGCAGTAT GAGGAGGACA TGCGTCACCC TGGTTCCAGG AAGTTCAACA

101 CCACGGAGAG AGTCCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA

201 AAAACGTGGG GCAGCCACCG GCGTGGACAC CATCTGCACT CACCGCCTTG

251 ACCCTCTAAA CCCAGGACTG GACAGAGAGC AGCTATACTG GGAGCTGAGC

301 AAACTGACCC GTGGCATCAT CGAGCTGGGC CCCTACCTCC TGGACAGAGG

351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GACCTCTGTG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGGACCTTG GAACCTCAGG GACTCCATTC

451 TCCCTCCCAA GCCCCGCA

(SEQ ID NO: 109)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

101 CCACNGAGAG GGTCCTGCAG ACTCTGCTTG GTCCTATGTT CAAGAACACC

151 AGTGTTGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTCCGA

201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTCTTG

251 ACCCCAAAAG CCCTGGAGTG GACAGGGAGC AACTATACTG GGAGCTGAGC

301 CAGCTGACCA ATGGCATTAA AGAACTGGGC CCCTACACCC TGGACAGGAA

351 CAGTCTCTAT GTCAATGGGT TCACCCATTG GATCCCTGTG CCCACCAGCA

401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGTCAGGGAC TCCATCCTCC

451 CTCCCCAGCC CCACA

(SEQ ID NO: 110)

1 ACTGCTGGCC CTCTCCTGGT GCCGTTCACC CTCAACTTCA CCATCACCAA

51 CCTGAAGTAC GAGGAGGACA TGCATTGCCC TGGCTCCAGG AAGTTCAACA

101 CCACAGAGAG AGTCCTGCAG AGTCTGCTTG GTCCCATGTT CAAGAACACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTCCGA

201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTCTTG

251 ACCCCAAAAG CCCTGGAGTG GACAGGGAGC AGCTATACTG GGAGCTGAGC

301 CAGCTGACCA ATGGCATCAA AGAGCTGGGT CCCTACACCC TGGACAGAAA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GACCTCTGCG CCCAACACCA

401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGACCTCAGG GACTCCATCC

451 TCCCTCCCCA GCCCTACA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

(SEQ ID NO: 111)

```
  1  NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
 51  CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA
101  CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNTNTT CAAGAACNCC
151  AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA
201  GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN
251  ANCCCAAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
301  CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
351  CAGTCTCTAT GTCAATGGTT TCACCCATTG GATCCCTGTG CCCACCAGCA
401  GCACTCCTGG GACCTCCACA GTGGACCTTG GGTCAGGGAC TCCATCCTCC
451  CTCCCCAGCC CCACA
```

(SEQ ID NO: 112)

```
  1  ACTGCTGGCC CTCTCCTGGT GCCGTTCACC CTCAACTTCA CCATCACCAA
 51  CCTGAAGTAC GAGGAGGACA TGCATTGCCC TGGCTCCAGG AAGTTCAACA
101  CCACAGAGAG AGTCCTGCAG AGTCTGCTTG GTCCCATGTT CAAGAACACC
151  AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCGC TCAGGTCCGA
201  GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTGTTG
251  ACCCCAAAAG CCCTGGAGTG GACAGGGAGC AGCTATACTG GGAGCTGAGC
301  CAGCTGACCA ATGGCATCAA AGAGCTGGGT CCCTACACCC TGGACAGAAA
351  CAGTCTCTAT GTCAATGGTT TCACCCATCA GACCTCTGCG CCCAACACCA
401  GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
```

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 113)

1 TCTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA

51 CCTGCAGTAC GAGGAGGACA TGCATCACCC AGGCTCCAGG AAGTTCAACA

101 CCACGGAGCG GGTCCTGCAG GGTCTGCTTG GTCCCATGTT CAAGAACACC

151 AGTGTCGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA

201 GAAGAATGGG GCAACCACTG GAATGGATGC CATCTGCACC CACCGTCTTG

251 ACCCCAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC

451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 114)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

101 CCACNGAGAG GGTTCTGCAG GGTCTGCTCA AACCCTTGTT CAGGAATAGC

151 AGTCTGGAAT ACCTCTATTC AGGCTGCAGA CTAGCCTCAC TCAGGCCAGA

201 GAAGGATAGC TCAGCCATGG CAGTGGATGC CATCTGCACA CATCGCCCTG

251 ACCCTGAAGA CCTCGGACTG GACAGAGAGC GACTGTACTG GGAGCTGAGC

301 AATCTGACAA ATGGCATCCA GGAGCTGGGC CCCTACACCC TGGACCGGAA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCG AAGCTCTATG CCCACCACCA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

401 GCACTCCTGG GACCTCCACA GTGGATGTGG GAACCTCAGG GACTCCATCC

451 TCCAGCCCCA GCCCCACG

(SEQ ID NO: 115)

1 ACTGCTGGCC CTCTCCTGAT ACCATTCACC CTCAACTTCA CCATCACCAA

51 CCTGCAGTAT GGGGAGGACA TGGGTCACCC TGGCTCCAGG AAGTTCAACA

101 CCACAGAGAG GGTCCTGCAG GGTCTGCTTG GTCCCATATT CAAGAACACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGTCTGA

201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCATC CATCATCTTG

251 ACCCCAAAAG CCCTGGACTC AACAGAGAGC GGCTGTACTG GGAGCTGAGC

301 CAACTGACCA ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACAGGAA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GACCTCTGTG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGGACCTTG GAACCTCAGG GACTCCATTC

451 TCCCTCCCAA GCCCCGCA

(SEQ ID NO: 116)

1 ACTGCTGGCC CTCTCCTGGT GCTGTTCACC CTCAACTTCA CCATCACCAA

51 CCTGAAGTAT GAGGAGGACA TGCATCGCCC TGGCTCCAGG AAGTTCAACA

101 CCACTGAGAG GGTCCTGCAG ACTCTGCTTG GTCCTATGTT CAAGAACACC

151 AGTGTTGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTCCGA

201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTCTTG

251 ACCCCAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC

451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 117)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

101 CCACNGAGAG AGTCCTTCAG GGTCTGCTCA GGCCTGTGTT CAAGAACACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCCAA

201 GAAGGATGGG GCAGCCACCA AAGTGGATGC CATCTGCACC TACCGCCCTG

251 ATCCCAAAAG CCCTGGACTG GACAGAGAGC AGCTATACTG GGAGCTGAGC

301 CAGCTAACCC ACAGCATCAC TGAGCTGGGC CCCTACACCC AGGACAGGGA

351 CAGTCTCTAT GTCAATGGCT TCACCCATCG GAGCTCTGTG CCAACCACCA

401 GTATTCCTGG GACCTCTGCA GTGCACCTGG AAACCACTGG GACTCCATCC

451 TCCTTCCCCG GCCACACA

(SEQ ID NO: 118)

1 GAGCCTGGCC CTCTCCTGAT ACCATTCACT TTCAACTTTA CCATCACCAA

51 CCTGCGTTAT GAGGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA

101 CCACGGAGAG GGTTCTGCAG GGTCTGCTCA CGCCCTTGTT CAAGAACACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA

201 GAAGCAGGAG GCAGCCACTG GAGTGGACAC CATCTGTACC CACCGCGTTG

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru 145)

```
251  ATCCCATCGG ACCTGGACTG GACAGAGAGC GGCTATACTG GGAGCTGAGC
301  CAGCTGACCA ACAGCATCAC AGAGCTGGGA CCCTACACCC TGGATAGGGA
351  CAGTCTCTAT GTCGATGGCT TCAACCCTTG GAGCTCTGTG CCAACCACCA
401  GCACTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC
451  CCCCTGCCTG GCCACACA
```

(SEQ ID NO: 119)

```
  1  GCCCCTGTCC CTCTCTTGAT ACCATTCACC CTCAACTTTA CCATCACCGA
 51  CCTGCATTAT GAAGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA
101  CCACGGAGAG GGTTCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC
151  AGCGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA
201  GAAACATGGG GCAGCCACTG GAGTGGACGC CATCTGCACC CTCCGCCTTG
251  ATCCCACTGG TCCTGGACTG GACAGAGAGC GGCTATACTG GGAGCTGAGC
301  CAGCTGACCA ACAGCATCAC AGAGCTGGGA CCCTACACCC TGGATAGGGA
351  CAGTCTCTAT GTCAATGGCT TCAACCCTTG GAGCTCTGTG CCAACCACCA
401  GCACTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC
451  TCCCTGCCTG GCCACACA
```

(SEQ ID NO: 120)

```
  1  ACTGCTGGCC CTCTCCTGGT GCCGTTCACC CTCAACTTCA CCATCACCAA
 51  CCTGAAGTAC GAGGAGGACA TGCATTGCCC TGGCTCCAGG AAGTTCAACA
101  CCACAGAGAG AGTCCTGCAG AGTCTGCATG GTCCCATGTT CAAGAACACC
151  AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTCCGA
```

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCACC CACCGTCTTG

251 ACCCCAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC

451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 121)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNTNTT CAAGAACNCC

151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA

201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN

251 ANCCCAAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ACAGCATCAC AGAGCTGGGA CCCTACACCC TGGATAGGGA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCG AAGCTCTATG CCCACCACCA

401 GTATTCCTGG GACCTCTGCA GTGCACCTGG AAACCTCTGG GACTCCAGCC

451 TCCCTCCCTG GCCACACA

(SEQ ID NO: 122)

1 GCCCCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CTATCACCAA

51 CCTGCAGTAT GAGGAGGACA TGCGTCACCC TGGTTCCAGG AAGTTCAACA

101 CCACGGAGAG AGTCCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA

201 AAAACGTGGG GCAGCCACCG GCGTGGACAC CATCTGCACT CACCGCCTTG

251 ACCCTCTAAA CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC

451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 123)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNTNTT CAAGAACNCC

151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA

201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN

251 ANCCCAAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TTCACCCTCG GAGCTCTGTG CCAACCACCA

401 GCACTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC

451 TCCCTGCCTG GCCACACA

(SEQ ID NO: 124)

1 GCCCCTGTCC CTCTCTTGAT ACCATTCACC CTCAACTTTA CCATCACCAA

51 CCTGCATTAT GAAGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

101 CCACGGAGCG GGTCCTGCAG GGTCTGCTTG GTCCCATGTT CAAGAACACA

151 AGTGTCGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA

201 GAAGAATGGG GCAGCCACTG GAATGGATGC CATCTGCAGC CACCGTCTTG

251 ACCCCAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC

451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 125)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNTNTT CAAGAACNCC

151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA

201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN

251 ANCCCAAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GAACTCTGTG CCCACCACCA

401 GTACTCCTGG GACCTCCACA GTGTACTGGG CAACCACTGG GACTCCATCC

451 TCCTTCCCCG GCCACACA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

(SEQ ID NO: 126)

```
   1  GAGCCTGGCC CTCTCCTGAT ACCATTCACT TTCAACTTTA CCATCACCAA
  51  CCTGCATTAT GAGGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA
 101  CCACGGAGAG GGTTCTGCAG GGTCTGCTCA CGCCCTTGTT CAAGAACACC
 151  AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA
 201  GAAGCAGGAG GCAGCCACTG GAGTGGACAC CATCTGTACC CACCGCGTTG
 251  ATCCCATCGG ACCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
 301  CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
 351  CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA
 401  GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC
 451  TCCNTCCCCN GCCNCACA
```

(SEQ ID NO: 127)

```
   1  NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA
  51  CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA
 101  CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNTNTT CAAGAACNCC
 151  AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA
 201  GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN
 251  ANCCCAAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC
 301  CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA
 351  CAGTCTCTAT GTCAATGGTT TCACCCATCG GAGCTCTGTG CCAACCACCA
 401  GCAGTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC
```

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

451 TCCCTGCCTG GCCACACA

(SEQ ID NO: 128)

1 GCCCCTGTCC CTCTCTTGAT ACCATTCACC CTCAACTTTA CCATCACCAA

51 CCTGCATTAT GAAGAAAACA TGCAACACCC TGGTTCCAGG AAGTTCAACA

101 CCACGGAGAG GGTTCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA

201 GAAACATGGG GCAGCCACTG GAGTGGACGC CATCTGCACC CTCCGCCTTG

251 ATCCCACTGG TCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC

451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 129)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNTNTT CAAGAACNCC

151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA

201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN

251 ANCCCAAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GACCTCTGTG CCCACCACCA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

401 GCACTCCTGG GACCTCCACA GTGCACCTGG CAACCTCTGG GACTCCATCC

451 TCCCTGCCTG GCCACACA

(SEQ ID NO: 130)

1 GCCCCTGTCC CTCTCTTGAT ACCATTCACC CTCAACTTTA CCATCACCAA

51 CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGATCTAGG AAGTTCAACA

101 CCACAGAGAG GGTCCTGCAG GGTCTGCTTA GTCCCATTTT CAAGAACTCC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGCCCGA

201 GAAGGATGGG GCAGCAACTG GAATGGATGC TGTCTGCCTC TACCACCCTA

251 ATCCCAAAAG ACCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC

451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 131)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNTNTT CAAGAACNCC

151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA

201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN

251 ANCCCAAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

351 CAGTCTCTAT GTCAATGGTT TCACCCATTG GAGCTCTGGG CTCACCACCA

401 GCACTCCTTG GACTTCCACA GTTGACCTTG GAACCTCAGG GACTCCATCC

451 CCCGTCCCCA GCCCCACA

(SEQ ID NO: 132)

1 ACTGCTGGCC CTCTCCTGGT GCCATTCACC CTAAACTTCA CCATCACCAA

51 CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGATCTAGG AAGTTCAACG

101 CCACAGAGAG GGTCCTGCAG GGTCTGCTTA GTCCCATATT CAAGAACACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGACCTGA

201 GAAGCAGGAG GCAGCCACTG GAGTGGACAC CATCTGTACC CACCGCGTTG

251 ATCCCATCGG ACCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC

451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 133)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNTNTT CAAGAACNCC

151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA

201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN

251 ANCCCAAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCG GAGCTTTGGG CTCACCACCA

401 GCACTCCTTG GACTTCCACA GTTGACCTTG GAACCTCAGG GACTCCATCC

451 CCCGTCCCCA GCCCCACA

(SEQ ID NO: 134)

1 ACTGCTGGCC CTCTCCTGGT GCCATTCACC CTAAACTTCA CCATCACCAA

51 CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGCTCCAGG AAGTTCAACA

101 CCACGGAGAG GGTCCTTCAG GGTCTGCTTA CGCCCTTGTT CAGGAACACC

151 AGTGTCAGCT CTCTGTACTC TGGTTGCAGA CTGACCTTGC TCAGGCCTGA

201 GAAGGATGGG GCAGCCACCA GAGTGGATGC TGTCTGCACC CATCGTCCTG

251 ACCCCAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC

451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 135)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNTNTT CAAGAACNCC

151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA

201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

251 ANCCCAAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATTG GATCCCTGTG CCCACCAGCA

401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGTCAGGGAC TCCATCCTCC

451 CTCCCCAGCC CCACA

(SEQ ID NO: 136)

1 ACTGCTGGCC CTCTCCTGGT ACCATTCACC CTCAACTTCA CCATCACCAA

51 CCTGCAGTAT GGGGAGGACA TGGGTCACCC TGGCTCCAGG AAGTTCAACA

101 CCACAGAGAG GGTCCTGCAG GGTCTGCTTG GTCCCATATT CAAGAACACC

151 AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGTCCGA

201 GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCATC CATCATCTTG

251 ACCCCAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC

451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 137)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

101 CCACNGAGNG NGTNCTGCAG GGTCTGCTNN NNCCCNTNTT CAAGAACNCC

151 AGTGTNGGCC NTCTGTACTC TGGCTGCAGA CTGACCTNNC TCAGGNCNGA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

201 GAAGNATGGN GCAGCCACTG GANTGGATGC CATCTGCANC CACCNNCNTN

251 ANCCCAAAAG NCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GACCTTTGCG CCCAACACCA

401 GCACTCCTGG GACCTCCACA GTGGACCTTG GGACCTCAGG GACTCCATCC

451 TCCCTCCCC AGCCCTACA

(SEQ ID NO: 138)

1 TCTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA

51 CCTGCAGTAC GAGGAGGACA TGCATCACCC AGGCTCCAGG AAGTTCAACA

101 CCACGGAGCG GGTCCTGCAG GGTCTGCTTG GTCCCATGTT CAAGAACACC

151 AGTGTCGGCC TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA

201 GAAGAATGGG GCAGCCACCA GAGTGGATGC TGTCTGCACC CATCGTCCTG

251 ACCCCAAAAG CCCTGGACTG NACAGNGAGC NGCTNTACTG GGAGCTNAGC

301 CANCTGACCA ANNNCATCNN NGAGCTGGGN CCCTACACCC TGGACAGGNA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCN GANCTCTGNG CCCACCACCA

401 GCACTCCTGG GACCTCCACA GTGNACNTNG GNACCTCNGG GACTCCATCC

451 TCCNTCCCCN GCCNCACA

(SEQ ID NO: 139)

1 NCNNCTGNCC CTCTCCTGNT NCCNTTCACC NTCAACTTNA CCATCACCAA

51 CCTGCANTAN GNGGANNACA TGCNNCNCCC NGGNTCCAGG AAGTTCAACA

101 CCACNGAGAG GGTTCTGCAG GGTCTGCTCA AGCCCTTGTT CAAGAGCACC

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

151 AGTGTTGGCC CTCTGTATTC TGGCTGCAGA CTGACCTTGC TCAGGCCTGA

201 GAAGGACGGA GTAGCCACCA GAGTGGACGC CATCTGCACC CACCGCCCTG

251 ACCCCAAAAT CCCTGGGCTA GACAGACAGC AGCTATACTG GGAGCTGAGC

301 CAGCTGACCC ACAGCATCAC TGAGCTGGGA CCCTACACCC TGGATAGGGA

351 CAGTCTCTAT GTCAATGGTT TCACCCAGCG GAGCTCTGTG CCCACCACCA

401 GCACTCCTGG GACTTTCACA GTACAGCCGG AAACCTCTGA GACTCCATCA

451 TCCCTCCCTG GCCCCACA

(SEQ ID NO: 140)

1 GCCACTGGCC CTGTCCTGCT GCCATTCACC CTCAATTTTA CCATCACTAA

51 CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGCTCCAGG AAGTTCAACA

101 CCACGGAGAG GGTCCTTCAG GGTCTGCTTA TGCCCTTGTT CAAGAACACC

151 AGTGTCAGCT CTCTGTACTC TGGTTGCAGA CTGACCTTGC TCAGGCCTGA

201 GAAGGATGGG GCAGCCACCA GAGTGGATGC TGTCTGCACC CATCGTCCTG

251 ACCCCAAAAG CCCTGGACTG GACAGAGAGC GGCTGTACTG GAAGCTGAGC

301 CAGCTGACCC ACGGCATCAC TGAGCTGGGC CCCTACACCC TGGACAGGCA

351 CAGTCTCTAT GTCAATGGTT TCACCCATCA GAGCTCTATG ACGACCACCA

401 GAACTCCTGA TACCTCCACA ATGCACCTGG CAACCTCGAG AACTCCAGCC

451 TCCCTGTCTG GACCTACG

(SEQ ID NO: 141)

1 ACCGCCAGCC CTCTCCTGGT GCTATTCACA ATTAACTTCA CCATCACTAA

51 CCTGCGGTAT GAGGAGAACA TGCATCACCC TGGCTCTAGA AAGTTTAACA

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

```
101  CCACGGAGAG AGTCCTTCAG GGTCTGCTCA GGCCTGTGTT CAAGAACACC
151  AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGCCCAA
201  GAAGGATGGG GCAGCCACCA AAGTGGATGC CATCTGCACC TACCGCCCTG
251  ATCCCAAAAG CCCTGGACTG GACAGAGAGC AGCTATACTG GGAGCTGAGC
301  CAGCTAACCC ACAGCATCAC TGAGCTGGGC CCCTACACCC TGGACAGGGA
351  CAGTCTCTAT GTCAATGGTT TCACACAGCG GAGCTCTGTG CCCACCACTA
401  GCATTCCTGG GACCCCCACA GTGGACCTGG GAACATCTGG GACTCCAGTT
451  TCTAAACCTG GTCCCTCG
```

(SEQ ID NO: 142)

```
  1  GCTGCCAGCC CTCTCCTGGT GCTATTCACT CTCAACTTCA CCATCACCAA
 51  CCTGCGGTAT GAGGAGAACA TGCAGCACCC TGGCTCCAGG AAGTTCAACA
101  CCACGGAGAG GGTCCTTCAG GGCCTGCTCA GGTCCCTGTT CAAGAGCACC
151  AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACTTTGC TCAGGCCTGA
201  AAAGGATGGG ACAGCCACTG GAGTGGATGC CATCTGCACC CACCACCCTG
251  ACCCCAAAAG CCCTAGGCTG GACAGAGAGC AGCTGTATTG GGAGCTGAGC
301  CAGCTGACCC ACAATATCAC TGAGCTGGGC CACTATGCCC TGGACAACGA
351  CAGCCTCTTT GTCAATGGTT TCACTCATCG GAGCTCTGTG TCCACCACCA
401  GCACTCCTGG GACCCCCACA GTGTATCTGG GAGCATCTAA GACTCCAGCC
451  TCGATATTTG GCCCTTCA
```

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

(SEQ ID NO: 143)

```
   1  GCTGCCAGCC ATCTCCTGAT ACTATTCACC CTCAACTTCA CCATCACTAA
  51  CCTGCGGTAT GAGGAGAACA TGTGGCCTGG CTCCAGGAAG TTCAACACTA
 101  CAGAGAGGGT CCTTCAGGGC CTGCTAAGGC CCTTGTTCAA GAACACCAGT
 151  GTTGGCCCTC TGTACTCTGG CTCCAGGCTG ACCTTGCTCA GGCCAGAGAA
 201  AGATGGGGAA GCCACCGGAG TGGATGCCAT CTGCACCCAC CGCCCTGACC
 251  CCACAGGCCC TGGGCTGGAC AGAGAGCAGC TGTATTTGGA GCTGAGCCAG
 301  CTGACCCACA GCATCACTGA GCTGGGCCCC TACACACTGG ACAGGGACAG
 351  TCTCTATGTC AATGGTTTCA CCCATCGGAG CTCTGTACCC ACCACCAGC
```

(SEQ ID NO: 144)

```
   1  ACCGGGGTGG TCAGCGAGGA GCCATTCACA CTGAACTTCA CCATCAACAA
  51  CCTGCGCTAC ATGGCGGACA TGGGCCAACC CGGCTCCCTC AAGTTCAACA
 101  TCACAGACAA CGTCATGAAG CACCTGCTCA GTCCTTTGTT CCAGAGGAGC
 151  AGCCTGGGTG CACGGTACAC AGGCTGCAGG GTCATCGCAC TAAGGTCTGT
 201  GAAGAACGGT GCTGAGACAC GGGTGGACCT CCTCTGCACC TACCTGCAGC
 251  CCCTCAGCGG CCCAGGTCTG CCTATCAAGC AGGTGTTCCA TGAGCTGAGC
 301  CAGCAGACCC ATGGCATCAC CCGGCTGGGC CCCTACTCTC TGGACAAAGA
 351  CAGCCTCTAC CTTAACGGTT ACAATGAACC TGGTCTAGAT GAGCCTCCTA
 401  CAACTCCCAA GCCAGCCACC ACATTCCTGC CTCCTCTGTC AGAAGCCACA
 451  ACA
```

TABLE 15-continued

CA125 Repeat Nucleotide Sequence
(SEQ ID NO: 83 thru SEQ ID NO: 145)

(SEQ ID NO: 145)

```
   1  GCCATGGGGT ACCACCTGAA GACCCTCACA CTCAACTTCA CCATCTCCAA
  51  TCTCCAGTAT TCACCAGATA TGGGCAAGGG CTCAGCTACA TTCAACTCCA
 101  CCGAGGGGGT CCTTCAGCAC CTGCTCAGAC CCTTGTTCCA GAAGAGCAGC
 151  ATGGGCCCCT TCTACTTGGG TTGCCAACTG ATCTCCCTCA GGCCTGAGAA
 201  GGATGGGGCA GCCACTGGTG TGGACACCAC CTGCACCTAC CACCCTGACC
 251  CTGTGGGCCC CGGGCTGGAC ATACAGCAGC TTTACTGGGA GCTGAGTCAG
 301  CTGACCCATG GTGTCACCCA ACTGGGCTTC TATGTCCTGG ACAGGGATAG
 351  CCTCTTCATC AATGGCTATG CACCCCAGAA TTTATCAATC CGGGGCGAGT
 401  ACCAGATAAA TTTCCACATT GTCAACTGGA ACCTCAGTAA TCCAGACCCC
 451  ACATCCTCAG AGTAC
```

TABLE 16

CA125 Repeat Domains
(SEQ ID NO: 146)

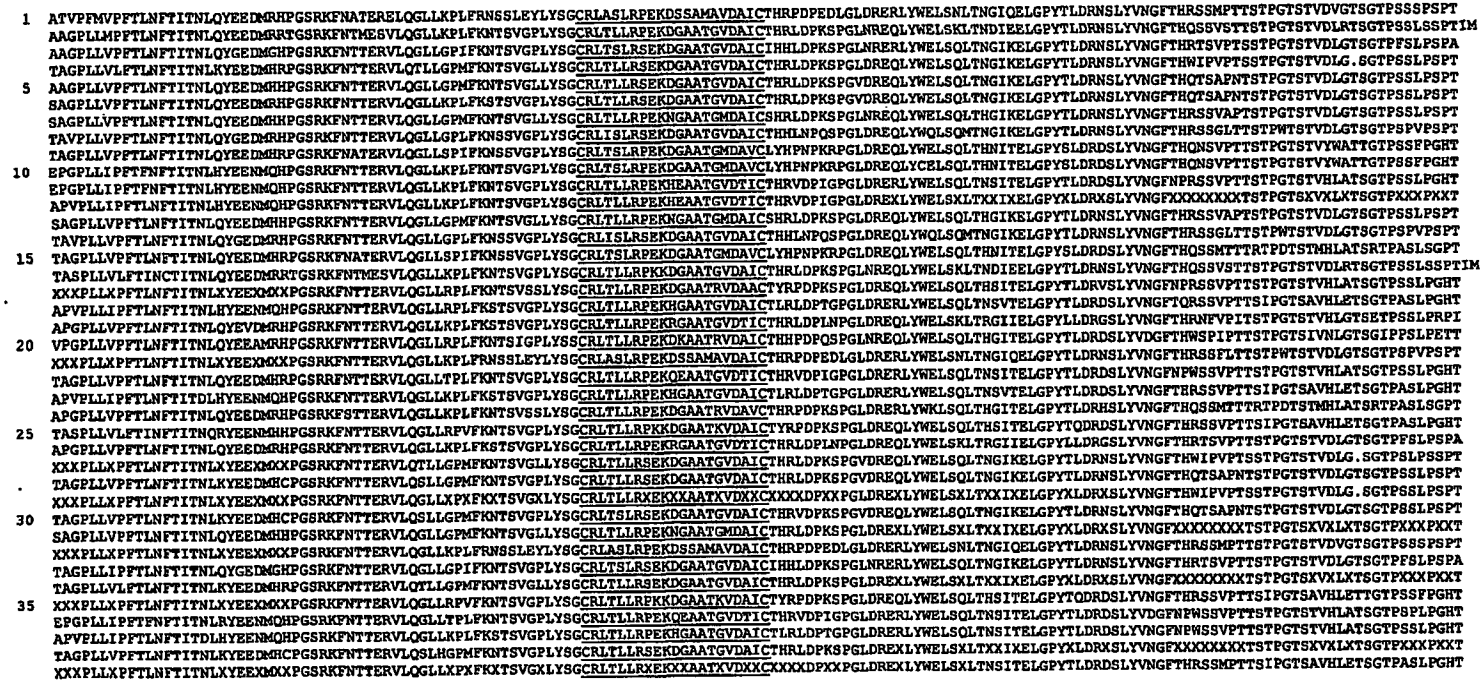

TABLE 16 - continued

CA125 Repeat Domains
(SEQ ID NO: 146)

```
40  APGPLLVPFTLNFTITNLQYEEDMRHPGSRKFNTTERVLQGLLKPLFKSTSVGPLYSGCRLTLLRPEKRGAATGVDTICTHRLDPLNPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFXXXXXXXXTSTPGTSKVXLXTSGTPXXXPXXT
    XXXPLLXPFTLNFTITNLXYEEXMXXPGSRKFNTTERVLQGLLXPXFKXTSVGXLYSGCRLTLLRXEKXXAATKVDXXCXXXXDPXXPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFHPRSSVPTTSTPGTSTVHLATSGTPSSLPGHT
    APVPLLIPFTLNFTITNLHYEENMQHPGSRKFNTTERVLQGLLGPMFKNTSVGLLYSGCRLTLLRPEKNGAATGMDAICSHRLDPKSPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFXXXXXXXXTSTPGTSKVXLXTSGTPXXXPXXT
    XXXPLLXPFTLNFTITNLXYEEXMXXPGSRKFNTTERVLQGLLXPXFKXTSVGXLYSGCRLTLLRXEKXXAATKVDXXCXXXXDPXXPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFTHQNSVPTTSTPGTSTVYWATTGTPSSFPGHT
    EPGPLLIPFTFNFTITNLHYEENMQHPGSRKFNTTERVLQGLLTPLFKNTSVGPLYSGCRLTLLRPEKQEAATGVDTICTHRVDPIGPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFXXXXXXXXTSTPGTSKVXLXTSGTPXXXPXXT
45  XXXPLLXPFTLNFTITNLXYEEXMXXPGSRKFNTTERVLQGLLXPXFKXTSVGXLYSGCRLTLLRXEKXXAATKVDXXCXXXXDPXXPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFTHRSSVPTTSSPGTSTVHLATSGTPSSLPGHT
    APVPLLIPFTLNFTITNLHYEENMQHPGSRKFNTTERVLQGLLKPLFKSTSVGPLYSGCRLTLLRPEKHGAATGVDAICTLRLDPTGPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFXXXXXXXXTSTPGTSKVXLXTSGTPXXXPXXT
    XXXPLLXPFTLNFTITNLXYEEXMXXPGSRKFNTTERVLQGLLXPXFKXTSVGXLYSGCRLTLLRXEKXXAATKVDXXCXXXXDPXXPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFTHRTSVPTTSTPGTSTVHLATSGTPSSLPGHT
    APVPLLIPFTLNFTITNLQYEEDMHRPGSRKFNTTERVLQGLLSPIFKNSSVGPLYSGCRLTSLRPEKDGAATGMDAVCLYHPNPKRPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFXXXXXXXXTSTPGTSKVXLXTSGTPXXXPXXT
    XXXPLLXPFTLNFTITNLXYEEXMXXPGSRKFNTTERVLQGLLXPXFKXTSVGXLYSGCRLTLLRXEKXXAATKVDXXCXXXXDPXXPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFTHWSSGLTTSTPWTSTVDLGTSGTPSPVPSPT
50  TAGPLLVPFTLNFTITNLQYEEDMHRPGSRKFNATERVLQGLLSPIFKNTSVGPLYSGCRLTLLRPEKQEAATGVDTICTHRVDPIGPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFXXXXXXXXTSTPGTSKVXLXTSGTPXXXPXXT
    XXXPLLXPFTLNFTITNLXYEEXMXXPGSRKFNTTERVLQGLLXPXFKXTSVGXLYSGCRLTLLRXEKXXAATKVDXXCXXXXDPXXPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFTHRSFGLTTSTPWTSTVDLGTSGTPSPVPSPT
    TAGPLLVPFTLNFTITNLQYEEDMHRPGSRKFNTTERVLQGLLTPLFRNTSVSSLYSGCRLTLLRPEKDGAATRVDAVCTHRPDPKSPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFXXXXXXXXTSTPGTSKVXLXTSGTPXXXPXXT
    XXXPLLXPFTLNFTITNLXYEEXMXXPGSRKFNTTERVLQGLLXPXFKXTSVGXLYSGCRLTLLRXEKXXAATKVDXXCXXXXDPXXPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFTHWIPVPTSSTPGTSTVDLG.SGTPSSLPSPT
    TAGPLLVPFTLNFTITNLQYGEDMGHPGSRKFNTTERVLQGLLGPIFKNTSVGPLYSGCRLTSLRSEKDGAATGVDAICIHHLDPKSPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFXXXXXXXXTSTPGTSKVXLXTSGTPXXXPXXT
55  XXXPLLXPFTLNFTITNLXYEEXMXXPGSRKFNTTERVLQGLLXPXFKXTSVGXLYSGCRLTLLRXEKXXAATKVDXXCXXXXDPXXPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFTHQTFAPNTSTPGTSTVDLGTSGTPSSLPSPT
    SAGPLLVPFTLNFTITNLQYEEDMHHPGSRKFNTTERVLQGLLGPMFKNTSVGLLYSGCRLTLLRPEKNGAATRVDAVCTHRPDPKSPGLDREKLYWELSXLTXXIXELGPYKLDRXSLYVNGFXXXXXXXXTSTPGTSKVXLXTSGTPXXXPXXT
    XXXPLLXPFTLNFTITNLXYEEXMXXPGSRKFNTTERVLQGLLKPLFKSTSVGPLYSGCRLTLLRPEKDGVATRVDAICTHRPDPKIPGLDRQQLYWELSQLTHSITELGPYTLDRDSLYVNGFTQRSSVPTTSTPGTFTVQPETSETPSSLPGPT
    ATGPVLLPFTLNFTITNLQYEEDMHRPGSRKFNTTERVLQGLLMPLFKNTSVSSLYSGCRLTLLRPEKDGAATRVDAVCTHRPDPKSPGLDRERLYWKLSQLTHGITELGPYTLDRHSLYVNGFTHQSSMTTTRTPDTSTMHLATSRTPASLSGPT
    TASPLLVLFTINFTITNLRYEENMHHPGSRKFNTTERVLQGLLRPVFKNTSVGPLYSGCRLTLLRPKKDGAATKVDAICTYRPDPKSPGLDREQLYWELSQLTHSITELGPYTQDRDSLYNVGFTQRSSVPTTSVPGTPTVDLGTSGTPVSKPGPS
60  AASPLLVLFTLNGTITNLRYEENMQHPGSRKFNTTERVLQGLLRSLFKSTSVGPLYSGCRLTLLRPEKDGTATGVDAICTHRPDPKSPRLDREQLYWELSQLTHNITELGHYALDNDSLFVNGFTHRSSVSTTSTPGTPTVYLGASKTPASIPGPS
    AASHLLILFTLNFTITNLRYEENMW.PGSRKFNTTERVLQGLLRPLFKNTSVGPLYSGSRLTLLRPEKDGEATGVDAICTHRPDPTGPGLDREQLYLELSQLTHSITELGPYTLDRDSLYVNGFTHRSSVPTTS.....................
    TGVVSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVMKHLLSPLFQRSSLGARYTGCRVIALRSVKNGAETRVDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNGYNEPGLDEPPTTPKPATTFLPPLSEATT.....
    AMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLLRPLFQKSSM.GPFYLGCQLISLRPEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTHGVTQLGFYVLDRDSLFINGYAPQNLSIRGEYQINFHIVNWNLSNPDPTSSEY
```

TABLE 17

Carboxy Terminal Nucleotide Sequence
(SEQ ID NO: 147)

```
   1  GCCATGGGGT ACCACCTGAA GACCCTCACA CTCAACTTCA CCATCTCCAA
  51  TCTCCAGTAT TCACCAGATA TGGGCAAGGG CTCAGCTACA TTCAACTCCA
 101  CCGAGGGGGT CCTTCAGCAC CTGCTCAGAC CCTTGTTCCA GAAGAGCAGC
 151  ATGGGCCCCT TCTACTTGGG TTGCCAACTG ATCTCCCTCA GGCCTGAGAA
 201  GGATGGGGCA GCCACTGGTG TGGACACCAC CTGCACCTAC CACCCTGACC
 251  CTGTGGGCCC CGGGCTGGAC ATACAGCAGC TTTACTGGGA GCTGAGTCAG
 301  CTGACCCATG GTGTCACCCA ACTGGGCTTC TATGTCCTGG ACAGGGATAG
 351  CCTCTTCATC AATGGCTATG CACCCCAGAA TTTATCAATC CGGGGCGAGT
 401  ACCAGATAAA TTTCCACATT GTCAACTGGA ACCTCAGTAA TCCAGACCCC
 451  ACATCCTCAG AGTACATCAC CCTGCTGAGG GACATCCAGG ACAAGGTCAC
 501  CACACTCTAC AAAGGCAGTC AACTACATGA CACATTCCGC TTCTGCCTGG
 551  TCACCAACTT GACGATGGAC TCCGTGTTGG TCACTGTCAA GGCATTGTTC
 601  TCCTCCAATT TGGACCCCAG CCTGGTGGAG CAAGTCTTTC TAGATAAGAC
 651  CCTGAATGCC TCATTCCATT GGCTGGGCTC CACCTACCAG TTGGTGGACA
 701  TCCATGTGAC AGAAATGGAG TCATCAGTTT ATCAACCAAC AAGCAGCTCC
 751  AGCACCCAGC ACTTCTACCT GAATTTCACC ATCACCAACC TACCATATTC
 801  CCAGGACAAA GCCCAGCCAG GCACCACCAA TTACCAGAGG AACAAAAGGA
 851  ATATTGAGGA TGCGCTCAAC CAACTCTTCC GAAACAGCAG CATCAAGAGT
901 TATTTTTCTG ACTGTCAAGT TTCAACATTC AGGTCTGTCC CCAACAGGCA
```

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TABLE 17-continued

Carboxy Terminal Nucleotide Sequence (SEQ ID NO: 147)	
951	CCACACCGGG GTGGACTCCC TGTGTAACTT CTCGCCACTG GCTCGGAGAG *
1001	TAGACAGAGT TGCCATCTAT GAGGAATTTC TGCGGATGAC CCGGAATGGT
1051	ACCCAGCTGC AGAACTTCAC CCTGGACAGG AGCAGTGTCC TTGTGGATGG
1101	GTATTCTCCC AACAGAAATG AGCCCTTAAC TGGGAATTCT GACCTTCCCT
1151	TCTGGGCTGT CATCCTCATC GGCTTGGCAG GACTCCTGGG ACTCATCACA
1201	TGCCTGATCT GCGGTGTCCT GGTGACCACC CGCCGGCGGA AGAAGGAAGG
1251	AGAATACAAC GTCCAGCAAC AGTGCCCAGG CTACTACCAG TCACACCTAG
1301	ACCTGGAGGA TCTGCAATGA CTGGAACTTG CCGGTGCCTG GGGTGCCTTT
1351	CCCCCAGCCA GGGTCCAAAG AAGCTTGGCT GGGGCAGAAA TAAACCATAT
1401	TGGTCGGAAA AAAAAAAAAA AA

TABLE 18

Carboxy Terminal Amino Acid Sequence
(SEQ ID NO: 148)

```
  1  AMGYHLKTLT LNFTISNLQY SPDMGKGSAT FNSTEGVLQH LLRPLFQKSS
 51  MGPFYLGCQL ISLRPEKDGA ATGVDTTCTY HPDPVGPGLD IQQLYWELSQ
101  LTHGVTQLGF YVLDRDSLFI NGYAPQNLSI RGEYQINFHI VNWNLSNPDP
151  TSSEYITLLR DIQDKVTTLY KGSQLHDTFR FCLVTNLTMD SVLVTVKALF
201  SSNLDPSLVE QVFLDKTLNA SFHWLGSTYQ LVDIHVTEME SSVYQPTSSS
251  STQHFYLNFT ITNLPYSQDK AQPGTTNYQR NKRNIEDALN QLFRNSSIKS
301  YFSDCQVSTF RSVPNRHHTG VDSLCNFSPL ARRVDRVAIY EEFLRMTRNG
351  TQLQNFTLDR SSVLVDGYSP NRNEPLTGNS DLPFWAVILI GLAGLLGLIT
401  CLICGVLVTT RRRKKEGEYN VQQQCPGYYQ SHLDLEDLQ
```

TABLE 19A

Serine/Threonine O-glycosylation Pattern Predicted for the Amino Terminal End of the CA125 Molecule (SEQ ID NO: 149)

SEQ ID NO: 149 Length: 1799

```
RTDGIMEHITKIPNEAAHRGTIRPVKGPQTSTSPASPKGLHTGGTKRMETTTTALKTTTTALKTTSRATLTTSVYTPTLG   80
TLTPLNASRQMASTILTEMMITTPYVFPDVPETTSSLATSLGAETSTALPRTTPSVLNRESETTASLVSRSGAERSPVIQ  160
TLDVSSSEPDTTASWVIHPAETIPTVSKTTPNFFHSELDTVSSTATSHGADVSSAIPTNISPSELDALTPLVTISGTDTS  240
TTFPTLTKSPHETETRTTWLTHPAETSSTIPRTIPNFSHHESDATPSIATSPGAETSSAIPIMTVSPGAEDLVTSQVTSS  320
GTDRNMTIPTLTLSPGEPKTIASLVTHPEAQTSSAIPTSTISPAVSRLVTSMVTSLAAKTSTTNRALTNSPGEPATTVSL  400
VTHPAQTSPTVPWTTSIFFHSKSDTTPSMTTSHGAESSSAVPTPTVSTEVPGVVTPLVTSSRAVISTTIPILTLSPGEPE  480
TTPSMATSHGEEASSAIPTPTVSPGVPGVVTSLVTSSRAVTSTTIPILTFSLGEPETTPSMATSHGTEAGSAVPTVLPEV  560
PGMVTSLVASSRAVTSTTLPTLTLSPGEPETTPSMATSHGAEASSTVPTVSPEVPGVVTSLVTSSSGVNSTSIPTLILSP  640
GELETTPSMATSHGAEASSAVPTPTVSPGVSGVVTPLVTSSRAVTSTTIPILTLSSSEPETTPSMATSHGVEASSAVLTV  720
SPEVPGMVTSLVTSSRAVTSTTIPTLTISSDEPETTTSLVTHSEAKMISAIPTLAVSPTVQGLVTSLVTSSGSETSAFSN  800
LTVASSQPETIDSWVAHPGTEASSVVPTLTVSTGEPFTNISLVTHPAESSSTLPRTTSRFSHSELDTMPSTVTSPEAESS  880
SAISTTISPGIPGVLTSLVTSSGRDISATFPTVPESPHESEATASWVTHPAVTSTTVPRTTPNYSHSEPDTTPSIATSPG  960
AEATSDFPTITVSPDVPDMVTSQVTSSGTDTSITIPTLTLSSGEPETTTSFITYSETHTSSAIPTLPVSPGASKMLTSLV 1040
ISSGTDSTTTFPTLTETPYEPETTAIQLIHPAETNTMVPRTTPKFSHSKSDTTLPVAITSPGPEASSAVSTTTISPDMSD 1120
LVTSLVPSSGTDTSTTFPTLSETPYEPETTATWLTHPAETSTTVSGTIPNFSHRGSDTAPSMVTSPGVDTRSGVPTTTIP 1200
PSIPGVVTSQVTSSATDTSTAIPTLTPSPGEPETTASSATHPGTQTGFTVPIRTVPSSEPDTMASWVTHPPQTSTPVSRT 1280
TSSFSHSSPDATPVMATSPRTEASSAVLTTISPGAPEMVTSQITSSGAATSTTVPTLTHSPGMPETTALLSTHPRTETSK 1360
TFPASTVFPQVSETTASLTIRPGAETSTALPTQTTSSLFTLLVTGTSRVDLSPTASPGVSAKTAPLSTHPGTETSTMIPT 1440
STLSLGLLETTGLLATSSSAETSTSTLTLTVSPAVSGLSSASITTDKPQTVTSWNTETSPSVTSVGPPEFSRTVTGTTMT 1520
LIPSEMPTPPKTSHGEGVSPTTILRTTMVEATNLATTGSSPTVAKTTTTFNTLAGSLFTPLTTPGMSTLASESVTSRTSY 1600
NHRSWISTTSSYNRRYWTPATSTPVTSTFSPGISTSSIPSSTAATVPFMVPFTLNFTITNLQYEEDMRHPGSRKFNATER 1680
ELQGLLKPLFRNSSLEYLYSGCRLASLRPEKDSSAMAVDAICTHRPDPEDLGLDRERLYWELSNLTNGIQELGPYTLDRN 1760
SLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTPSSSPSPT
```

TABLE 19B

```
.....T.....TSTS.....TTT....TTTT...TT.....TT...T....   80
.....ST....TT.....                                    160
.....S.....T.....T.S.....T.....S.....S.....S.T..S     240
T...T.T.....TSS....T.....S..T.S..TS.....S.....T.....T...TS.  320
.....T.S.....T..S.....TSS...TST.....T.....STT....T.S.....TT.S.  400
.T....TS.T...T.....S..T...TTS....SSS...T.T.ST.....T.....T.S.....  480
TT.S..T.....SS...T.T.S.....S.....T.....T.S..TS.....S...T.....  560
.....T.....T.S.....TT.S..TS.....SST..T.S.....TS.S....T.....  640
.....T.S..T.....SS...T.T.S...S.....S.....T.....T.SSS....T.S..TS.....S.....  720
S.....S.....STT..T.T.SS.....TT.....S.....T.....  800
....S.....SS.....T.....T....SSS....T.....ST.T.....S  880
S...TT.S.....S....T.....S..T....T....TSTT...TT...S.S....T.S..TS..  960
...TS.....T.....T...TS.....T.T.SS.....T....T.....T.S...T.....  1040
.S..T.STTT..T.T.T.....T....TT.....S.....S.....SS....TT.....  1120
.....S..T..STT..T.S.T.....TT....T.....ST.....TS.....S....TT..  1200
.S.....T...TS..T.TST...T.T.S.....TT.SS.T.....T..SS...T..S..T....TST..S.T  1280
TSS.S.SS...T....TS..T..SS....T.S.....T...TS....TSTT....T.S.....ST...T..S.  1360
....ST.....S.TT...T.....ST...T.TT.S.....T.S...S.....ST...T..ST...T  1440
ST.....T..S..TSTS....T.....S..S..S..T....T.TS..T..S.S.TS.....S.....T  1520
```

TABLE 19B-continued

Serine/Threonine O-glycosylation Pattern Predicted for the Amino Terminal End of the CA125 Molecule

...S...T....S.....T.....TT.SS.T.....T...ST..S.....	1600
.....TST..TST.S...STSS..SST.....	1680
.....	1760
.....TTST...ST....TS.T.SSS.S.T	

TABLE 20

Nucleotide and Amino Acid Sequences of Recombinant CA125 Repeat Showing Peptides (Underlined 1-4) which are Antigenically Matched for Immune Stimulation of Patients with the HLA-2 Histocompatibility Subtype

CA 125 Recombinant Nucleotide and Amino Acid Sequences (SEQ ID NO: 151 and SEQ ID NO: 152, respectively) CA 125 Recombinant Nucleotide (Anti-Sense Strand) Sequence (SEQ ID NO: 153) Peptide 1 (SEQ ID NO: 154); Peptide 2 (SEQ ID NO: 155); Peptide 3 (SEQ ID NO: 156) and Peptide 4 (SEQ ID NO: 157)

```
   ATGAGAGGATCGCATCACCATCACCATCACGGATCCATGGGCCACACAGAGCCTGGCCCT
 1 ---------+---------+---------+---------+---------+---------+ 60
   TACTCTCCTAGCGTAGTGGTAGTGGTAGTGCCTAGGTACCCGGTGTGTCTCGGACCGGGA

   M  R  G  S  H  H  H  H  H  H  G  S  M  G  H  T  E  P  G  P  -
                                                   ↑
   CTCCTGATACCATTCACTTTCAACTTTACCATCACCAACCTGCATTATGAGGAAAACATG
61 ---------+---------+---------+---------+---------+---------+ 120
   GAGGACTATGGTAAGTGAAAGTTGAAATGGTAGTGGTTGGACGTAATACTCCTTTTGTAC

   L  L  I  P  F  T  F  N  F  T  I  T  N  L  H  Y  E  E  N  M  -

   CAACACCCTGGTTCCAGGAAGTTCAACACCACGGAGAGGGTTCTGCAGGGTCTGCTCAAG
121 ---------+---------+---------+---------+---------+---------+ 180
   GTTGTGGGACCAAGGTCCTTCAAGTTGTGGTGCCTCTCCCAAGACGTCCCAGACGAGTTC
                                                3
   Q  H  P  G  S  R  K  F  N  T  T  E  R  V  L  Q  G  L  L  K  -

   CCCTTGTTCAAGAACACCAGTGTTGGCCCTCTGTACTCTGGCTGCAGACTGACCTTGCTC
181 ---------+---------+---------+---------+---------+---------+ 240
   GGGAACAAGTTCTTGTGGTCACAACCGGGAGACATGAGACCGACGTCTGACTGGAACGAG

   P  L  F  K  N  T  S  V  G  P  L  Y  S  G  C  R  L  T  L  L  -

   AGACCTGAGAAGCATGAGGCAGCCACTGGAGTGGACACCATCTGTACCCACCGCGTTGAT
241 ---------+---------+---------+---------+---------+---------+ 300
   TCTGGACTCTTCGTACTCCGTCGGTGACCTCACCTGTGGTAGACATGGGTGGCGCAACTA

   R  P  E  K  H  E  A  A  T  G  V  D  T  I  C  T  H  R  V  D  -

   CCCATCGGACCTGGACTGGACAGAGAGCGGCTATACTGGGAGCTGAGCCAGCTGACCAAC
301 ---------+---------+---------+---------+---------+---------+ 360
   GGGTAGCCTGGACCTGACCTGTCTCTCGCCGATATGACCCTCGACTCGGTCGACTGGTTG
                                1                   4
   P  I  G  P  G  L  D  R  E  R  L  Y  W  E  L  S  Q  L  T  N  -

   AGCATCACAGAGCTGGGACCCTACACCCTGGACAGGGACAGTCTCTATGTCAATGGCTTC
361 ---------+---------+---------+---------+---------+---------+ 420
   TCGTAGTGTCTCGACCCTGGGATGTGGGACCTGTCCCTGTCAGAGATACAGTTACCGAAG
```

TABLE 20 (continued)

Nucleotide and Amino Acid Sequences of Recombinant CA125 Repeat Showing Peptides (Underlined 1-4) which are Antigenically Matched for Immune Stimulation of Patients with the HLA-2 Histocompatibility Subtype

CA 125 Recombinant Nucleotide and Amino Acid Sequences
(SEQ ID NO: 151 and SEQ ID NO: 152, respectively)
CA 125 Recombinant Nucleotide (Anti-Sense Strand) Sequence (SEQ ID NO: 153)
Peptide 1 (SEQ ID NO: 154); Peptide 2 (SEQ ID NO: 155);
Peptide 3 (SEQ ID NO: 156) and Peptide 4 (SEQ ID NO: 157)

```
                                    2
    S  I  T  E  L  G  P  Y  T  L  D  R  D  S  L  Y  V  N  G  F  -

    AACCCTCGGAGCTCTGTGCCAACCACCAGCACTCCTGGGACCTCCACAGTGCACCTGGCA
421 ---------+---------+---------+---------+---------+---------+ 480
    TTGGGAGCCTCGAGACACGGTTGGTGGTCGTGAGGACCCTGGAGGTGTCACGTGGACCGT

    N  P  R  S  S  V  P  T  T  S  T  P  G  T  S  T  V  H  L  A  -

    ACCTCTGGGACTCCATCCTCCCTGCCT
481 ---------+---------+------- 507
    TGGAGACCCTGAGGTAGGAGGGACGGA

    T  S  G  T  P  S  S  L  P  -
```

(SEQ ID NO: 154)
Peptide 1 R L Y W E L S Q L

(SEQ ID NO: 155)
Peptide 2 T L D R D S L Y V

(SEQ ID NO: 156)
Peptide 3 V L Q G L L K P L

(SEQ ID NO: 157)
Peptide 4 Q L T N S I T E L

TABLE 21

CA125 Protein Sequence

(SEQ ID NO: 162)

```
   1  MEHITKIPNE AAHRGTIRPV KGPQTSTSPA SPKGLHTGGT KRMETTTTAL
  51  KTTTTALKTT SRATLTTSVY TPTLGTLTPL NASRQMASTI LTEMMITTPY
 101  VFPDVPETTS SLATSLGAET STALPRTTPS VLNRESETTA SLVSRSGAER
 151  SPVIQTLDVS SSEPDTTASW VIHPAETIPT VSKTTPNFFH SELDTVSSTA
 201  TSHGADVSSA IPTNISPSEL DALTPLVTIS GTDTSTTFPT LTKSPHETET
 251  RTTWLTHPAE TSSTIPRTIP NFSHHESDAT PSIATSPGAE TSSAIPIMTV
 301  SPGAEDLVTS QVTSSGTDRN MTIPTLTLSP GEPKTIASLV THPEAQTSSA
 351  IPTSTISPAV SRLVTSMVTS LAAKTSTTNR ALTNSPGEPA TTVSLVTHPA
 401  QTSPTVPWTT SIFFHSKSDT TPSMTTSHGA ESSSAVPTPT VSTEVPGVVT
 451  PLVTSSRAVI STTIPILTLS PGEPETTPSM ATSHGEEASS AIPTPTVSPG
 501  VPGVVTSLVT SSRAVTSTTI PILTFSLGEP ETTPSMATSH GTEAGSAVPT
 551  VLPEVPGMVT SLVASSRAVT STTLPTLTLS PGEPETTPSM ATSHGAEASS
 601  TVPTVSPEVP GVVTSLVTSS SGVNSTSIPT LILSPGELET TPSMATSHGA
 651  EASSAVPTPT VSPGVSGVVT PLVTSSRAVT STTIPILTLS SSEPETTPSM
 701  ATSHGVEASS AVLTVSPEVP GMVTSLVTSS RAVTSTTIPT LTISSDEPET
 751  TTSLVTHSEA KMISAIPTLA VSPTVQGLVT SLVTSSGSET SAFSNLTVAS
 801  SQPETIDSWV AHPGTEASSV VPTLTVSTGE PFTNISLVTH PAESSSTLPR
 851  TTSRFSHSEL DTMPSTVTSP EAESSSAIST TISPGIPGVL TSLVTSSGRD
 901  ISATFPTVPE SPHESEATAS WVTHPAVTST TVPRTTPNYS HSEPDTTPSI
 951  ATSPGAEATS DFPTITVSPD VPDMVTSQVT SSGTDTSITI PTLTLSSGEP
1001  ETTTSFITYS ETHTSSAIPT LPVSPGASKM LTSLVISSGT DSTTTFPTLT
1051  ETPYEPETTA IQLIHPAETN TMVPRTTPKF SHSKSDTTLP VAITSPGPEA
1101  SSAVSTTTIS PDMSDLVTSL VPSSGTDTST TFPTLSETPY EPETTATWLT
1151  HPAETSTTVS GTIPNFSHRG SDTAPSMVTS PGVDTRSGVP TTTIPPSIPG
1201  VVTSQVTSSA TDTSTAIPTL TPSPGEPETT ASSATHPGTQ TGFTVPIRTV
1251  PSSEPDTMAS WVTHPPQTST PVSRTTSSFS HSSPDATPVM ATSPRTEASS
1301  AVLTTISPGA PEMVTSQITS SGAATSTTVP TLTHSPGMPE TTALLSTHPR
1351  TETSKTFPAS TVFPQVSETT ASLTIRPGAE TSTALPTQTT SSLFTLLVTG
1401  TSRVDLSPTA SPGVSAKTAP LSTHPGTETS TMIPTSTLSL GLLETTGLLA
1451  TSSSAETSTS TLTLTVSPAV SGLSSASITT DKPQTVTSWN TETSPSVTSV
1501  GPPEFSRTVT GTTMTLIPSE MPTPPKTSHG EGVSPTTILR TTMVEATNLA
1551  TTGSSPTVAK TTTTFNTLAG SLFTPLTTPG MSTLASESVT SRTSYNHRSW
1601  ISTTSSYNRR YWTPATSTPV TSTFSPGIST SSIPSSTA
```

Amino Terminal Domain

TABLE 21 - continued

CA125 Protein Sequence

(SEQ ID NO: 162)

```
                                                                AT VPFMVPFTLN
1651  FTITNLQYEE DMRHPGSRKF NATERELQGL LKPLFRNSSL EYLYSGCRLA
1701  SLRPEKDSSA MAVDAICTHR PDPEDLGLDR ERLYWELSNL TNGIQELGPY
1751  TLDRNSLYVN GFTHRSSMPT TSTPGTSTVD VGTSGTPSSS PSPTAAGPLL
1801  MPFTLNFTIT NLQYEEDMRR TGSRKFNTME SVLQGLLKPL FKNTSVGPLY
1851  SGCRLTLLRP EKDGAATGVD AICTHRLDPK SPGLNREQLY WELSKLTNDI
1901  EELGPYTLDR NSLYVNGFTH QSSVSTTSTP GTSTVDLRTS GTPSSLSSPT
1951  IMAAGPLLVP FTLNFTITNL QYGEDMGHPG SRKFNTTERV LQGLLGPIFK
2001  NTSVGPLYSG CRLTSLRSEK DGAATGVDAI CIHHLDPKSP GLNRERLYWE
2051  LSQLTNGIKE LGPYTLDRNS LYVNGFTHRT SVPTSSTPGT STVDLGTSGT
2101  PFSLPSPATA GPLLVLFTLN FTITNLKYEE DMHRPGSRKF NTTERVLQTL
2151  LGPMFKNTSV GLLYSGCRLT LLRSEKDGAA TGVDAICTHR LDPKSPGLDR
2201  EQLYWELSQL TNGIKELGPY TLDRNSLYVN GFTHWIPVPT SSTPGTSTVD
2251  LGSGTPSSLP SPTAAGPLLV PFTLNFTITN LQYEEDMHHP GSRKFNTTER
2301  VLQGLLGPMF KNTSVGLLYS GCRLTLLRSE KDGAATGVDA ICTHRLDPKS
2351  PGVDREQLYW ELSQLTNGIK ELGPYTLDRN SLYVNGFTHQ TSAPNTSTPG
2401  TSTVDLGTSG TPSSLPSPTS AGPLLVPFTL NFTITNLQYE EDMRHPGSRK
2451  FNTTERVLQG LLKPLFKSTS VGPLYSGCRL TLLRSEKDGA ATGVDAICTH
2501  RLDPKSPGVD REQLYWELSQ LTNGIKELGP YTLDRNSLYV NGFTHQTSAP
2551  NTSTPGTSTV DLGTSGTPSS LPSPTSAGPL LVPFTLNFTI TNLQYEEDMH
2601  HPGSRKFNTT ERVLQGLLGP MFKNTSVGLL YSGCRLTLLR PEKNGAATGM
2651  DAICSHRLDP KSPGLNREQL YWELSQLTHG IKELGPYTLD RNSLYVNGFT
2701  HRSSVAPTST PGTSTVDLGT SGTPSSLPSP TTAVPLLVPF TLNFTITNLQ
2751  YGEDMRHPGS RKFNTTERVL QGLLGPLFKN SSVGPLYSGC RLISLRSEKD
2801  GAATGVDAIC THHLNPQSPG LDREQLYWQL SQMTNGIKEL GPYTLDRNSL
2851  YVNGFTHRSS GLTTSTPWTS TVDLGTSGTP SPVPSPTTAG PLLVPFTLNF
2901  TITNLQYEED MHRPGSRKFN ATERVLQGLL SPIFKNSSVG PLYSGCRLTS
2951  LRPEKDGAAT GMDAVCLYHP NPKRPGLDRE QLYWELSQLT HNITELGPYS
3001  LDRDSLYVNG FTHQNSVPTT STPGTSTVYW ATTGTPSSFP GHTEPGPLLI
3051  PFTFNFTITN LHYEENMQHP GSRKFNTTER VLQGLLKPLF KNTSVGPLYS
3101  GCRLTSLRPE KDGAATGMDA VCLYHPNPKR PGLDREQLYC ELSQLTHNIT
3151  ELGPYSLDRD SLYVNGFTHQ NSVPTTSTPG TSTVYWATTG TPSSFPGHTE
3201  PGPLLIPFTF NFTITNLHYE ENMQHPGSRK FNTTERVLQG LLKPLFKNTS
3251  VGPLYSGCRL TLLRPEKHEA ATGVDTICTH RVDPIGPGLD RERLYWELSQ
3301  LTNSITELGP YTLDRDSLYV NGFNPRSSVP TTSTPGTSTV HLATSGTPSS
3351  LPGHTAPVPL LIPFTLNFTI TNLHYEENMQ HPGSRKFNTT ERVLQGLLKP
3401  LFKNTSVGPL YSGCRLTLLR PEKHEAATGV DTICTHRVDP IGPGLDREXL
3451  YWELSXLTXX IXELGPYXLD RXSLYVNGFX XXXXXXXTST PGTSXVXLXT
3501  SGTPXXXPXX TSAGPLLVPF TLNFTITNLQ YEEDMHHPGS RKFNTTERVL
3551  QGLLGPMFKN TSVGLLYSGC RLTLLRPEKN GAATGMDAIC SHRLDPKSPG
3601  LDREQLYWEL SQLTHGIKEL GPYTLDRNSL YVNGFTHRSS VAPTSTPGTS
```

Repeat Domain

TABLE 21 - continued

CA125 Protein Sequence

(SEQ ID NO: 162)

3651	TVDLGTSGTP SSLPSPTTAV PLLVPFTLNF TITNLQYGED MRHPGSRKFN	
3701	TTERVLQGLL GPLFKNSSVG PLYSGCRLIS LRSEKDGAAT GVDAICTHHL	
3751	NPQSPGLDRE QLYWQLSQMT NGIKELGPYT LDRNSLYVNG FTHRSSGLTT	
3801	STPWTSTVDL GTSGTPSPVP SPTTAGPLLV PFTLNFTITN LQYEEDMHRP	
3851	GSRKFNATER VLQGLLSPIF KNSSVGPLYS GCRLTSLRPE KDGAATGMDA	
3901	VCLYHPNPKR PGLDREQLYW ELSQLTHNIT ELGPYSLDRD SLYVNGFTHQ	
3951	SSMTTTRTPD TSTMHLATSR TPASLSGPTT ASPLLVLFTI NCTITNLQYE	
4001	EDMRRTGSRK FNTMESVLQG LLKPLFKNTS VGPLYSGCRL TLLRPKKDGA	
4051	ATGVDAICTH RLDPKSPGLN REQLYWELSK LTNDIEELGP YTLDRNSLYV	
4101	NGFTHQSSVS TTSTPGTSTV DLRTSGTPSS LSSPTIMXXX PLLXPFTLNF	
4151	TITNLXYEEX MXXPGSRKFN TTERVLQGLL RPLFKNTSVS SLYSGCRLTL	
4201	LRPEKDGAAT RVDAACTYRP DPKSPGLDRE QLYWELSQLT HSITELGPYT	
4251	LDRVSLYVNG FNPRSSVPTT STPGTSTVHL ATSGTPSSLP GHTXX XPLL	
4301	XPFTLNFTIT NLXYEEXMXX PGSRKFNTTE RVLQGLLKPL FRNSSLEYLY	
4351	SGCRLASLRP EKDSSAMAVD AICTHRPDPE DLGLDRERLY WELSNLTNGI	
4401	QELGPYTLDR NSLYVNGFTH RSSFLTTSTP WTSTVDLGTS GTPSPVPSPT	
4451	TAGPLLVPFT LNFTITNLQY EEDMHRPGSR RFNTTERVLQ GLLTPLFKNT	
4501	SVGPLYSGCR LTLLRPEKQE AATGVDTICT HRVDPIGPGL DRERLYWELS	
4551	QLTNSITELG PYTLDRDSLY VNGFNPWSSV PTTSTPGTST VHLATSGTPS	
4601	SLPGHTAPVP LLIPFTLNFT ITDLHYEENM QHPGSRKFNT TERVLQGLLK	
4651	PLFKSTSVGP LYSGCRLTLL RPEKHGAATG VDAICTLRLD PTGPGLDRER	
4701	LYWELSQLTN SVTELGPYTL DRDSLYVNGF THRSSVPTTS IPGTSAVHLE	
4751	TSGTPASLPG HTAPGPLLVP FTLNFTITNL QYEEDMRHPG SRKFSTTERV	
4801	LQGLLKPLFK NTSVSSLYSG CRLTLLRPEK DGAATRVDAV CTHRPDPKSP	
4851	GLDRERLYWK LSQLTHGITE LGPYTLDRHS LYVNGFTHQS SMTTTRTPDT	R
4901	STMHLATSRT PASLSGPTTA SPLLVLFTIN FTITNQRYEE NMHHPGSRKF	e
4951	NTTERVLQGL LRPVFKNTSV GPLYSGCRLT LLRPKKDGAA TKVDAICTYR	p
5001	PDPKSPGLDR EQLYWELSQL THSITELGPY TQDRDSLYVN GFTHRSSVPT	e
5051	TSIPGTSAVH LETSGTPASL PGHTAPGPLL VPFTLNFTIT NLQYEEDMRH	a
5101	PGSRKFNTTE RVLQGLLKPL FKSTSVGPLY SGCRLTLLRP EKRGAATGVD	t
5151	TICTHRLDPL NPGLDREQLY WELSKLTRGI IELGPYLLDR GSLYVNGFTH	
5201	RTSVPTTSTP GTSTVDLGTS GTPFSLPSPA XXXPLLXPFT LNFTITNLXY	D
5201	EEXMXXPGSR KFNTTERVLQ TLLGPMFKNT SVGLLYSGCR LTLLRSEKDG	o
5251	AATGVDAICT HRLDPKSPGV DREQLYWELS QLTNGIKELG PYTLDRNSLY	m
5301	VNGFTHWIPV PTSSTPGTST VDLGSGTPSL PSSPTTAGPL LVPFTLNFTI	a
5351	TNLKYEEDMH CPGSRKFNTT ERVLQSLLGP MFKNTSVGPL YSGCRLTLLR	i
5401	SEKDGAATGV DAICTHRLDP KSPGVDREQL YWELSQLTNG IKELGPYTLD	n
5451	RNSLYVNGFT HQTSAPNTST PGTSTVDLGT SGTPSSLPSP TXXXPLLXPF	
5501	TLNFTITNLX YEEXMXXPGS RKFNTTERVL QGLLXPXFKX TSVGXLYSGC	
5551	RLTLLRXEKX XAATXVDXXC XXXXDPXXPG LDREXLYWEL SXLTXXIXEL	
5601	GPYXLDRXSL YVNGFTHWIP VPTSSTPGTS TVDLGSGTPS SLPSPTTAGP	
5651	LLVPFTLNFT ITNLKYEEDM HCPGSRKFNT TERVLQSLLG PMFKNTSVGP	

TABLE 21 - continued

CA125 Protein Sequence

(SEQ ID NO: 162)

```
5701  LYSGCRLTSL RSEKDGAATG VDAICTHRVD PKSPGVDREQ LYWELSQLTN
5751  GIKELGPYTL DRNSLYVNGF THQTSAPNTS TPGTSTVDLG TSGTPSSLPS
5801  PTSAGPLLVP FTLNFTITNL QYEEDMHHPG SRKFNTTERV LQGLLGPMFK
5851  NTSVGLLYSG CRLTLLRPEK NGAATGMDAI CTHRLDPKSP GLDREXLYWE
5901  LSXLTXXIXE LGPYXLDRXS LYVNGFXXXX XXXXTSTPGT SXVXLXTSGT
5951  PXXXPXXTXX XPLLXPFTLN FTITNLXYEE XMXXPGSRKF NTTERVLQGL
6001  LKPLFRNSSL EYLYSGCRLA SLRPEKDSSA MAVDAICTHR PDPEDLGLDR
6051  ERLYWELSNL TNGIQELGPY TLDRNSLYVN GFTHRSSMPT TSTPGTSTVD
6101  VGTSGTPSSS PSPTTAGPLL IPFTLNFTIT NLQYGEDMGH PGSRKFNTTE
6151  RVLQGLLGPI FKNTSVGPLY SGCRLTSLRS EKDGAATGVD AICIHHLDPK
6201  SPGLNRERLY WELSQLTNGI KELGPYTLDR NSLYVNGFTH RTSVPTTSTP
6251  GTSTVDLGTS GTPFSLPSPA TAGPLLVLFT LNFTITNLKY EEDMHRPGSR
6301  KFNTTERVLQ TLLGPMFKNT SVGLLYSGCR LTLLRSEKDG AATGVDAICT
6351  HRLDPKSPGL DREXLYWELS XLTXXIXELG PYXLDRXSLY VNGFXXXXXX
6401  XXTSTPGTSX VXLXTSGTPX XXPXXTXXXP LLXPFTLNFT ITNLXYEEXM
6451  XXPGSRKFNT TERVLQGLLR PVFKNTSVGP LYSGCRLTLL RPKKDGAATK
6501  VDAICTYRPD PKSPGLDREQ LYWELSQLTH SITELGPYTQ DRDSLYVNGF
6551  THRSSVPTTS IPGTSAVHLE TTGTPSSFPG HTEPGPLLIP FTFNFTITNL
6601  RYEENMQHPG SRKFNTTERV LQGLLTPLFK NTSVGPLYSG CRLTLLRPEK
6651  QEAATGVDTI CTHRVDPIGP GLDRERLYWE LSQLTNSITE LGPYTLDRDS
6701  LYVDGFNPWS SVPTTSTPGT STVHLATSGT PSPLPGHTAP VPLLIPFTLN
6751  FTITDLHYEE NMQHPGSRKF NTTERVLQGL LKPLFKSTSV GPLYSGCRLT
6801  LLRPEKHGAA TGVDAICTLR LDPTGPGLDR ERLYWELSQL TNSITELGPY
6851  TLDRDSLYVN GFNPWSSVPT TSTPGTSTVH LATSGTPSSL PGHTTAGPLL
6901  VPFTLNFTIT NLKYEEDMHC PGSRKFNTTE RVLQSLHGPM FKNTSVGPLY
6951  SGCRLTLLRS EKDGAATGVD AICTHRLDPK SPGLDREXLY WELSXLTXXI
7001  XELGPYXLDR XSLYVNGFXX XXXXXXTSTP GTSXVXLXTS GTPXXXPXXT
7051  XXXPLLXPFT LNFTITNLXY EEXMXXPGSR KFNTTERVLQ GLLXPXFKXT
7101  SVGXLYSGCR LTLLRXEKXX AATXVDXXCX XXXDPXXPGL DREXLYWELS
7151  XLTNSITELG PYTLDRDSLY VNGFTHRSSM PTTSIPGTSA VHLETSGTPA
7201  SLPGHTAPGP LLVPFTLNFT ITNLQYEEDM RHPGSRKFNT TERVLQGLLK
7251  PLFKSTSVGP LYSGCRLTLL RPEKRGAATG VDTICTHRLD PLNPGLDREX
7301  LYWELSXLTX XIXELGPYXL DRXSLYVNGF XXXXXXXXTS TPGTSXVXLX
7351  TSGTPXXXPX XTXXXPLLXP FTLNFTITNL XYEEXMXXPG SRKFNTTERV
7401  LQGLLXPXFK XTSVGXLYSG CRLTLLRXEK XXAATXVDXX CXXXXDPXXP
7451  GLDREXLYWE LSXLTXXIXE LGPYXLDRXS LYVNGFHPRS SVPTTSTPGT
7501  STVHLATSGT PSSLPGHTAP VPLLIPFTLN FTITNLHYEE NMQHPGSRKF
7551  NTTERVLQGL LGPMFKNTSV GLLYSGCRLT LLRPEKNGAA TGMDAICSHR
7601  LDPKSPGLDR EXLYWELSXL TXXIXELGPY XLDRXSLYVN GFXXXXXXXX
7651  TSTPGTSXVX LXTSGTPXXX PXXTXXXPLL XPFTLNFTIT NLXYEEXMXX
7701  PGSRKFNTTE RVLQGLLXPX FKXTSVGXLY SGCRLTLLRX EKXXAATXVD
7751  XXCXXXXDPX XPGLDREXLY WELSXLTXXI XELGPYXLDR XSLYVNGFTH
```

Repeat Domain

TABLE 21 - continued

CA125 Protein Sequence

(SEQ ID NO: 162)

```
7801  QNSVPTTSTP GTSTVYWATT GTPSSFPGHT EPGPLLIPFT FNFTITNLHY
7851  EENMQHPGSR KFNTTERVLQ GLLTPLFKNT SVGPLYSGCR LTLLRPEKQE
7901  AATGVDTICT HRVDPIGPGL DREXLYWELS XLTXXIXELG PYXLDRXSLY
7951  VNGFXXXXXX XXTSTPGTSX VXLXTSGTPX XXPXXTXXXP LLXPFTLNFT
8001  ITNLXYEEXM XXPGSRKFNT TERVLQGLLX PXFKXTSVGX LYSGCRLTLL
8051  RXEKXXAATX VDXXCXXXXD PXXPGLDREX LYWELSXLTX XIXELGPYXL
8101  DRXSLYVNGF THRSSVPTTS SPGTSTVHLA TSGTPSSLPG HTAPVPLLIP
8151  FTLNFTITNL HYEENMQHPG SRKFNTTERV LQGLLKPLFK STSVGPLYSG
8201  CRLTLLRPEK HGAATGVDAI CTLRLDPTGP GLDREXLYWE LSXLTXXIXE
8251  LGPYXLDRXS LYVNGFXXXX XXXXTSTPGT SXVXLXTSGT PXXXPXXTXX
8301  XPLLXPFTLN FTITNLXYEE XMXXPGSRKF NTTERVLQGL LXPXFKXTSV
8351  GXLYSGCRLT LLRXEKXXAA TXVDXXCXXX XDPXXPGLDR EXLYWELSXL
8401  TXXIXELGPY XLDRXSLYVN GFTHRTSVPT TSTPGTSTVH LATSGTPSSL
8451  PGHTAPVPLL IPFTLNFTIT NLQYEEDMHR PGSRKFNTTE RVLQGLLSPI
8501  FKNSSVGPLY SGCRLTSLRP EKDGAATGMD AVCLYHPNPK RPGLDREQLY
8551  CELSQLTHNI TELGPYSLDR DSLYVNGFTH QNSVPTTSTP GTSTVYWATT
8601  GTPSSFPGHT XXXPLLXPFT LNFTITNLXY EEXMXXPGSR KFNTTERVLQ
8651  GLLXPXFKXT SVGXLYSGCR LTLLRXEKXX AATXVDXXCX XXXDPXXPGL
8701  DREXLYWELS XLTXXIXELG PYXLDRXSLY VNGFTHWSSG LTTSTPWTST
8751  VDLGTSGTPS PVPSPTTAGP LLVPFTLNFT ITNLQYEEDM HRPGSRKFNA
8801  TERVLQGLLS PIFKNTSVGP LYSGCRLTLL RPEKQEAATG VDTICTHRVD
8851  PIGPGLDREX LYWELSXLTX XIXELGPYXL DRXSLYVNGF XXXXXXXXTS
8901  TPGTSXVXLX TSGTPXXXPX XTXXXPLLXP FTLNFTITNL XYEEXMXXPG
8951  SRKFNTTERV LQGLLXPXFK XTSVGXLYSG CRLTLLRXEK XXAATXVDXX
9001  CXXXXDPXXP GLDREXLYWE LSXLTXXIXE LGPYXLDRXS LYVNGFTHRS
9051  FGLTTSTPWT STVDLGTSGT PSPVPSPTTA GPLLVPFTLN FTITNLQYEE
9101  DMHRPGSRKF NTTERVLQGL LTPLFRNTSV SSLYSGCRLT LLRPEKDGAA
9151  TRVDAVCTHR PDPKSPGLDR EXLYWELSXL TXXIXELGPY XLDRXSLYVN
9201  GFXXXXXXXX TSTPGTSXVX LXTSGTPXXX PXXTXXXPLL XPFTLNFTIT
9251  NLXYEEXMXX PGSRKFNTTE RVLQGLLXPX FKXTSVGXLY SGCRLTLLRX
9301  EKXXAATXVD XXCXXXXDPX XPGLDREXLY WELSXLTXXI XELGPYXLDR
9351  XSLYVNGFTH WIPVPTSSTP GTSTVDLGSG TPSSLPSPTT AGPLLVPFTL
9401  NFTITNLQYG EDMGHPGSRK FNTTERVLQG LLGPIFKNTS VGPLYSGCRL
9451  TSLRSEKDGA ATGVDAICIH HLDPKSPGLD REXLYWELSX LTXXIXELGP
9501  YXLDRXSLYV NGFXXXXXXX XTSTPGTSXV XLXTSGTPXX XPXXTXXXPL
9551  LXPFTLNFTI TNLXYEEXMX XPGSRKFNTT ERVLQGLLXP XFKXTSVGXL
9601  YSGCRLTLLR XEKXXAATXV DXXCXXXXDP XXPGLDREXL YWELSXLTXX
9651  IXELGPYXLD RXSLYVNGFT HQTFAPNTST PGTSTVDLGT SGTPSSLPSP
9701  TSAGPLLVPF TLNFTITNLQ YEEDMHHPGS RKFNTTERVL QGLLGPMFKN
9751  TSVGLLYSGC RLTLLRPEKN GAATRVDAVC THRPDPKSPG LDREXLYWEL
9801  SXLTXXIXEL GPYXLDRXSL YVNGFXXXXX XXXTSTPGTS XVXLXTSGTP
9851  XXXPXXTAPV PLLIPFTLNF TITNLHYEEN MQHPGSRKFN TTERVLQGLL
```

Repeat Domain

TABLE 21 - continued

CA125 Protein Sequence

(SEQ ID NO: 162)

```
 9901  RPLFKSTSVG PLYSGCRLTL LRPEKHGAAT GVDAICTLRL DPTGPGLDRE
 9951  RLYWELSQLT NSVTELGPYT LDRDSLYVNG FTQRSSVPTT SIPGTSAVHL
10001  ETSGTPASLP GHTAPGPLLV PFTLNFTITN LQYEVDMRHP GSRKFNTTER
10051  VLQGLLKPLF KSTSVGPLYS GCRLTLLRPE KRGAATGVDT ICTHRLDPLN
10101  PGLDREQLYW ELSKLTRGII ELGPYLLDRG SLYVNGFTHR NFVPITSTPG
10151  TSTVHLGTSE TPSSLPRPIV PGPLLVPFTL NFTITNLQYE EAMRHPGSRK
10201  FNTTERVLQG LLRPLFKNTS IGPLYSSCRL TLLRPEKDKA ATRVDAICTH
10251  HPDPQSPGLN REQLYWELSQ LTHGITELGP YTLDRDSLYV DGFTHWSPIP
10301  TTSTPGTSIV NLGTSGIPPS LPETTXXXPL LXPFTLNFTI TNLXYEEXMX
10351  XPGSRKFNTT ERVLQGLLKP LFKSTSVGPL YSGCRLTLLR PEKDGVATRV
10451  DAICTHRPDP KIPGLDRQQL YWELSQLTHS ITELGPYTLD RDSLYVNGFT
10501  QRSSVPTTST PGTFTVQPET SETPSSLPGP TATGPVLLPF TLNFTITNLQ
10551  YEEDMHRPGS RKFNTTERVL QGLLMPLFKN TSVSSLYSGC RLTLLRPEKD
10601  GAATRVDAVC THRPDPKSPG LDRERLYWKL SQLTHGITEL GPYTLDRHSL
10651  YVNGFTHQSS MTTTRTPDTS TMHLATSRTP ASLSGPTTAS PLLVLFTINF
10701  TITNLRYEEN MHHPGSRKFN TTERVLQGLL RPVFKNTSVG PLYSGCRLTL
10751  LRPKKDGAAT KVDAICTYRP DPKSPGLDRE QLYWELSQLT HSITELGPYT
10801  QDRDSLYNVG FTQRSSVPTT SVPGTPTVDL GTSGTPVSKP GPSAASPLLV
10851  LFTLNGTITN LRYEENMQHP GSRKFNTTER VLQGLLRSLF KSTSVGPLYS
10901  GCRLTLLRPE KDGTATGVDA ICTHHPDPKS PRLDREQLYW ELSQLTHNIT
10951  ELGHYALDND SLFVNGFTHR SSVSTTSTPG TPTVYLGASK TPASIFGPSA
11001  ASHLLILFTL NFTITNLRYE ENMWPGSRKF NTTERVLQGL LRPLFKNTSV
11051  GPLYSGSRLT LLRPEKDGEA TGVDAICTHR PDPTGPGLDR EQLYLELSQL
11101  THSITELGPY TLDRDSLYVN GFTHRSSVPT TSTGVVSEEP FTLNFTINNL
11151  RYMADMGQPG SLKFNITDNV MKHLLSPLFQ RSSLGARYTG CRVIALRSVK
11201  NGAETRVDLL CTYLQPLSGP GLPIKQVFHE LSQQTHGITR LGPYSLDKDS
11251  LYLNGYNEPG LDEPPTTPKP ATTFLPPLSE ATTAMGYHLK TLTLNFTISN
11301  LQYSPDMGKG SATFNSTEGV LQHLLRPLFQ KSSMGPFYLG CQLISLRPEK
11351  DGAATGVDTT CTYHPDPVGP GLDIQQLYWE LSQLTHGVTQ LGFYVLDRDS
11401  LFINGYAPQN LSIRGEYQIN FHIVNWNLSN PDPTSSEY
                                      IT LLRDIQDKVT
11451  TLYKGSQLHD TFRFCLVTNL TMDSVLVTVK ALFSSNLDPS LVEQVFLDKT
11501  LNASFHWLGS TYQLVDIHVT EMESSVYQPT SSSSTQHFYL NFTITNLPYS
11551  QDKAQPGTTN YQRNKRNIED ALNQLFRNSS IKSYFSDCQV STFRSVPNRH
11601  HTGVDSLCNF SPLARRVDRV AIYEEFLRMT RNGTQLQNFT LDRSSVLVDG
11651  YSPNRNEPLT GNSDLPFWAV ILIGLAGLLG LITCLICGVL VTTRRRKKEG
11701  EYNVQQQCPG YYQSHLDLED LQ
```

Carboxy Terminal Domain

TABLE 22

CA125 Repeat Nucleotide Sequence

(SEQ ID NO: 307)

```
  1  ACTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA
 51  CCTGCAGTAT GAGGAGGACA TGCATCGCCC TGGATCTAGG AAGTTCAACA
101  CCACAGAGAG GGTCCTGCAG GGTCTGCTTA GTCCCATATT CAAGAACACC
151  AGTGTTGGCC CTCTGTACTC TGGCTGCAGA CTGACCTCTC TCAGGTCTGA
201  GAAGGATGGA GCAGCCACTG GAGTGGATGC CATCTGCATC CATCATCTTG
251  ACCCCAAAAG CCCTGGACTC AACAGAGAGC GGCTGTACTG GGAGCTGAGC
301  CGACTGACCA ATGGCATCAA AGAGCTGGGC CCCTACACCC TGGACAGGAA
351  CAGTCTCTAT GTCAATGGTT TCACCCATCG GACCTCTGTG CCCACCACCA
401  GCACTCCTGG GACCTCCACA GTGGACCTTG GAACCTCAGG GACTCCATTC
451  TCCCTCCCAA GCCCCGCA
```

TABLE 23

CA125 Repeat Amino Acid Sequence
(SEQ ID NO: 308)

```
  1  TAGPLLVPFT LNFTITNLQY EEDMHRPGSR KFNTTERVLQ GLLSPIFKNT
 51  SVGPLYSGCR LTSLRSEKDG AATGVDAICI HHLDPKSPGL NRERLYWELS
101  RLTNGIKELG PYTLDRNSLY VNGFTHRTSV PTTSTPGTST VDLGTSGTPF
151  SLPSPA
```

Table 24

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

```
   1  AAGCGTTGCA CAATTCCCCC AACCTCCATA CATACGGCAG CTCTTCTAGA
  51  CACAGGTTTT CCCAGGTCAA ATGCGGGGAC CCCAGCCATA TCTCCCACCC
 101  TGAGAAATTT TGGAGTTTCA GGGAGCTCAG AAGCTCTGCA GAGGCCACCC
 151  TCTCTGAGGG GATTCTTCTT AGACCTCCAT CCAGAGGCAA ATGTTGACCT
 201  GTCCATGCTG AAACCCTCAG GCCTTCCTGG GTCATCTTCT CCCACCCGCT
 251  CCTTGATGAC AGGGAGCAGG AGCACTAAAG CCACACCAGA AATGGATTCA
 301  GGACTGACAG GAGCCACCTT GTCACCTAAG ACATCTACAG GTGCAATCGT
 351  GGTGACAGAA CATACTCTGC CCTTTACTTC CCCAGATAAG ACCTTGGCCA
 401  GTCCTACATC TTCGGTTGTG GGAAGAACCA CCCAGTCTTT GGGGGTGATG
 451  TCCTCTGCTC TCCCTGAGTC AACCTCTAGA GGAATGACAC ACTCCGAGCA
 501  AAGAACCAGC CCATCGCTGA GTCCCCAGGT CAATGGAACT CCCTCTAGGA
 551  ACTACCCTGC TACAAGCATG GTTTCAGGAT TGAGTTCCCC AAGGACCAGG
 601  ACCAGTTCCA CAGAAGGAAA TTTTACCAAA GAAGCATCTA CATACACACT
 651  CACTGTAGAG ACCACAAGTG GCCCAGTCAC TGAGAAGTAC ACAGTCCCCA
 701  CTGAGACCTC AACAACTGAA GGTGACAGCA CAGAGACCCC CTGGGACACA
 751  AGATATATTC CTGTAAAAAT CACATCTCCA ATGAAAACAT TTGCAGATTC
 801  AACTGCATCC AAGGAAAATG CCCCAGTGTC TATGACTCCA GCTGAGACCA
 851  CAGTTACTGA CTCACATACT CCAGGAAGGA CAAACCCATC ATTTGGGACA
 901  CTTTATTCTT CCTTCCTTGA CCTATCACCT AAAGGGACCC CAAATTCCAG
```

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

```
 951  AGGTGAAACA AGCCTGGAAC TGATTCTATC AACCACTGGA TATCCCTTCT
1001  CCTCTCCTGA ACCTGGCTCT GCAGGACACA GCAGAATAAG TACCAGTGCG
1051  CCTTTGTCAT CATCTGCTTC AGTTCTCGAT AATAAAATAT CAGAGACCAG
1101  CATATTCTCA GGCCAGAGTC TCACCTCCCC TCTGTCTCCT GGGGTGCCCG
1151  AGGCCAGAGC CAGCACAATG CCCAACTCAG CTATCCCTTT TTCCATGACA
1201  CTAAGCAATG CAGAAACAAG TGCCGAAAGG GTCAGAAGCA CAATTTCCTC
1251  TCTGGGGACT CCATCAATAT CCACAAAGCA GACAGCAGAG ACTATCCTTA
1301  CCTTCCATGC CTTCGCTGAG ACCATGGATA TACCCAGCAC CCACATAGCC
1351  AAGACTTTGG CTTCAGAATG GTTGGGAAGT CCAGGTACCC TTGGTGGCAC
1401  CAGCACTTCA GCGCTGACAA CCACATCTCC ATCTACCACT TTAGTCTCAG
1451  AGGAGACCAA CACCCATCAC TCCACGAGTG GAAAGGAAAC AGAAGGAACT
1501  TTGAATACAT CTATGACTCC ACTTGAGACC TCTGCTCCTG GAGAAGAGTC
1551  CGAAATGACT GCCACCTTGG TCCCCACTCT AGGTTTTACA ACTCTTGACA
1601  GCAAGATCAG AAGTCCATCT CAGGTCTCTT CATCCCACCC AACAAGAGAG
1651  CTCAGAACCA CAGGCAGCAC CTCTGGGAGG CAGAGTTCCA GCACAGCTGC
1701  CCACGGGAGC TCTGACATCC TGAGGGCAAC CACTTCCAGC ACCTCAAAAG
1751  CATCATCATG GACCAGTGAA AGCACAGCTC AGCAATTTAG TGAACCCCAG
1801  CACACACAGT GGGTGGAGAC AAGTCCTAGC ATGAAAACAG AGAGACCCCC
1851  AGCATCAACC AGTGTGGCAG CCCCTATCAC CACTTCTGTT CCCTCAGTGG
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Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

1901 TCTCTGGCTT CACCACCCTG AAGACCAGCT CCACAAAAGG GATTTGGCTT

1951 GAAGAAACAT CTGCAGACAC ACTCATCGGA GAATCCACAG CTGGCCCAAC

2001 CACCCATCAG TTTGCTGTTC CCACTGGGAT TTCAATGACA GGAGGCAGCA

2051 GCACCAGGGG AAGCCAGGGC ACAACCCACC TACTCACCAG AGCCACAGCA

2101 TCATCTGAGA CATCCGCAGA TTTGACTCTG GCCACGAACG GTGTCCCAGT

2151 CTCCGTGTCT CCAGCAGTGA GCAAGACGGC TGCTGGCTCA AGTCCTCCAG

2201 GAGGGACAAA GCCATCATAT ACAATGGTTT CTTCTGTCAT CCCTGAGACA

2251 TCATCTCTAC AGTCCTCAGC TTTCAGGGAA GGAACCAGCC TGGGACTGAC

2301 TCCATTAAAC ACTAGACATC CCTTCTCTTC CCCTGAACCA GACTCTGCAG

2351 GACACACCAA GATAAGCACC AGCATTCCTC TGTTGTCATC TGCTTCAGTT

2401 CTTGAGGATA AAGTGTCAGC GACCAGCACA TTCTCACACC ACAAAGCCAC

2451 CTCATCTATT ACCACAGGGA CTCCTGAAAT CTCAACAAAG ACAAAGCCCA

2501 GCTCAGCCGT TCTTTCCTCC ATGACCCTAA GCAATGCAGC AACAAGTCCT

2551 GAAAGAGTCA GAAATGCAAC TTCCCCTCTG ACTCATCCAT CTCCATCAGG

2601 GGAAGAGACA GCAGGGAGTG TCCTCACTCT CAGCACCTCT GCTGAGACTA

2651 CAGACTCACC TAACATCCAC CCAACTGGGA CACTGACTTC AGAATCGTCA

2701 GAGAGTCCTA GCACTCTCAG CCTCCCAAGT GTCTCTGGAG TCAAAACCAC

2751 ATTTTCTTCA TCTACTCCTT CCACTCATCT ATTTACTAGT GGAGAAGAAA

2801 CAGAGGAAAC TTCGAATCCA TCTGTGTCTC AACCTGAGAC TTCTGTTTCC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

2851 AGAGTAAGGA CCACCTTGGC CAGCACCTCT GTCCCTACCC CAGTATTCCC

2901 CACCATGGAC ACCTGGCCTA CACGTTCAGC TCAGTTCTCT TCATCCCACC

2951 TAGTGAGTGA GCTCAGAGCT ACGAGCAGTA CCTCAGTTAC AAACTCAACT

3001 GGTTCAGCTC TTCCTAAAAT ATCTCACCTC ACTGGGACGG CAACAATGTC

3051 ACAGACCAAT AGAGACACGT TTAATGACTC TGCTGCACCC CAAAGCACAA

3101 CTTGGCCAGA GACTAGTCCC AGATTCAAGA CAGGGTTACC TTCAGCAACA

3151 ACCACTGTTT CAACCTCTGC CACTTCTCTC TCTGCTACTG TAATGGTCTC

3201 TAAATTCACT TCTCCAGCAA CTAGTTCCAT GGAAGCAACT TCTATCAGGG

3251 AACCATCAAC AACCATCCTC ACAACAGAGA CCACGAATGG CCCAGGCTCT

3301 ATGGCTGTGG CTTCTACCAA CATCCCAATT GGAAAGGGCT ACATTACTGA

3351 AGGAAGATTG GACACAAGCC ATCTGCCCAT TGGAACCACA GCTTCCTCTG

3401 AGACATCTAT GGATTTTACC ATGGCCAAAG AAAGTGTCTC AATGTCAGTA

3451 TCTCCATCTC AGTCCATGGA TGCTGCTGGC TCAAGCACTC CAGGAAGGAC

3501 AAGCCAATTC GTTGACACAT TTTCTGATGA TGTCTATCAT TTAACATCCA

3551 GAGAAATTAC AATACCTAGA GATGGAACAA GCTCAGCTCT GACTCCACAA

3601 ATGACTGCAA CTCACCCTCC ATCTCCTGAT CCTGGCTCTG CTAGAAGCAC

3651 CTGGCTTGGC ATCTTGTCCT CATCTCCTTC TTCTCCTACT CCCAAAGTCA

3701 CAATGAGCTC CACATTTTCA ACTCAGAGAG TCACCACAAG CATGATAATG

3751 GACACAGTTG AAACTAGTCG GTGGAACATG CCCAACTTAC CTTCCACGAC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

3801	TTCCCTGACA	CCAAGTAATA	TTCCAACAAG	TGGTGCCATA	GGAAAAAGCA
3851	CCCTGGTTCC	CTTGGACACT	CCATCTCCAG	CCACATCATT	GGAGGCATCA
3901	GAAGGGGGAC	TTCCAACCCT	CAGCACCTAC	CCTGAATCAA	CAAACACACC
3951	CAGCATCCAC	CTCGGAGCAC	ACGCTAGTTC	AGAAAGTCCA	AGCACCATCA
4001	AACTTACCAT	GGCTTCAGTA	GTAAAACCTG	GCTCTTACAC	ACCTCTCACC
4051	TTCCCCTCAA	TAGAGACCCA	CATTCATGTA	TCAACAGCCA	GAATGGCTTA
4101	CTCTTCTGGG	TCTTCACCTG	AGATGACAGC	TCCTGGAGAG	ACTAACACTG
4151	GTAGTACCTG	GGACCCCACC	ACCTACATCA	CCACTACGGA	TCCTAAGGAT
4201	ACAAGTTCAG	CTCAGGTCTC	TACACCCCAC	TCAGTGAGGA	CACTCAGAAC
4251	CACAGAAAAC	CATCCAAAGA	CAGAGTCCGC	CACCCCAGCT	GCTTACTCTG
4301	GAAGTCCTAA	AATCTCAAGT	TCACCCAATC	TCACCAGTCC	GGCCACAAAA
4351	GCATGGACCA	TCACAGACAC	AACTGAACAC	TCCACTCAAT	TACATTACAC
4401	AAAATTGGCA	GAAAAATCAT	CTGGATTTGA	GACACAGTCA	GCTCCAGGAC
4451	CTGTCTCTGT	AGTAATCCCT	ACCTCCCCTA	CCATTGGAAG	CAGCACATTG
4501	GAACTAACTT	CTGATGTCCC	AGGGGAACCC	CTGGTCCTTG	CTCCCAGTGA
4551	GCAGACCACA	ATCACTCTCC	CCATGGCAAC	ATGGCTGAGT	ACCAGTTTGA
4601	CAGAGGAAAT	GGCTTCAACA	GACCTTGATA	TTTCAAGTCC	AAGTTCACCC
4651	ATGAGTACAT	TTGCTATTTT	TCCACCTATG	TCCACACCTT	CTCATGAACT
4701	TTCAAAGTCA	GAGGCAGATA	CCAGTGCCAT	TAGAAATACA	GATTCAACAA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

4751 CGTTGGATCA GCACCTAGGA ATCAGGAGTT TGGGCAGAAC TGGGGACTTA

4801 ACAACTGTTC CTATCACCCC ACTGACAACC ACGTGGACCA GTGTGATTGA

4851 ACACTCAACA CAAGCACAGG ACACCCTTTC TGCAACGATG AGTCCTACTC

4901 ACGTGACACA GTCACTCAAA GATCAAACAT CTATACCAGC CTCAGCATCC

4951 CCTTCCCATC TTACTGAAGT CTACCCTGAG CTCGGGACAC AAGGGAGAAG

5001 CTCCTCTGAG GCAACCACTT TTTGGAAACC ATCTACAGAC ACACTGTCCA

5051 GAGAGATTGA GACTGGCCCA ACAAACATTC AATCCACTCC ACCCATGGAC

5101 AACACAACAA CAGGGAGCAG TAGTAGTGGA GTCACCCTGG GCATAGCCCA

5151 CCTTCCCATA GGAACATCCT CCCCAGCTGA GACATCCACA AACATGGCAC

5201 TGGAAAGAAG AAGTTCTACA GCCACTGTCT CTATGGCTGG GACAATGGGA

5251 CTCCTTGTTA CTAGTGCTCC AGGAAGAAGC ATCAGCCAGT CATTAGGAAG

5301 AGTTTCCTCT GTCCTTTCTG AGTCAACTAC TGAAGGAGTC ACAGATTCTA

5351 GTAAGGGAAG CAGCCCAAGG CTGAACACAC AGGGAAATAC AGCTCTCTCC

5401 TCCTCTCTTG AACCCAGCTA TGCTGAAGGA AGCCAGATGA GCACAAGCAT

5451 CCCTCTAACC TCATCTCCTA CAACTCCTGA TGTGGAATTC ATAGGGGGCA

5501 GCACATTTTG GACCAAGGAG GTCACCACAG TTATGACCTC AGACATCTCC

5551 AAGTCTTCAG CAAGGACAGA GTCCAGCTCA GCTACCCTTA TGTCCACAGC

5601 TTTGGGAAGC ACTGAAAATA CAGGAAAAGA AAAACTCAGA ACTGCCTCTA

5651 TGGATCTTCC ATCTCCAACT CCATCAATGG AGGTGACACC ATGGATTTCT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

5701 CTCACTCTCA GTAATGCCCC CAATACCACA GATTCACTTG ACCTCAGCCA

5751 TGGGGTGCAC ACCAGCTCTG CAGGGACTTT GGCCACTGAC AGGTCATTGA

5801 ATACTGGTGT CACTAGAGCC TCCAGATTGG AAAACGGCTC TGATACCTCT

5851 TCTAAGTCCC TGTCTATGGG AAACAGCACT CACACTTCCA TGACTGACAC

5901 AGAGAAGAGT GAAGTGTCTT CTTCAATCCA TCCCCGACCT GAGACCTCAG

5951 CTCCTGGAGC AGAGACCACT TTGACTTCCA CTCCTGGAAA CAGGGCCATA

6001 AGCTTAACAT TGCCTTTTTC ATCCATTCCA GTGGAAGAAG TCATTTCTAC

6051 AGGCATAACC TCAGGACCAG ACATCAACTC AGCACCCATG ACACATTCTC

6101 CCATCACCCC ACCAACAATT GTATGGACCA GTACAGGCAC AATTGAACAG

6151 TCCACTCAAC CACTACATGC AGTTTCTTCA GAAAAAGTTT CTGTGCAGAC

6201 ACAGTCAACT CCATATGTCA ACTCTGTGGC AGTGTCTGCT TCCCCTACCC

6251 ATGAGAATTC AGTCTCTTCT GGAAGCAGCA CATCCTCTCC ATATTCCTCA

6301 GCCTCACTTG AATCCTTGGA TTCCACAATC AGTAGGAGGA ATGCAATCAC

6351 TTCCTGGCTA TGGGACCTCA CTACATCTCT CCCCACTACA ACTTGGCCAA

6401 GTACTAGTTT ATCTGAGGCA CTGTCCTCAG GCCATTCTGG GGTTTCAAAC

6451 CCAAGTTCAA CTACGACTGA ATTTCCACTC TTTTCAGCTG CATCCACATC

6501 TGCTGCTAAG CAAAGAAATC CAGAAACAGA GACCCATGGT CCCCAGAATA

6551 CAGCCGCGAG TACTTTGAAC ACTGATGCAT CCTCGGTCAC AGGTCTTTCT

6601 GAGACTCCTG TGGGGGCAAG TATCAGCTCT GAAGTCCCTC TTCCAATGGC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

6651 CATAACTTCT AGATCAGATG TTTCTGGCCT TACATCTGAG AGTACTGCTA

6701 ACCCGAGTTT AGGCACAGCC TCTTCAGCAG GGACCAAATT AACTAGGACA

6751 ATATCCCTGC CCACTTCAGA GTCTTTGGTT TCCTTTAGAA TGAACAAGGA

6801 TCCATGGACA GTGTCAATCC CTTTGGGGTC CCATCCAACT ACTAATACAG

6851 AAACAAGCAT CCCAGTAAAC AGCGCAGGTC CACCTGGCTT GTCCACAGTA

6901 GCATCAGATG TAATTGACAC ACCTTCAGAT GGGGCTGAGA GTATTCCCAC

6951 TGTCTCCTTT TCCCCCTCCC CTGATACTGA AGTGACAACT ATCTCACATT

7001 TCCCAGAAAA GACAACTCAT TCATTTAGAA CCATTTCATC TCTCACTCAT

7051 GAGTTGACTT CAAGAGTGAC ACCTATTCCT GGGGATTGGA TGAGTTCAGC

7101 TATGTCTACA AAGCCCACAG GAGCCAGTCC CTCCATTACA CTGGGAGAGA

7151 GAAGGACAAT CACCTCTGCT GCTCCAACCA CTTCCCCCAT AGTTCTCACT

7201 GCTAGTTTCA CAGAGACCAG CACAGTTTCA CTGGATAATG AAACTACAGT

7251 AAAAACCTCA GATATCCTTG ACGCACGGAA AACAAATGAG CTCCCCTCAG

7301 ATAGCAGTTC TTCTTCTGAT CTGATCAACA CCTCCATAGC TTCTTCAACT

7351 ATGGATGTCA CTAAAACAGC CTCCATCAGT CCCACTAGCA TCTCAGGAAT

7401 GACAGCAAGT TCCTCCCCAT CTCTCTTCTC TTCAGATAGA CCCCAGGTTC

7451 CCACATCTAC AACAGAGACA AATACAGCCA CCTCTCCATC TGTTTCCAGT

7501 AACACCTATT CTCTTGATGG GGGCTCCAAT GTGGGTGGCA CTCCATCCAC

7551 TTTACCACCC TTTACAATCA CCCACCCTGT CGAGACAAGC TCGGCCCTAT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

7601 TAGCCTGGTC TAGACCAGTA AGAACTTTCA GCACCATGGT CAGCACTGAC

7651 ACTGCCTCCG GAGAAAATCC TACCTCTAGC AATTCTGTGG TGACTTCTGT

7701 TCCAGCACCA GGTACATGGA CCAGTGTAGG CAGTACTACT GACTTACCTG

7751 CCATGGGCTT TCTCAAGACA AGTCCTGCAG GAGAGGCACA CTCACTTCTA

7801 GCATCAACTA TTGAACCAGC CACTGCCTTC ACTCCCCATC TCTCAGCAGC

7851 AGTGGTCACT GGATCCAGTG CTACATCAGA AGCCAGTCTT CTCACTACGA

7901 GTGAAAGCAA AGCCATTCAT TCTTCACCAC AGACCCCAAC TACACCCACC

7951 TCTGGAGCAA ACTGGGAAAC TTCAGCTACT CCTGAGAGCC TTTTGGTAGT

8001 CACTGAGACT TCAGACACAA CACTTACCTC AAAGATTTTG GTCACAGATA

8051 CCATCTTGTT TTCAACTGTG TCCACGCCAC CTTCTAAATT TCCAAGTACG

8101 GGGACTCTGT CTGGAGCTTC CTTCCCTACT TTACTCCCGG ACACTCCAGC

8151 CATCCCTCTC ACTGCCACTG AGCCAACAAG TTCATTAGCT ACATCCTTTG

8201 ATTCCACCCC ACTGGTGACT ATAGCTTCGG ATAGTCTTGG CACAGTCCCA

8251 GAGACTACCC TGACCATGTC AGAGACCTCA AATGGTGATG CACTGGTTCT

8301 TAAGACAGTA AGTAACCCAG ATAGGAGCAT CCCTGGAATC ACTATCCAAG

8351 GAGTAACAGA AAGTCCACTC CATCCTTCTT CCACTTCCCC CTCTAAGATT

8401 GTTGCTCCAC GGAATACAAC CTATGAAGGT TCGATCACAG TGGCACTTTC

8451 TACTTTGCCT GCGGGAACTA CTGGTTCCCT TGTATTCAGT CAGAGTTCTG

8501 AAAACTCAGA GACAACGGCT TTGGTAGACT CATCAGCTGG GCTTGAGAGG

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

8551 GCATCTGTGA TGCCACTAAC CACAGGAAGC CAGGGTATGG CTAGCTCTGG

8601 AGGAATCAGA AGTGGGTCCA CTCACTCAAC TGGAACCAAA ACATTTTCTT

8651 CTCTCCCTCT GACCATGAAC CCAGGTGAGG TTACAGCCAT GTCTGAAATC

8701 ACCACGAACA GACTGACAGC TACTCAATCA ACAGCACCCA AAGGGATACC

8751 TGTGAAGCCC ACCAGTGCTG AGTCAGGCCT CCTAACACCT GTCTCTGCCT

8801 CCTCAAGCCC ATCAAAGGCC TTTGCCTCAC TGACTACAGC TCCCCCAACT

8851 TGGGGGATCC CACAGTCTAC CTTGACATTT GAGTTTTCTG AGGTCCCAAG

8901 TTTGGATACT AAGTCCGCTT CTTTACCAAC TCCTGGACAG TCCCTGAACA

8951 CCATTCCAGA CTCAGATGCA AGCACAGCAT CTTCCTCACT GTCCAAGTCT

9001 CCAGAAAAAA ACCCAAGGGC AAGGATGATG ACTTCCACAA AGGCCATAAG

9051 TGCAAGCTCA TTTCAATCAA CAGGTTTTAC TGAAACCCCT GAGGGATCTG

9101 CCTCCCCTTC TATGGCAGGG CATGAACCCA GAGTCCCCAC TTCAGGAACA

9151 GGGGACCCTA GATATGCCTC AGAGAGCATG TCTTATCCAG ACCCAAGCAA

9201 GGCATCATCA GCTATGACAT CGACCTCTCT TGCATCAAAA CTCACAACTC

9251 TCTTCAGCAC AGGTCAAGCA GCAAGGTCTG GTTCTAGTTC CTCTCCCATA

9301 AGCCTATCCA CTGAGAAAGA AACAAGCTTC CTTTCCCCCA CTGCATCCAC

9351 CTCCAGAAAG ACTTCACTAT TTCTTGGGCC TTCCATGGCA AGGCAGCCCA

9401 ACATATTGGT GCATCTTCAG ACTTCAGCTC TGACACTTTC TCCAACATCC

9451 ACTCTAAATA TGTCCCAGGA GGAGCCTCCT GAGTTAACCT CAAGCCAGAC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

9501	CATTGCAGAA	GAAGAGGGAA	CAACAGCTGA	AACACAGACG	TTAACCTTCA
9551	CACCATCTGA	GACCCCAACA	TCCTTGTTAC	CTGTCTCTTC	TCCCACAGAA
9601	CCCACAGCCA	GAAGAAAGAG	TTCTCCAGAA	ACATGGGCAA	GCTCTATTTC
9651	AGTTCCTGCC	AAGACCTCCT	TGGTTGAAAC	AACTGATGGA	ACGCTAGTGA
9701	CCACCATAAA	GATGTCAAGC	CAGGCAGCAC	AAGGAAATTC	CACGTGGCCT
9751	GCCCCAGCAG	AGGAGACGGG	GACCAGTCCA	GCAGGCACAT	CCCCAGGAAG
9801	CCCAGAAATG	TCTACCACTC	TCAAAATCAT	GAGCTCCAAG	GAACCCAGCA
9851	TCAGCCCAGA	GATCAGGTCC	ACTGTGCGAA	ATTCTCCTTG	GAAGACTCCA
9901	GAAACAACTG	TTCCCATGGA	GACCACAGTG	GAACCAGTCA	CCCTTCAGTC
9951	CACAGCCCTA	GGAAGTGGCA	GCACCAGCAT	CTCTCACCTG	CCCACAGGAA
10001	CCACATCACC	AACCAAGTCA	CCAACAGAAA	ATATGTTGGC	TACAGAAAGG
10051	GTCTCCCTCT	CCCCATCCCC	ACCTGAGGCT	TGGACCAACC	TTTATTCTGG
10101	AACTCCAGGA	GGGACCAGGC	AGTCACTGGC	CACAATGTCC	TCTGTCTCCC
10151	TAGAGTCACC	AACTGCTAGA	AGCATCACAG	GGACTGGTCA	GCAAAGCAGT
10201	CCAGAACTGG	TTTCAAAGAC	AACTGGAATG	GAATTCTCTA	TGTGGCATGG
10251	CTCTACTGGA	GGGACCACAG	GGGACACACA	TGTCTCTCTG	AGCACATCTT
10301	CCAATATCCT	TGAAGACCCT	GTAACCAGCC	CAAACTCTGT	GAGCTCATTG
10351	ACAGATAAAT	CCAAACATAA	AACCGAGACA	TGGGTAAGCA	CCACAGCCAT
10401	TCCCTCCACT	GTCCTGAATA	ATAAGATAAT	GGCAGCTGAA	CAACAGACAA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

10451 GTCGATCTGT GGATGAGGCT TATTCATCAA CTAGTTCTTG GTCAGATCAG

10501 ACATCTGGGA GTGACATCAC CCTTGGTGCA TCTCCTGATG TCACAAACAC

10551 ATTATACATC ACCTCCACAG CACAAACCAC CTCACTAGTG TCTCTGCCCT

10601 CTGGAGACCA AGGCATTACA AGCCTCACCA ATCCCTCAGG AGGAAAAACA

10651 AGCTCTGCGT CATCTGTCAC ATCTCCTTCA ATAGGGCTTG AGACTCTGAG

10701 GGCCAATGTA AGTGCAGTGA AAAGTGACAT TGCCCCTACT GCTGGGCATC

10751 TATCTCAGAC TTCATCTCCT GCGGAAGTGA GCATCCTGGA CGTAACCACA

10801 GCTCCTACTC CAGGTATCTC CACCACCATC ACCACCATGG GAACCAACTC

10851 AATCTCAACT ACCACACCCA ACCCAGAAGT GGGTATGAGT ACCATGGACA

10901 GCACCCCGGC CACAGAGAGG CGCACAACTT CTACAGAACA CCCTTCCACC

10951 TGGTCTTCCA CAGCTGCATC AGATTCCTGG ACTGTCACAG ACATGACTTC

11001 AAACTTGAAA GTTGCAAGAT CTCCTGGAAC AATTTCCACA ATGCATACAA

11051 CTTCATTCTT AGCCTCAAGC ACTGAATTAG ACTCCATGTC TACTCCCCAT

11101 GGCCGTATAA CTGTCATTGG AACCAGCCTG GTCACTCCAT CCTCTGATGC

11151 TTCAGCTGTA AAGACAGAGA CCAGTACAAG TGAAAGAACA TTGAGTCCTT

11201 CAGACACAAC TGCATCTACT CCCATCTCAA CTTTTTCTCG TGTCCAGAGG

11251 ATGAGCATCT CAGTTCCTGA CATTTTAAGT ACAAGTTGGA CTCCCAGTAG

11301 TACAGAAGCA GAAGATGTGC CTGTTTCAAT GGTTTCTACA GATCATGCTA

11351 GTACAAAGAC TGACCCAAAT ACGCCCCTGT CCACTTTTCT GTTTGATTCT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

11401 CTGTCCACTC TTGACTGGGA CACTGGGAGA TCTCTGTCAT CAGCCACAGC

11451 CACTACCTCA GCTCCTCAGG GGGCCACAAC TCCCCAGGAA CTCACTTTGG

11501 AAACCATGAT CAGCCCAGCT ACCTCACAGT TGCCCTTCTC TATAGGGCAC

11551 ATTACAAGTG CAGTCACACC AGCTGCAATG GCAAGGAGCT CTGGAGTTAC

11601 TTTTTCAAGA CCAGATCCCA CAAGCAAAAA GGCAGAGCAG ACTTCCACTC

11651 AGCTTCCCAC CACCACTTCT GCACATCCAG GGCAGGTGCC CAGATCAGCA

11701 GCAACAACTC TGGATGTGAT CCCACACACA GCAAAAACTC CAGATGCAAC

11751 TTTTCAGAGA CAAGGGCAGA CAGCTCTTAC AACAGAGGCA AGAGCTACAT

11801 CTGACTCCTG GAATGAGAAA GAAAAATCAA CCCCAAGTGC ACCTTGGATC

11851 ACTGAGATGA TGAATTCTGT CTCAGAAGAT ACCATCAAGG AGGTTACCAG

11901 CTCCTCCAGT GTATTAAAGG ACCCTGAATA CGCTGGACAT AAACTTGGAA

11951 TCTGGGACGA CTTCATCCCC AAGTTTGGAA AAGCAGCCCA TATGAGAGAG

12001 TTGCCCCTTC TGAGTCCACC ACAGGACAAA GAGGCAATTC ACCCTTCTAC

12051 AAACACAGTA GAGACCACAG GCTGGGTCAC AAGTTCCGAA CATGCTTCTC

12101 ATTCCACTAT CCCAGCCCAC TCAGCGTCAT CCAAACTCAC ATCTCCAGTG

12151 GTTACAACCT CCACCAGGGA ACAAGCAATA GTTTCTATGT CAACAACCAC

12201 ATGGCCAGAG TCTACAAGGG CTAGAACAGA GCCTAATTCC TTCTTGACTA

12251 TTGAACTGAG GGACGTCAGC CCTTACATGG ACACCAGCTC AACCACACAA

12301 ACAAGTATTA TCTCTTCCCC AGGTTCCACT GCGATCACCA AGGGGCCTAG

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

12351 AACAGAAATT ACCTCCTCTA AGAGAATATC CAGCTCATTC CTTGCCCAGT

12401 CTATGAGGTC GTCAGACAGC CCCTCAGAAG CCATCACCAG GCTGTCTAAC

12451 TTTCCTGCCA TGACAGAATC TGGAGGAATG ATCCTTGCTA TGCAAACAAG

12501 TCCACCTGGC GCTACATCAC TAAGTGCACC TACTTTGGAT ACATCAGCCA

12551 CAGCCTCCTG GACAGGGACT CCACTGGCTA CGACTCAGAG ATTTACATAC

12601 TCAGAGAAGA CCACTCTCTT TAGCAAAGGT CCTGAGGATA CATCACAGCC

12651 AAGCCCTCCC TCTGTGGAAG AAACCAGCTC TTCCTCTTCC CTGGTACCTA

12701 TCCATGCTAC AACCTCGCCT TCCAATATTT TGTTGACATC ACAAGGGCAC

12751 AGTCCCTCCT CTACTCCACC TGTGACCTCA GTTTTCTTGT CTGAGACCTC

12801 TGGCCTGGGG AAGACCACAG ACATGTCGAG GATAAGCTTG GAACCTGGCA

12851 CAAGTTTACC TCCCAATTTG AGCAGTACAG CAGGTGAGGC GTTATCCACT

12901 TATGAAGCCT CCAGAGATAC AAAGGCAATT CATCATTCTG CAGACACAGC

12951 AGTGACGAAT ATGGAGGCAA CCAGTTCTGA ATATTCTCCT ATCCCAGGCC

13001 ATACAAAGCC ATCCAAAGCC ACATCTCCAT TGGTTACCTC CCACATCATG

13051 GGGGACATCA CTTCTTCCAC ATCAGTATTT GGCTCCTCCG AGACCACAGA

13101 GATTGAGACA GTGTCCTCTG TGAACCAGGG ACTTCAGGAG AGAAGCACAT

13151 CCCAGGTGGC CAGCTCTGCT ACAGAGACAA GCACTGTCAT TACCCATGTG

13201 TCTAGTGGTG ATGCTACTAC TCATGTCACC AAGACACAAG CCACTTTCTC

13251 TAGCGGAACA TCCATCTCAA GCCCTCATCA GTTTATAACT TCTACCAACA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

13301 CATTTACAGA TGTGAGCACC AACCCCTCCA CCTCTCTGAT AATGACAGAA

13351 TCTTCAGGAG TGACCATCAC CACCCAAACA GGTCCTACTG GAGCTGCAAC

13401 ACAGGGTCCA TATCTCTTGG ACACATCAAC CATGCCTTAC TTGACAGAGA

13451 CTCCATTAGC TGTGACTCCA GATTTTATGC AATCAGAGAA GACCACTCTC

13501 ATAAGCAAAG GTCCCAAGGA TGTGACCTGG ACAAGCCCTC CCTCTGTGGC

13551 AGAAACCAGC TATCCCTCTT CCCTGACACC TTTCTTGGTC ACAACCATAC

13601 CTCCTGCCAC TTCCACGTTA CAAGGGCAAC ATACATCCTC TCCTGTTTCT

13651 GCGACTTCAG TTCTTACCTC TGGACTGGTG AAGACCACAG ATATGTTGAA

13701 CACAAGCATG GAACCTGTGA CCAATTCACC TCAAAATTTG AACAATCCAT

13751 CAAATGAGAT ACTGGCCACT TTGGCAGCCA CCACAGATAT AGAGACTATT

13801 CATCCTTCCA TAAACAAAGC AGTGACCAAT ATGGGGACTG CCAGTTCAGC

13851 ACATGTACTG CATTCCACTC TCCCAGTCAG CTCAGAACCA TCTACAGCCA

13901 CATCTCCAAT GGTTCCTGCC TCCAGCATGG GGGACGCTCT TGCTTCTATA

13951 TCAATACCTG GTTCTGAGAC CACAGACATT GAGGGAGAGC CAACATCCTC

14001 CCTGACTGCT GGACGAAAAG AGAACAGCAC CCTCCAGGAG ATGAACTCAA

14051 CTACAGAGTC AAACATCATC CTCTCCAATG TGTCTGTGGG GGCTATTACT

14101 GAAGCCACAA AAATGGAAGT CCCCTCTTTT GATGCAACAT TCATACCAAC

14151 TCCTGCTCAG TCAACAAAGT TCCCAGATAT TTTCTCAGTA GCCAGCAGTA

14201 GACTTTCAAA CTCTCCTCCC ATGACAATAT CTACCCACAT GACCACCACC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

14251 CAGACAGGGT CTTCTGGAGC TACATCAAAG ATTCCACTTG CCTTAGACAC

14301 ATCAACCTTG GAAACCTCAG CAGGGACTCC ATCAGTGGTG ACTGAGGGGT

14351 TTGCCCACTC AAAAATAACC ACTGCAATGA ACAATGATGT CAAGGACGTG

14401 TCACAGACAA ACCCTCCCTT TCAGGATGAA GCCAGCTCTC CCTCTTCTCA

14451 AGCACCTGTC CTTGTCACAA CCTTACCTTC TTCTGTTGCT TTCACACCGC

14501 AATGGCACAG TACCTCCTCT CCTGTTTCTA TGTCCTCAGT TCTTACTTCT

14551 TCACTGGTAA AGACCGCAGG CAAGGTGGAT ACAAGCTTAG AAACAGTGAC

14601 CAGTTCACCT CAAAGTATGA GCAACACTTT GGATGACATA TCGGTCACTT

14651 CAGCAGCCAC CACAGATATA GAGACAACGC ATCCTTCCAT AAACACAGTA

14701 GTTACCAATG TGGGGACCAC CGGTTCAGCA TTTGAATCAC ATTCTACTGT

14751 CTCAGCTTAC CCAGAGCCAT CTAAAAGTCA CATTCTCCCA ATGTTACCAC

14801 CTCCACCATG GAAGACACCA CAATTTCCAC GATCAATACC TAAATCCTCT

14851 AAGACTACAA GAACTGAGAC TGAGACAACT TCCTCCCTGA CTCCTAAACT

14901 GAGGGAGACC AGCATCTCCC AGGAGATCAC CTCGTCCACA GAGACAAGCA

14951 CTGTTCCTTA CAAAGAGCTC ACTGGTGCCA CTACCGAGGT ATCCAGGACA

15001 GATGTCACTT CCTCTAGCAG TACATCCTTC CCTGGCCCTG ATCAGTCCAC

15051 AGTGTCACTA GACATCTCCA CAGAAACCAA CACCAGGCTG TCTACCTCCC

15101 CAATAATGAC AGAATCTGCA GAAATAACCA TCACCACCCA AACAGGTCCT

15151 CATGGGGCTA CATCACAGGA TACTTTTACC ATGGACCCAT CAAATACAAC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

15201 CCCCCAGGCA GGGATCCACT CAGCTATGAC TCATGGATTT TCACAATTGG

15251 ATGTGACCAC TCTTATGAGC AGAATTCCAC AGGATGTATC ATGGACAAGT

15301 CCTCCCTCTG TGGATAAAAC CAGCTCCCCC TCTTCCTTTC TGTCCTCACC

15351 TGCAATGACC ACACCTTCCC TGATTTCTTC TACCTTACCA GAGGATAAGC

15401 TCTCCTCTCC TATGACTTCA CTTCTCACCT CTGGCCTAGT GAAGATTACA

15451 GACATATTAC GTACACGCTT GGAACCTGTG ACCAGCTCAC TTCCAAATTT

15501 CAGCAGCACC TCAGATAAGA TACTGGCCAC TTCTAAAGAC AGTAAAGACA

15551 CAAAGGAAAT TTTTCCTTCT ATAAACACAG AAGAGACCAA TGTGAAAGCC

15601 AACAACTCTG GACATGAATC CCATTCCCCT GCACTGGCTG ACTCAGAGAC

15651 ACCCAAAGCC ACAACTCAAA TGGTTATCAC CACCACTGTG GGAGATCCAG

15701 CTCCTTCCAC ATCAATGCCA GTGCATGGTT CCTCTGAGAC TACAAACATT

15751 AAGAGAGAGC CAACATATTT CTTGACTCCT AGACTGAGAG AGACCAGTAC

15801 CTCTCAGGAG TCCAGCTTTC CCACGGACAC AAGTTTTCTA CTTTCCAAAG

15851 TCCCCACTGG TACTATTACT GAGGTCTCCA GTACAGGGGT CAACTCTTCT

15901 AGCAAAATTT CCACCCCAGA CCATGATAAG TCCACAGTGC CACCTGACAC

15951 CTTCACAGGA GAGATCCCCA GGGTCTTCAC CTCCTCTATT AAGACAAAAT

16001 CTGCAGAAAT GACGATCACC ACCCAAGCAA GTCCTCCTGA GTCTGCATCG

16051 CACAGTACCC TTCCCTTGGA CACATCAACC ACACTTTCCC AGGGAGGGAC

16101 TCATTCAACT GTGACTCAGG GATTCCCATA CTCAGAGGTG ACCACTCTCA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

16151 TGGGCATGGG TCCTGGGAAT GTGTCATGGA TGACAACTCC CCCTGTGGAA

16201 GAAACCAGCT CTGTGTCTTC CCTGATGTCT TCACCTGCCA TGACATCCCC

16251 TTCTCCTGTT TCCTCCACAT CACCACAGAG CATCCCCTCC TCTCCTCTTC

16301 CTGTGACTGC ACTTCCTACT TCTGTTCTGG TGACAACCAC AGATGTGTTG

16351 GGCACAACAA GCCCAGAGTC TGTAACCAGT TCACCTCCAA ATTTGAGCAG

16401 CATCACTCAT GAGAGACCGG CCACTTACAA AGACACTGCA CACACAGAAG

16451 CCGCCATGCA TCATTCCACA AACACCGCAG TGACCAATGT AGGGACTTCC

16501 GGGTCTGGAC ATAAATCACA ATCCTCTGTC CTAGCTGACT CAGAGACATC

16551 GAAAGCCACA CCTCTGATGA GTACCACCTC CACCCTGGGG GACACAAGTG

16601 TTTCCACATC AACTCCTAAT ATCTCTCAGA CTAACCAAAT TCAAACAGAG

16651 CCAACAGCAT CCCTGAGCCC TAGACTGAGG GAGAGCAGCA CGTCTGAGAA

16701 GACCAGCTCA ACAACAGAGA CAAATACTGC CTTTTCTTAT GTGCCCACAG

16751 GTGCTATTAC TCAGGCCTCC AGAACAGAAA TCTCCTCTAG CAGAACATCC

16801 ATCTCAGACC TTGATCGGCC CACAATAGCA CCCGACATCT CCACAGGAAT

16851 GATCACCAGG CTCTTCACCT CCCCCATCAT GACAAAATCT GCAGAAATGA

16901 CCGTCACCAC TCAAACAACT ACTCCTGGGG CTACATCACA GGGTATCCTT

16951 CCTTGGGACA CATCAACCAC ACTTTTCCAG GGAGGGACTC ATTCAACCGT

17001 GTCTCAGGGA TTCCCACACT CAGAGATAAC CACTCTTCGG AGCAGAACCC

17051 CTGGAGATGT GTCATGGATG ACAACTCCCC CTGTGGAAGA AACCAGCTCT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

17101 GGGTTTTCCC TGATGTCACC TTCCATGACA TCCCCTTCTC CTGTTTCCTC

17151 CACATCACCA GAGAGCATCC CCTCCTCTCC TCTCCCTGTG ACTGCACTTC

17201 TTACTTCTGT TCTGGTGACA ACCACCAATG TATTGGGCAC AACAAGCCCA

17251 GAGACCGTAA CGAGTTCACC TCCAAATTTA AGCAGCCCCA CACAGGAGAG

17301 ACTGACCACT TACAAAGACA CTGCGCACAC AGAAGCCATG CATGCTTCCA

17351 TGCATACAAA CACTGCAGTG GCCAACGTCG GGACCTCCAT TTCTGGACAT

17401 GAATCACAAT CTTCTGTCCC AGCTGATTCA CACACATCCA AAGCCACATC

17451 TCCAATGGGT ATCACCTTCG CCATGGGGGA TACAAGTGTT TCTACATCAA

17501 CTCCTGCCTT CTTTGAGACT AGAATTCAGA CTGAATCAAC ATCCTCTTTG

17551 ATTCCTGGAT TAAGGGACAC CAGGACGTCT GAGGAGATCA ACACTGTGAC

17601 AGAGACCAGC ACTGTCCTTT CAGAAGTGCC CACTACTACT ACTACTGAGG

17651 TCTCCAGGAC AGAAGTTATC ACTTCCAGCA GAACAACCAT CTCAGGGCCT

17701 GATCATTCCA AAATGTCACC CTACATCTCC ACAGAAACCA TCACCAGGCT

17751 CTCCACTTTT CCTTTTGTAA CAGGATCCAC AGAAATGGCC ATCACCAACC

17801 AAACAGGTCC TATAGGGACT ATCTCACAGG CTACCCTTAC CCTGGACACA

17851 TCAAGCACAG CTTCCTGGGA AGGGACTCAC TCACCTGTGA CTCAGAGATT

17901 TCCACACTCA GAGGAGACCA CTACTATGAG CAGAAGTACT AAGGGCGTGT

17951 CATGGCAAAG CCCTCCCTCT GTGGAAGAAA CCAGTTCTCC TTCTTCCCCA

18001 GTGCCTTTAC CTGCAATAAC CTCACATTCA TCTCTTTATT CCGCAGTATC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

18051 AGGAAGTAGC CCCACTTCTG CTCTCCCTGT GACTTCCCTT CTCACCTCTG

18101 GCAGGAGGAA GACCATAGAC ATGTTGGACA CACACTCAGA ACTTGTGACC

18151 AGCTCCTTAC CAAGTGCAAG TAGCTTCTCA GGTGAGATAC TCACTTCTGA

18201 AGCCTCCACA AATACAGAGA CAATTCACTT TTCAGAGAAC ACAGCAGAAA

18251 CCAATATGGG GACCACCAAT TCTATGCATA AACTACATTC CTCTGTCTCA

18301 ATCCACTCCC AGCCATCCGG ACACACACCT CCAAAGGTTA CTGGATCTAT

18351 GATGGAGGAC GCTATTGTTT CCACATCAAC ACCTGGTTCT CCTGAGACTA

18401 AAAATGTTGA CAGAGACTCA ACATCCCCTC TGACTCCTGA ACTGAAAGAG

18451 GACAGCACCG CCCTGGTGAT GAACTCAACT ACAGAGTCAA ACACTGTTTT

18501 CTCCAGTGTG TCCCTGGATG CTGCTACTGA GGTCTCCAGG GCAGAAGTCA

18551 CCTACTATGA TCCTACATTC ATGCCAGCTT CTGCTCAGTC AACAAAGTCC

18601 CCAGACATTT CACCTGAAGC CAGCAGCAGT CATTCTAACT CTCCTCCCTT

18651 GACAATATCT ACACACAAGA CCATCGCCAC ACAAACAGGT CCTTCTGGGG

18701 TGACATCTCT TGGCCAACTG ACCCTGGACA CATCAACCAT AGCCACCTCA

18751 GCAGGAACTC CATCAGCCAG AACTCAGGAT TTTGTAGATT CAGAAACAAC

18801 CAGTGTCATG AACAATGATC TCAATGATGT GTTGAAGACA AGCCCTTTCT

18851 CTGCAGAAGA AGCCAACTCT CTCTCTTCTC AGGCACCTCT CCTTGTGACA

18901 ACCTCACCTT CTCCTGTAAC TTCCACATTG CAAGAGCACA GTACCTCCTC

18951 TCTTGTTTCT GTGACCTCAG TACCCACCCC TACACTGGCG AAGATCACAG

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Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

19001 ACATGGACAC AAACTTAGAA CCTGTGACTC GTTCACCTCA AAATTTAAGG

19051 AACACCTTGG CCACTTCAGA AGCCACCACA GATACACACA CAATGCATCC

19101 TTCTATAAAC ACAGCAATGG CCAATGTGGG GACCACCAGT TCACCAAATG

19151 AATTCTATTT TACTGTCTCA CCTGACTCAG ACCCATATAA AGCCACATCC

19201 GCAGTAGTTA TCACTTCCAC CTCGGGGGAC TCAATAGTTT CCACATCAAT

19251 GCCTAGATCC TCTGCGATGA AAAAGATTGA GTCTGAGACA ACTTTCTCCC

19301 TGATATTTAG ACTGAGGGAG ACTAGCACCT CCCAGAAAAT TGGCTCATCC

19351 TCAGACACAA GCACGGTCTT TGACAAAGCA TTCACTGCTG CTACTACTGA

19401 GGTCTCCAGA ACAGAACTCA CCTCCTCTAG CAGAACATCC ATCCAAGGCA

19451 CTGAAAAGCC CACAATGTCA CCGGACACCT CCACAAGATC TGTCACCATG

19501 CTTTCTACTT TTGCTGGCCT GACAAAATCC GAAGAAAGGA CCATTGCCAC

19551 CCAAACAGGT CCTCATAGGG CGACATCACA GGGTACCCTT ACCTGGGACA

19601 CATCAATCAC AACCTCACAG GCAGGGACCC ACTCAGCTAT GACTCATGGA

19651 TTTTCACAAT TAGATTTGTC CACTCTTACG AGTAGAGTTC CTGAGTACAT

19701 ATCAGGGACA AGCCCACCCT CTGTGGAAAA AACCAGCTCT TCCTCTTCCC

19751 TTCTGTCTTT ACCAGCAATA ACCTCACCGT CCCCTGTACC TACTACATTA

19801 CCAGAAAGTA GGCCGTCTTC TCCTGTTCAT CTGACTTCAC TCCCCACCTC

19851 TGGCCTAGTG AAGACCACAG ATATGCTGGC ATCTGTGGCC AGTTTACCTC

19901 CAAACTTGGG CAGCACCTCA CATAAGATAC CGACTACTTC AGAAGACATT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

19951 AAAGATACAG AGAAAATGTA TCCTTCCACA AACATAGCAG TAACCAATGT

20001 GGGGACCACC ACTTCTGAAA AGGAATCTTA TTCGTCTGTC CCAGCCTACT

20051 CAGAACCACC CAAAGTCACC TCTCCAATGG TTACCTCTTT CAACATAAGG

20101 GACACCATTG TTTCCACATC CATGCCTGGC TCCTCTGAGA TTACAAGGAT

20151 TGAGATGGAG TCAACATTCT CCGTGGCTCA TGGGCTGAAG GGAACCAGCA

20201 CCTCCCAGGA CCCCATCGTA TCCACAGAGA AAAGTGCTGT CCTTCACAAG

20251 TTGACCACTG GTGCTACTGA GACCTCTAGG ACAGAAGTTG CCTCTTCTAG

20301 AAGAACATCC ATTCCAGGCC CTGATCATTC CACAGAGTCA CCAGACATCT

20351 CCACTGAAGT GATCCCCAGC CTGCCTATCT CCCTTGGCAT TACAGAATCT

20401 TCAAATATGA CCATCATCAC TCGAACAGGT CCTCCTCTTG GCTCTACATC

20451 ACAGGGCACA TTTACCTTGG ACACACCAAC TACATCCTCC AGGGCAGGAA

20501 CACACTCGAT GGCGACTCAG GAATTTCCAC ACTCAGAAAT GACCACTGTC

20551 ATGAACAAGG ACCCTGAGAT TCTATCATGG ACAATCCCTC CTTCTATAGA

20601 GAAAACCAGC TTCTCCTCTT CCCTGATGCC TTCACCAGCC ATGACTTCAC

20651 CTCCTGTTTC CTCAACATTA CCAAAGACCA TTCACACCAC TCCTTCTCCT

20701 ATGACCTCAC TGCTCACCCC TAGCCTAGTG ATGACCACAG ACACATTGGG

20751 CACAAGCCCA GAACCTACAA CCAGTTCACC TCCAAATTTG AGCAGTACCT

20801 CACATGAGAT ACTGACAACA GATGAAGACA CCACAGCTAT AGAAGCCATG

20851 CATCCTTCCA CAAGCACAGC AGCGACTAAT GTGGAAACCA CCAGTTCTGG

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

20901 ACATGGGTCA CAATCCTCTG TCCTAGCTGA CTCAGAAAAA ACCAAGGCCA

20951 CAGCTCCAAT GGATACCACC TCCACCATGG GGCATACAAC TGTTTCCACA

21001 TCAATGTCTG TTTCCTCTGA GACTACAAAA ATTAAGAGAG AGTCAACATA

21051 TTCCTTGACT CCTGGACTGA GAGAGACCAG CATTTCCCAA AATGCCAGCT

21101 TTTCCACTGA CACAAGTATT GTTCTTTCAG AAGTCCCCAC TGGTACTACT

21151 GCTGAGGTCT CCAGGACAGA AGTCACCTCC TCTGGTAGAA CATCCATCCC

21201 TGGCCCTTCT CAGTCCACAG TTTTGCCAGA AATATCCACA AGAACAATGA

21251 CAAGGCTCTT TGCCTCGCCC ACCATGACAG AATCAGCAGA AATGACCATC

21301 CCCACTCAAA CAGGTCCTTC TGGGTCTACC TCACAGGATA CCCTTACCTT

21351 GGACACATCC ACCACAAAGT CCCAGGCAAA GACTCATTCA ACTTTGACTC

21401 AGAGATTTCC ACACTCAGAG ATGACCACTC TCATGAGCAG AGGTCCTGGA

21451 GATATGTCAT GGCAAAGCTC TCCCTCTCTG GAAAATCCCA GCTCTCTCCC

21501 TTCCCTGCTG TCTTTACCTG CCACAACCTC ACCTCCTCCC ATTTCCTCCA

21551 CATTACCAGT GACTATCTCC TCCTCTCCTC TTCCTGTGAC TTCACTTCTC

21601 ACCTCTAGCC CGGTAACGAC CACAGACATG TTACACACAA GCCCAGAACT

21651 TGTAACCAGT TCACCTCCAA AGCTGAGCCA CACTTCAGAT GAGAGACTGA

21701 CCACTGGCAA GGACACCACA AATACAGAAG CTGTGCATCC TTCCACAAAC

21751 ACAGCAGCGT CCAATGTGGA GATTCCCAGC TCTGGACATG AATCCCCTTC

21801 CTCTGCCTTA GCTGACTCAG AGACATCCAA AGCCACATCA CCAATGTTTA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

21851	TTACCTCCAC	CCAGGAGGAT	ACAACTGTTG	CCATATCAAC CCCTCACTTC
21901	TTGGAGACTA	GCAGAATTCA	GAAAGAGTCA	ATTTCCTCCC TGAGCCCTAA
21951	ATTGAGGGAG	ACAGGCAGTT	CTGTGGAGAC	AAGCTCAGCC ATAGAGACAA
22001	GTGCTGTCCT	TTCTGAAGTG	TCCGTTGGTG	CTACTACTGA GATCTCCAGG
22051	ACAGAAGTCA	CCTCCTCTAG	CAGAACATCC	ATCTCTGGTT CTGCTGAGTC
22101	CACAATGTTG	CCAGAAATAT	CCACCACAAG	AAAAATCATT AAGTTCCCTA
22151	CTTCCCCCAT	CCTGGCAGAA	TCATCAGAAA	TGACCATCAA GACCCAAACA
22201	AGTCCTCCTG	GGTCTACATC	AGAGAGTACC	TTTACATTAG ACACATCAAC
22251	CACTCCCTCC	TTGGTAATAA	CCCATTCGAC	TATGACTCAG AGATTGCCAC
22301	ACTCAGAGAT	AACCACTCTT	GTGAGTAGAG	GTGCTGGGGA TGTGCCACGG
22351	CCCAGCTCTC	TCCCTGTGGA	AGAAACAAGC	CCTCCATCTT CCCAGCTGTC
22401	TTTATCTGCC	ATGATCTCAC	CTTCTCCTGT	TTCTTCCACA TTACCAGCAA
22451	GTAGCCACTC	CTCTTCTGCT	TCTGTGACTT	CACTTCTCAC ACCAGGCCAA
22501	GTGAAGACTA	CTGAGGTGTT	GGACGCAAGT	GCAGAACCTG AAACCAGTTC
22551	ACCTCCAAGT	TTGAGCAGCA	CCTCAGTTGA	AATACTGGCC ACCTCTGAAG
22601	TCACCACAGA	TACGGAGAAA	ATTCATCCTT	TCTCAAACAC GGCAGTAACC
22651	AAAGTTGGAA	CTTCCAGTTC	TGGACATGAA	TCCCCTTCCT CTGTCCTACC
22701	TGACTCAGAG	ACAACCAAAG	CCACATCGGC	AATGGGTACC ATCTCCATTA
22751	TGGGGGATAC	AAGTGTTTCT	ACATTAACTC	CTGCCTTATC TAACACTAGG

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

22801 AAAATTCAGT CAGAGCCAGC TTCCTCACTG ACCACCAGAT TGAGGGAGAC

22851 CAGCACCTCT GAAGAGACCA GCTTAGCCAC AGAAGCAAAC ACTGTTCTTT

22901 CTAAAGTGTC CACTGGTGCT ACTACTGAGG TCTCCAGGAC AGAAGCCATC

22951 TCCTTTAGCA GAACATCCAT GTCAGGCCCT GAGCAGTCCA CAATGTCACA

23001 AGACATCTCC ATAGGAACCA TCCCCAGGAT TTCTGCCTCC TCTGTCCTGA

23051 CAGAATCTGC AAAAATGACC ATCACAACCC AAACAGGTCC TTCGGAGTCT

23101 ACACTAGAAA GTACCCTTAA TTTGAACACA GCAACCACAC CCTCTTGGGT

23151 GGAAACCCAC TCTATAGTAA TTCAGGGATT TCCACACCCA GAGATGACCA

23201 CTTCCATGGG CAGAGGTCCT GGAGGTGTGT CATGGCCTAG CCCTCCCTTT

23251 GTGAAAGAAA CCAGCCCTCC ATCCTCCCCG CTGTCTTTAC CTGCCGTGAC

23301 CTCACCTCAT CCTGTTTCCA CCACATTCCT AGCACATATC CCCCCCTCTC

23351 CCCTTCCTGT GACTTCACTT CTCACCTCTG GCCCGGCGAC AACCACAGAT

23401 ATCTTGGGTA CAAGCACAGA ACCTGGAACC AGTTCATCTT CAAGTTTGAG

23451 CACCACCTCC CATGAGAGAC TGACCACTTA CAAAGACACT GCACATACAG

23501 AAGCCGTGCA TCCTTCCACA AACACAGGAG GGACCAATGT GGCAACCACC

23551 AGCTCTGGAT ATAAATCACA GTCCTCTGTC CTAGCTGACT CATCTCCAAT

23601 GTGTACCACC TCCACCATGG GGGATACAAG TGTTCTCACA TCAACTCCTG

23651 CCTTCCTTGA GACTAGGAGG ATTCAGACAG AGCTAGCTTC CTCCCTGACC

23701 CCTGGATTGA GGGAGTCCAG TGGCTCTGAA GGGACCAGCT CAGGCACCAA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

23751 GATGAGCACT GTCCTCTCTA AAGTGCCCAC TGGTGCTACT ACTGAGATCT

23801 CCAAGGAAGA CGTCACCTCC ATCCCAGGTC CCGCTCAATC CACAATATCA

23851 CCAGACATCT CCACAAGAAC CGTCAGCTGG TTCTCTACAT CCCCTGTCAT

23901 GACAGAATCA GCAGAAATAA CCATGAACAC CCATACAAGT CCTTTAGGGG

23951 CCACAACACA AGGCACCAGT ACTTTGGCCA CGTCAAGCAC AACCTCTTTG

24001 ACAATGACAC ACTCAACTAT ATCTCAAGGA TTTTCACACT CACAGATGAG

24051 CACTCTTATG AGGAGGGGTC CTGAGGATGT ATCATGGATG AGCCCTCCCC

24101 TTCTGGAAAA AACTAGACCT TCCTTTTCTC TGATGTCTTC ACCAGCCACA

24151 ACTTCACCTT CTCCTGTTTC CTCCACATTA CCAGAGAGCA TCTCTTCCTC

24201 TCCTCTTCCT GTGACTTCAC TCCTCACGTC TGGCTTGGCA AAAACTACAG

24251 ATATGTTGCA CAAAAGCTCA GAACCTGTAA CCAACTCACC TGCAAATTTG

24301 AGCAGCACCT CAGTTGAAAT ACTGGCCACC TCTGAAGTCA CCACAGATAC

24351 AGAGAAAACT CATCCTTCTT CAAACAGAAC AGTGACCGAT GTGGGGACCT

24401 CCAGTTCTGG ACATGAATCC ACTTCCTTTG TCCTAGCTGA CTCACAGACA

24451 TCCAAAGTCA CATCTCCAAT GGTTATTACC TCCACCATGG AGGATACGAG

24501 TGTCTCCACA TCAACTCCTG GCTTTTTTGA GACTAGCAGA ATTCAGACAG

24551 AACCAACATC CTCCCTGACC CTTGGACTGA GAAAGACCAG CAGCTCTGAG

24601 GGGACCAGCT TAGCCACAGA GATGAGCACT GTCCTTTCTG GAGTGCCCAC

24651 TGGTGCCACT GCTGAAGTCT CCAGGACAGA AGTCACCTCC TCTAGCAGAA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

24701 CATCCATCTC AGGCTTTGCT CAGCTCACAG TGTCACCAGA GACTTCCACA

24751 GAAACCATCA CCAGACTCCC TACCTCCAGC ATAATGACAG AATCAGCAGA

24801 AATGATGATC AAGACACAAA CAGATCCTCC TGGGTCTACA CCAGAGAGTA

24851 CTCATACTGT GGACATATCA ACAACACCCA ACTGGGTAGA AACCCACTCG

24901 ACTGTGACTC AGAGATTTTC ACACTCAGAG ATGACCACTC TTGTGAGCAG

24951 AAGCCCTGGT GATATGTTAT GGCCTAGTCA ATCCTCTGTG GAAGAAACCA

25001 GCTCTGCCTC TTCCCTGCTG TCTCTGCCTG CCACGACCTC ACCTTCTCCT

25051 GTTTCCTCTA CATTAGTAGA GGATTTCCCT TCCGCTTCTC TTCCTGTGAC

25101 TTCTCTTCTC ACCCCTGGCC TGGTGATAAC CACAGACAGG ATGGGCATAA

25151 GCAGAGAACC TGGAACCAGT TCCACTTCAA ATTTGAGCAG CACCTCCCAT

25201 GAGAGACTGA CCACTTTGGA AGACACTGTA GATACAGAAG ACATGCAGCC

25251 TTCCACACAC ACAGCAGTGA CCAACGTGAG GACCTCCATT TCTGGACATG

25301 AATCACAATC TTCTGTCCTA TCTGACTCAG AGACACCCAA AGCCACATCT

25351 CCAATGGGTA CCACCTACAC CATGGGGGAA ACGAGTGTTT CCATATCCAC

25401 TTCTGACTTC TTTGAGACCA GCAGAATTCA GATAGAACCA ACATCCTCCC

25451 TGACTTCTGG ATTGAGGGAG ACCAGCAGCT CTGAGAGGAT CAGCTCAGCC

25501 ACAGAGGGAA GCACTGTCCT TTCTGAAGTG CCCAGTGGTG CTACCACTGA

25551 GGTCTCCAGG ACAGAAGTGA TATCCTCTAG GGGAACATCC ATGTCAGGGC

25601 CTGATCAGTT CACCATATCA CCAGACATCT CTACTGAAGC GATCACCAGG

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

25651 CTTTCTACTT CCCCCATTAT GACAGAATCA GCAGAAAGTG CCATCACTAT

25701 TGAGACAGGT TCTCCTGGGG CTACATCAGA GGGTACCCTC ACCTTGGACA

25751 CCTCAACAAC AACCTTTTGG TCAGGGACCC ACTCAACTGC ATCTCCAGGA

25801 TTTTCACACT CAGAGATGAC CACTCTTATG AGTAGAACTC CTGGAGATGT

25851 GCCATGGCCG AGCCTTCCCT CTGTGGAAGA AGCCAGCTCT GTCTCTTCCT

25901 CACTGTCTTC ACCTGCCATG ACCTCAACTT CTTTTTTCTC CACATTACCA

25951 GAGAGCATCT CCTCCTCTCC TCATCCTGTG ACTGCACTTC TCACCCTTGG

26001 CCCAGTGAAG ACCACAGACA TGTTGCGCAC AAGCTCAGAA CCTGAAACCA

26051 GTTCACCTCC AAATTTGAGC AGCACCTCAG CTGAAATATT AGCCACGTCT

26101 GAAGTCACCA AAGATAGAGA GAAAATTCAT CCCTCCTCAA ACACACCTGT

26151 AGTCAATGTA GGGACTGTGA TTTATAAACA TCTATCCCCT TCCTCTGTTT

26201 TGGCTGACTT AGTGACAACA AAACCCACAT CTCCAATGGC TACCACCTCC

26251 ACTCTGGGGA ATACAAGTGT TTCCACATCA ACTCCTGCCT TCCCAGAAAC

26301 TATGATGACA CAGCCAACTT CCTCCCTGAC TTCTGGATTA AGGGAGATCA

26351 GTACCTCTCA AGAGACCAGC TCAGCAACAG AGAGAAGTGC TTCTCTTTCT

26401 GGAATGCCCA CTGGTGCTAC TACTAAGGTC TCCAGAACAG AAGCCCTCTC

26451 CTTAGGCAGA ACATCCACCC CAGGTCCTGC TCAATCCACA ATATCACCAG

26501 AAATCTCCAC GGAAACCATC ACTAGAATTT CTACTCCCCT CACCACGACA

26551 GGATCAGCAG AAATGACCAT CACCCCCAAA ACAGGTCATT CTGGGGCATC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

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26601  CTCACAAGGT ACCTTTACCT TGGACACATC AAGCAGAGCC TCCTGGCCAG
26651  GAACTCACTC AGCTGCAACT CACAGATCTC CACACTCAGG GATGACCACT
26701  CCTATGAGCA GAGGTCCTGA GGATGTGTCA TGGCCAAGCC GCCCATCAGT
26751  GGAAAAAACT AGCCCTCCAT CTTCCCTGGT GTCTTTATCT GCAGTAACCT
26801  CACCTTCGCC ACTTTATTCC ACACCATCTG AGAGTAGCCA CTCATCTCCT
26851  CTCCGGGTGA CTTCTCTTTT CACCCCTGTC ATGATGAAGA CCACAGACAT
26901  GTTGGACACA AGCTTGGAAC CTGTGACCAC TTCACCTCCC AGTATGAATA
26951  TCACCTCAGA TGAGAGTCTG GCCACTTCTA AAGCCACCAT GGAGACAGAG
27001  GCAATTCAGC TTTCAGAAAA CACAGCTGTG ACTCAGATGG GCACCATCAG
27051  CGCTAGACAA GAATTCTATT CCTCTTATCC AGGCCTCCCA GAGCCATCCA
27101  AAGTGACATC TCCAGTGGTC ACCTCTTCCA CCATAAAAGA CATTGTTTCT
27151  ACAACCATAC CTGCTTCCTC TGAGATAACA AGAATTGAGA TGGAGTCAAC
27201  ATCCACCCTG ACCCCCACAC CAAGGGAGAC CAGCACCTCC CAGGAGATCC
27251  ACTCAGCCAC AAAGCCAAGC ACTGTTCCTT ACAAGGCACT CACTAGTGCC
27301  ACGATTGAGG ACTCCATGAC ACAAGTCATG TCCTCTAGCA GAGGACCTAG
27351  CCCTGATCAG TCCACAATGT CACAAGACAT ATCCAGTGAA GTGATCACCA
27401  GGCTCTCTAC CTCCCCCATC AAGGCAGAAT CTACAGAAAT GACCATTACC
27451  ACCCAAACAG GTTCTCCTGG GGCTACATCA AGGGGTACCC TTACCTTGGA
27501  CACTTCAACA ACTTTTATGT CAGGGACCCA CTCAACTGCA TCTCAAGGAT
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Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

27551 TTTCACACTC ACAGATGACC GCTCTTATGA GTAGAACTCC TGGAGATGTG

27601 CCATGGCTAA GCCATCCCTC TGTGGAAGAA GCCAGCTCTG CCTCTTTCTC

27651 ACTGTCTTCA CCTGTCATGA CCTCATCTTC TCCCGTTTCT TCCACATTAC

27701 CAGACAGCAT CCACTCTTCT TCGCTTCCTG TGACATCACT TCTCACCTCA

27751 GGGCTGGTGA AGACCACAGA GCTGTTGGGC ACAAGCTCAG AACCTGAAAC

27801 CAGTTCACCC CCAAATTTGA GCAGCACCTC AGCTGAAATA CTGGCCACCA

27851 CTGAAGTCAC TACAGATACA GAGAAACTGG AGATGACCAA TGTGGTAACC

27901 TCAGGTTATA CACATGAATC TCCTTCCTCT GTCCTAGCTG ACTCAGTGAC

27951 AACAAAGGCC ACATCTTCAA TGGGTATCAC CTACCCCACA GGAGATACAA

28001 ATGTTCTCAC ATCAACCCCT GCCTTCTCTG ACACCAGTAG GATTCAAACA

28051 AAGTCAAAGC TCTCACTGAC TCCTGGGTTG ATGGAGACCA GCATCTCTGA

28101 AGAGACCAGC TCTGCCACAG AAAAAAGCAC TGTCCTTTCT AGTGTGCCCA

28151 CTGGTGCTAC TACTGAGGTC TCCAGGACAG AAGCCATCTC TTCTAGCAGA

28201 ACATCCATCC CAGGCCCTGC TCAATCCACA ATGTCATCAG ACACCTCCAT

28251 GGAAACCATC ACTAGAATTT CTACCCCCCT CACAAGGAAA GAATCAACAG

28301 ACATGGCCAT CACCCCCAAA ACAGGTCCTT CTGGGGCTAC CTCGCAGGGT

28351 ACCTTTACCT TGGACTCATC AAGCACAGCC TCCTGGCCAG GAACTCACTC

28401 AGCTACAACT CAGAGATTTC CACAGTCAGT GGTGACAACT CCTATGAGCA

28451 GAGGTCCTGA GGATGTGTCA TGGCCAAGCC CGCTGTCTGT GGAAAAAAAC

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

28501 AGCCCTCCAT CTTCCCTGGT ATCTTCATCT TCAGTAACCT CACCTTCGCC

28551 ACTTTATTCC ACACCATCTG GGAGTAGCCA CTCCTCTCCT GTCCCTGTCA

28601 CTTCTCTTTT CACCTCTATC ATGATGAAGG CCACAGACAT GTTGGATGCA

28651 AGTTTGGAAC CTGAGACCAC TTCAGCTCCC AATATGAATA TCACCTCAGA

28701 TGAGAGTCTG GCCGCTTCTA AAGCCACCAC GGAGACAGAG GCAATTCACG

28751 TTTTTGAAAA TACAGCAGCG TCCCATGTGG AAACCACCAG TGCTACAGAG

28801 GAACTCTATT CCTCTTCCCC AGGCTTCTCA GAGCCAACAA AAGTGATATC

28851 TCCAGTGGTC ACCTCTTCCT CTATAAGAGA CAACATGGTT TCCACAACAA

28901 TGCCTGGCTC CTCTGGCATT ACAAGGATTG AGATAGAGTC AATGTCATCT

28951 CTGACCCCTG GACTGAGGGA GACCAGAACC TCCCAGGACA TCACCTCATC

29001 CACAGAGACA AGCACTGTCC TTTACAAGAT GCCCTCTGGT GCCACTCCTG

29051 AGGTCTCCAG GACAGAAGTT ATGCCCTCTA GCAGAACATC CATTCCTGGC

29101 CCTGCTCAGT CCACAATGTC ACTAGACATC TCCGATGAAG TTGTCACCAG

29151 GCTGTCTACC TCTCCCATCA TGACAGAATC TGCAGAAATA ACCATCACCA

29201 CCCAAACAGG TTATTCTCTG GCTACATCCC AGGTTACCCT TCCCTTGGGC

29251 ACCTCAATGA CCTTTTTGTC AGGGACCCAC TCAACTATGT CTCAAGGACT

29301 TTCACACTCA GAGATGACCA ATCTTATGAG CAGGGGTCCT GAAAGTCTGT

29351 CATGGACGAG CCCTCGCTTT GTGGAAACAA CTAGATCTTC CTCTTCTCTG

29401 ACATCATTAC CTCTCACGAC CTCACTTTCT CCTGTGTCCT CCACATTACT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

29451 AGACAGTAGC CCCTCCTCTC CTCTTCCTGT GACTTCACTT ATCCTCCCAG

29501 GCCTGGTGAA GACTACAGAA GTGTTGGATA CAAGCTCAGA GCCTAAAACC

29551 AGTTCATCTC CAAATTTGAG CAGCACCTCA GTTGAAATAC CGGCCACCTC

29601 TGAAATCATG ACAGATACAG AGAAAATTCA TCCTTCCTCA AACACAGCGG

29651 TGGCCAAAGT GAGGACCTCC AGTTCTGTTC ATGAATCTCA TTCCTCTGTC

29701 CTAGCTGACT CAGAAACAAC CATAACCATA CCTTCAATGG GTATCACCTC

29751 CGCTGTGGAC GATACCACTG TTTTCACATC AAATCCTGCC TTCTCTGAGA

29801 CTAGGAGGAT TCCGACAGAG CCAACATTCT CATTGACTCC TGGATTCAGG

29851 GAGACTAGCA CCTCTGAAGA GACCACCTCA ATCACAGAAA CAAGTGCAGT

29901 CCTTTATGGA GTGCCCACTA GTGCTACTAC TGAAGTCTCC ATGACAGAAA

29951 TCATGTCCTC TAATAGAACA CACATCCCTG ACTCTGATCA GTCCACGATG

30001 TCTCCAGACA TCATCACTGA AGTGATCACC AGGCTCTCTT CCTCATCCAT

30051 GATGTCAGAA TCAACACAAA TGACCATCAC CACCCAAAAA AGTTCTCCTG

30101 GGGCTACAGC ACAGAGTACT CTTACCTTGG CCACAACAAC AGCCCCCTTG

30151 GCAAGGACCC ACTCAACTGT TCCTCCTAGA TTTTTACACT CAGAGATGAC

30201 AACTCTTATG AGTAGGAGTC CTGAAAATCC ATCATGGAAG AGCTCTCCCT

30251 TTGTGGAAAA AACTAGCTCT TCATCTTCTC TGTTGTCCTT ACCTGTCACG

30301 ACCTCACCTT CTGTTTCTTC CACATTACCG CAGAGTATCC CTTCCTCCTC

30351 TTTTTCTGTG ACTTCACTCC TCACCCCAGG CATGGTGAAG ACTACAGACA

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension
(SEQ ID NO: 309)

30401 CAAGCACAGA ACCTGGAACC AGTTTATCTC CAAATCTGAG TGGCACCTCA

30451 GTTGAAATAC TGGCTGCCTC TGAAGTCACC ACAGATACAG AGAAAATTCA

30501 TCCTTCTTCA AGCATGGCAG TGACCAATGT GGGAACCACC AGTTCTGGAC

30551 ATGAACTATA TTCCTCTGTT TCAATCCACT CGGAGCCATC CAAGGCTACA

30601 TACCCAGTGG GTACTCCCTC TTCCATGGCT GAAACCTCTA TTTCCACATC

30651 AATGCCTGCT AATTTTGAGA CCACAGGATT TGAGGCTGAG CCATTTTCTC

30701 ATTTGACTTC TGGATTTAGG AAGACAAACA TGTCCCTGGA CACCAGCTCA

30751 GTCACACCAA CAAATACACC TTCTTCTCCT GGGTCCACTC ACCTTTTACA

30801 GAGTTCCAAG ACTGATTTCA CCTCTTCTGC AAAAACATCA TCCCCAGACT

30851 GGCCTCCAGC CTCACAGTAT ACTGAAATTC CAGTGGACAT AATCACCCCC

30901 TTTAATGCTT CTCCATCTAT TACGGAGTCC ACTGGGATAA CCTCCTTCCC

30951 AGAATCCAGG TTTACTATGT CTGTAACAGA AAGTACTCAT CATCTGAGTA

31001 CAGATTTGCT GCCTTCAGCT GAGACTATTT CCACTGGCAC AGTGATGCCT

31051 TCTCTATCAG AGGCCATGAC TTCATTTGCC ACCACTGGAG TTCCACGAGC

31101 CATCTCAGGT TCAGGTAGTC CATTCTCTAG GACAGAGTCA GGCCCTGGGG

31151 ATGCTACTCT GTCCACCATT GCAGAGAGCC TGCCTTCATC CACTCCTGTG

31201 CCATTCTCCT CTTCAACCTT CACTACCACT GATTCTTCAA CCATCCCAGC

31251 CCTCCATGAG ATAACTTCCT CTTCAGCTAC CCCATATAGA GTGGACACCA

31301 GTCTTGGGAC AGAGAGCAGC ACTACTGAAG GACGCTTGGT TATGGTCAGT

Table 24 (continued)

DNA Sequence of the CA125 Amino Terminal Extension

(SEQ ID NO: 309)

31351 ACTTTGGACA CTTCAAGCCA ACCAGGCAGG ACATCTTCAA CACCCATTTT

31401 GGATACCAGA ATGACAGAGA GCGTTGAGCT GGGAACAGTG ACAAGTGCTT

31451 ATCAAGTTCC TTCACTCTCA ACACGGTTGA CAAGAACTGA TGGCATT

Table 25

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

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  1  MLKPSGLPGS SSPTRSLMTG SRSTKATPEM DSGLTGATLS PKTSTGAIVV
 51  TEHTLPFTSP DKTLASPTSS VVGRTTQSLG VMSSALPEST SRGMTHSEQR
101  TSPSLSPQVN GTPSRNYPAT SMVSGLSSPR TRTSSTEGNF TKEASTYTLT
151  VETTSGPVTE KYTVPTETST TEGDSTETPW DTRYIPVKIT SPMKTFADST
201  ASKENAPVSM TPAETTVTDS HTPGRTNPSF GTLYSSFLDL SPKGTPNSRG
251  ETSLELILST TGYPFSSPEP GSAGHSRIST SAPLSSSASV LDNKISETSI
301  FSGQSLTSPL SPGVPEARAS TMPNSAIPFS MTLSNAETSA ERVRSTISSL
351  GTPSISTKQT AETILTFHAF AETMDIPSTH IAKTLASEWL GSPGTLGGTS
401  TSALTTTSPS TTLVSEETNT HHSTSGKETE GTLNTSMTPL ETSAPGEESE
451  MTATLVPTLG FTTLDSKIRS PSQVSSSHPT RELRTTGSTS GRQSSSTAAH
501  GSSDILRATT SSTSKASSWT SESTAQQFSE PQHTQWVETS PSMKTERPPA
551  STSVAAPITT SVPSVVSGFT TLKTSSTKGI WLEETSADTL IGESTAGPTT
601  HQFAVPTGIS MTGGSSTRGS QGTTHLLTRA TASSETSADL TLATNGVPVS
651  VSPAVSKTAA GSSPPGGTKP SYTMVSSVIP ETSSLQSSAF REGTSLGLTP
701  LNTRHPFSSP EPDSAGHTKI STSIPLLSSA SVLEDKVSAT STFSHHKATS
751  SITTGTPEIS TKTKPSSAVL SSMTLSNAAT SPERVRNATS PLTHPSPSGE
801  ETAGSVLTLS TSAETTDSPN IHPTGTLTSE SSESPSTLSL PSVSGVKTTF
851  SSSTPSTHLF TSGEETEETS NPSVSQPETS VSRVRTTLAS TSVPTPVFPT
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Table 25 (continued)

Amino Terminal Extension of the CA125 Gene Protein Sequence)
(SEQ ID NO: 310)

901 MDTWPTRSAQ FSSSHLVSEL RATSSTSVTN STGSALPKIS HLTGTATMSQ

951 TNRDTFNDSA APQSTTWPET SPRFKTGLPS ATTTVSTSAT SLSATVMVSK

1001 FTSPATSSME ATSIREPSTT ILTTETTNGP GSMAVASTNI PIGKGYITEG

1051 RLDTSHLPIG TTASSETSMD FTMAKESVSM SVSPSQSMDA AGSSTPGRTS

1101 QFVDTFSDDV YHLTSREITI PRDGTSSALT PQMTATHPPS PDPGSARSTW

1151 LGILSSSPSS PTPKVTMSST FSTQRVTTSM IMDTVETSRW NMPNLPSTTS

1201 LTPSNIPTSG AIGKSTLVPL DTPSPATSLE ASEGGLPTLS TYPESTNTPS

1251 IHLGAHASSE SPSTINLTMA SVVKPGSYTP LTFPSIETHI HVSTARMAYS

1301 SGSSPEMTAP GETNTGSTWD PTTYITTTDP KDTSSAQVST PHSVRTLRTT

1351 ENHPKTESAT PAAYSGSPKI SSSPNLTSPA TKAWTITDTT EHSTQLHYTK

1401 LAEKSSGFET QSAPGPVSVV IPTSPTIGSS TLELTSDVPG EPLVLAPSEQ

1451 TTITLPMATW LSTSLTEEMA STDLDISSPS SPMSTFAIFP PMSTPSHELS

1501 KSEADTSAIR NTDSTTLDQH LGIRSLGRTG DLTTVPITPL TTTWTSVIEH

1551 STQAQDTLSA TMSPTHVTQS LKDQTSIPAS ASPSHLTEVY PELGTQGRSS

1601 SEATTFWKPS TDTLSREIET GPTNIQSTPP MDNTTTGSSS SGVTLGIAHL

1651 PIGTSSPAET STNMALERRS STATVSMAGT MGLLVTSAPG RSISQSLGRV

1701 SSVLSESTTE GVTDSSKGSS PRLNTQGNTA LSSSLEPSYA EGSQMSTSIP

1751 LTSSPTTPDV EFIGGSTFWT KEVTTVMTSD ISKSSARTES SSATLMSTAL

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

1801 GSTENTGKEK LRTASMDLPS PTPSMEVTPW ISLTLSNAPN TTDSLDLSHG

1851 VHTSSAGTLA TDRSLNTGVT RASRLENGSD TSSKSLSMGN STHTSMTDTE

1901 KSEVSSSIHP RPETSAPGAE TTLTSTPGNR AISLTLPFSS IPVEEVISTG

1951 ITSGPDINSA PMTHSPITPP TIVWTSTGTI EQSTQPLHAV SSEKVSVQTQ

2001 STPYVNSVAV SASPTHENSV SSGSSTSSPY SSASLESLDS TISRRNAITS

2051 WLWDLTTSLP TTTWPSTSLS EALSSGHSGV SNPSSTTTEF PLFSAASTSA

2101 AKQRNPETET HGPQNTAAST LNTDASSVTG LSETPVGASI SSEVPLPMAI

2151 TSRSDVSGLT SESTANPSLG TASSAGTKLT RTISLPTSES LVSFRMNKDP

2201 WTVSIPLGSH PTTNTETSIP VNSAGPPGLS TVASDVIDTP SDGAESIPTV

2251 SFSPSPDTEV TTISHFPEKT THSFRTISSL THELTSRVTP IPGDWMSSAM

2301 STKPTGASPS ITLGERRTIT SAAPTTSPIV LTASFTETST VSLDNETTVK

2351 TSDILDARKT NELPSDSSSS SDLINTSIAS STMDVTKTAS ISPTSISGMT

2401 ASSSPSLFSS DRPQVPTSTT ETNTATSPSV SSNTYSLDGG SNVGGTPSTL

2451 PPFTITHPVE TSSALLAWSR PVRTFSTMVS TDTASGENPT SSNSVVTSVP

2501 APGTWTSVGS TTDLPAMGFL KTSPAGEAHS LLASTIEPAT AFTPHLSAAV

2551 VTGSSATSEA SLLTTSESKA IHSSPQTPTT PTSGANWETS ATPESLLVVT

2601 ETSDTTLTSK ILVTDTILFS TVSTPPSKFP STGTLSGASF PTLLPDTPAI

2651 PLTATEPTSS LATSFDSTPL VTIASDSLGT VPETTLTMSE TSNGDALVLK

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

2701 TVSNPDRSIP GITIQGVTES PLHPSSTSPS KIVAPRNTTY EGSITVALST

2751 LPAGTTGSLV FSQSSENSET TALVDSSAGL ERASVMPLTT GSQGMASSGG

2801 IRSGSTHSTG TKTFSSLPLT MNPGEVTAMS EITTNRLTAT QSTAPKGIPV

2851 KPTSAESGLL TPVSASSSPS KAFASLTTAP PTWGIPQSTL TFEFSEVPSL

2901 DTKSASLPTP GQSLNTIPDS DASTASSSLS KSPEKNPRAR MMTSTKAISA

2951 SSFQSTGFTE TPEGSASPSM AGHEPRVPTS GTGDPRYASE SMSYPDPSKA

3001 SSAMTSTSLA SKLTTLFSTG QAARSGSSSS PISLSTEKET SFLSPTASTS

3051 RKTSLFLGPS MARQPNILVH LQTSALTLSP TSTLNMSQEE PPELTSSQTI

3101 AEEEGTTAET QTLTFTPSET PTSLLPVSSP TEPTARRKSS PETWASSISV
Contig 27

3151 PAKTSLVETT DGTLVTTIKM SSQAAQGNST QPAPAEETGT SPAGTSPGSP

3201 EMSTTLKIMS SKEPSISPEI RSTVRNSPWK TPETTVPMET TVEPVTLQST

3251 ALGSGSTSIS HLPTGTTSPT KSPTENMLAT ERVSLSPSPP EAWTNLYSGT

3301 PGGTRQSLAT MSSVSLESPT ARSITGTGQQ SSPELVSKTT GMEFSMWHGS

3351 TGGTTGDTHV SLSTSSNILE DPVTSPNSVS SLTDKSKHKT ETWVSTTAIP

3401 STVLNNKIMA AEQQTSRSVD EAYSSTSSWS DQTSGSDITL GASPDVTNTL

3451 YITSTAQTTS LVSLPSGDQG ITSLTNPSGG KTSSASSVTS PSIGLETLRA

3501 NVSAVKSDIA PTAGHLSQTS SPAEVSILDV TTAPTPGIST TITTMGTNSI

3551 STTTPNPEVG MSTMDSTPAT ERRTTSTEHP STWSSTAASD SWTVTDMTSN

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

3601 LKVARSPGTI STMHTTSFLA SSTELDSMST PHGRITVIGT SLVTPSSDAS

3651 AVKTETSTSE RTLSPSDTTA STPISTFSRV QRMSISVPDI LSTSWTPSST

3701 EAEDVPVSMV PTDHASTKTD PNTPLSTFLF DSLSTLDWDT GRSLSSATAT

3751 TSAPQGATTP QELTLETMIS PATSQLPFSI GHITSAVTPA AMARSSGVTF

3801 SRPDPTSKKA EQTSTQLPTT TSAHPGQVPR SAATTLDVIP HTAKTPDATF

3851 QRQGQTALTT EARATSDSWN EKEKSTPSAP WITEMMNSVS EDTIKEVTSS

3901 SSVLKDPEYA GHKLGIWDDF IPKFGKAAHM RELPLLSPPQ DKEAIHPSTN

3951 TVETTGWVTS SEHASHSTIP AHSASSKLTS PVVTTSTREQ AIVSMSTTTW

4001 PESTRARTEP NSFLTIELRD VSPYMDTSST TQTSIISSPG STAITKGHRT

4051 EITSYKRISS SFLAQSMRSS DSPSEAITRL SNFPAMTESG GMILAMQTSP

4101 PGATSISAPT LDTSATASWT GTPLATTQRF TYSEKTTLFS KGREDTSQPS

4151 PPCVEETSSS SSVVPIHATT SPSNILLTSQ GHSPSSTPPV TSVFLSETSG

4201 LGKTTDMSRI SLEPGTSLPP NLSSTAGEAL STYEASRDTK AIHHSADTAV

4251 TNMEATSSEY SPIPGHTKPS KATSPLVTSH IMGDITSSTS VFGSSETTEI

4301 ETVSSVNQGL QERSTSQVAS SATETSTVIT HVSSGDATTH VTKTQATFSS

4351 GTSISSPHQF ITSTNTFTDV STNPSTSLIM TESSGVTITT QTGPTGAATQ

4401 GPYLLDTSTM PYLTETPLAV TPDFMQSEKT TLISKGPKDV TWTSPPSVAE

4451 TSYPSSLTPF LVTTIPPATS TLQGQHTSSP VSATSVLTSG LVKTTDMLNT

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

4501 SMEPVTNSPQ NLNNPSNEIL ATLAATTDIE TIHPSINKAV TNMGTASSAH

4551 VLHSTLPVSS EPSTATSPMV PASSMGDALA SISIPGSETT DIEGEPTSSL

4601 TAGRKENSTL QEMNSTTESN IILSNVSVGA ITEATKMEVP SFDATFIPTP

4651 AQSTKFPDIF SVASSRLSNS PPMTISTHMT TTQTGSSGAT SKIPLALDTS

4701 TLETSAGTPS VVTEGFAHSK ITTAMNNDVK DVSQTNPPFQ DEASSPSSQA

4751 PVLVTTLPSS VAFTPQWHST SSPVSMSSVL TSSLVKTAGK VDTSLETVTS

4801 SPQSMSNTLD DISVTSAATT DIETTHPSIN TVVTNVGTTG SAFESHSTVS

4851 AYPEPSKSHI LPMLPPPPWK TPQFPRSIPK SSKTTRTETE TTSSLTPKLR

4901 ETSISQEITS STETSTVPYK ELTGATTEVS RTDVTSSSST SFPGPDQSTV

4951 SLDISTETNT RLSTSPIMTE SAEITITTQT GPHGATSQDT FTMDPSNTTP

5001 QAGIHSAMTH GFSQLDVTTL MSRIPQDVSW TSPPSVDKTS SPSSFLSSPA

5051 MTTPSLISST LPEDKLSSPM TSLLTSGLVK ITDILRTRLE PVTSSLPNFS

5101 STSDKILATS KDSKDTKEIF PSINTEETNV KANNSGHESH SPALADSETP

5151 KATTQMVITT TVGDPAPSTS MPVHGSSETT NIKREPTYFL TPRLRETSTS

5201 QESSFPTDTS FLLSKVPTGT ITEVSSTGVI SSSKISTPDH DKSTVPPDTF

5251 TGEIPRVFTS SIKTKSAEMT ITTQASPPES ASHSTLPLDT STTLSQGGTH

5301 STVSQGFPYS EVTTLMGMGP GNVSWMTTPP VEETSSVSSL MSSPAMTSPS

5351 PVSSTSPQSI PSSPLPVTAL PTSVLVTTTD VLGTTSPESV TSSPPNLSSI

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

5401 THERPATYKD TAHTEAAMHH STNTAVTNVG TSGSGHKSQS SVLADSETSK

5451 ATPLMSTAST LGDTSVSTST PNISQTNQIQ TEPTASLSPR LRESSTSEKT

5501 SSTTETNTAF SYVPTGAITQ ASRTEISSSR TSISDLDRST IAPDISTGMI

5551 TRLFTSPIMT KSAEMTVTTQ TTTPGATSQG ILPWDTSTTL FQGGTHSTVS

5601 QGFPHSEITT LRSRTPGDVS WMTTPPVEET SSGFSLMSPS MTSPSPVSST

5651 SPESIPSSPL PVTALLTSVL VTTTNVLGTT SPEPVTSSPP NLSSPTQERL

5701 TTYKDTAHTE AMHASMHTNT AVANVGTSIS GHESQSSVPA DSHTSKATSP

5751 MGITFAMGDT SVYTSTPAFF ETRIQSESTS SLIPGLRDTR TSEEINTVTE

5801 TSTVLSEVPT TTTTEVSRTE VITSSRTTIS GPDHSKMSPY ISTETITRLS

5851 TFPFVTGSTE MAITNQTGPI GTISQATLTL DTSSTASWEG THSPVTQRFP

5901 HSEETTTMSR STKGVSWQSP PSVEETSSPS SPVPLPAITS HSSLYSAVSG

5951 SSPTSALPVT SLLTSGRRKT IDMLDTHSEL VTSSLPSASS FSGEILTSEA

6001 STNTETIHFS ENTAETNMGT TNSMHKLHSS VSIHSQPSGH TPPKVTGSMM

6051 EDAIVSTSTP GSPETKNVDR DSTSPLTPEL KEDSTALVMN STTESNTVFS

6101 SVSLDAATEV SRAEVTYYDP TFMPASAQST KSPDISPEAS SSHSNSPPLT

6151 ISTHKTIATQ TGPSGVTSLG QLTLDTSTIA TSAGTPSART QDFVDSETTS

6201 VMNNDLNDVL KTSPFSAEEA NSLSSQAPLL VTTSPSPVTS TLQEHSTSSL

6251 VSVTSVPTPT LAKITDMDTN LEPVTRSPQN LRNTLATSEA TTDTHTMHPS

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)

(SEQ ID NO: 310)

6301 INTAMANVGT TSSPNEFYFT VSPDSDPYKA TSAVVITSTS GDSIVSTSMP

6351 RSSAMKKIES ETTFSLIFRL RETSTSQKIG SSSDTSTVFD KAFTAATTEV

Contig16

6401 SRTELTSSSR TSIQGTEKPT MSPDTSTRSV TMLSTFAGLT KSEERTIATQ

6451 TGPHRATSQG TLTWDTSITT SQAGTHSAMT HGFSQLDLST LTSRVPEYIS

6501 GTSPPSVEKT SSSSSLLSLP AITSPSPVPT TLPESRPSSP VHLTSLPTSG

6551 LVKTTDMLAS VASLPPNLGS TSHKIPTTSE DIKDTEKMYP STNIAVTNVG

6601 TTTSEKESYS SVPAYSEPPK VTSPMVTSFN IRDTIVSTSM PGSSEITRIE

6651 MESTFSLAHG LKGTSTSQDP IVSTEKSAVL HKLTTGATET SRTEVASSRR

6701 TSIPGPDHST ESPDISTEVI PSLPISLGIT ESSNMTIITR TGPPLGSTSQ

6751 GTFTLDTPTT SSRAGTHSMA TQEFPHSEMT TVMNKDPEIL SWTIPPSIEK

6801 TSFSSSLMPS PAMTSPPVSS TLPKTIHTTP SPMTSLLTPS LVMTTDTLGT

6851 SPEPTTSSPP NLSSTSHEIL TTDEDTTAIE AMHPSTSTAA TNVETTSSGH

6901 GSQSSVLADS EKTKATAPMD TTSTMGHTTV STSMSVSSET TKIKRESTYS

6951 LTPGLRETSI SQNASFSTDT SIVLSEVPTG TTAEVSRTEV TSSGRTSIPG

7001 PSQSTVLPEI STRTMTRLFA SPTMTESAEM TIPTQTGPSG STSQDTLTLD

7051 TSTTKSQAKT HSTLTQRFPH SEMTTLMSRG PGDMSWQSSP SLENPSSLPS

7101 LLSLPATTSP PPISSTLPVT ISSSPLPVTS LLTSSPVTTT DMLHTSPELV

7151 TSSPPKLSHT SDERLTTGKD TTNTEAVHPS TNTAASNVEI PSSGHESPSS

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

7201 ALADSETSKA TSPMFITSTQ EDTTVAISTP HFLETSRIQK ESISSLSPKL
Contig10
7251 RETGSSVETS SAIETSAVLS EVSVGATTEI SRTEVTSSSR TSISGSAIST
7301 MLPEISTTRK IIKFPTSPIL AISSEMTIKT QTSPPGSTSE STFTLDTSTT
7351 PSLVITHSTM TQRLPHSEIT TLVSRGAGDV PRPSSLPVEE TSPPSSQLSL
7401 SAMISPSPVS STLPASSHSS SASVTSLLTP GQVKTTEVLD ASAEPETSSP
7451 PSLSSTSVEI LATSEVTTDT EKIHPFSNTA VTKVGTSSSG HESPSSVLPD
7501 SETTKATSAM GTISIMGDTS VSTLTPALSM TRKIQSEPAS SLTTRLRETS
7551 TSEETSLATE ANTVLSKVST GATTEVSRTE AISFSRTSMS GPEQSTMSQD
7601 ISIGTIPRIS ASSVLTESAK MTITTQTGPS ESTLESTLNL NTATTPSWVE
7651 THSIVIQGFP HPEMTTSMGR GPGGVSWPSP PFVKETSPPS SPLSLPAVTS
Contig22
7701 PHPVSTTFLA HIPPSPLPVT SLLTSGPATT TDILGTSTEP GTSSSSSLST
7751 TSHERLTTYK DTAHTEAVHP STNTGGTNVA TTSSGYKSQS SVLADSSPMC
7801 TTSTMGDTSV LTSTPAFLET RRIQTELASS LTPGLRESSG SEGTSSGTKM
7851 STVLSKVPTG ATTEISKEDV TSIPGPAQST ISPDTSTRTV SWFSTSPVMT
7901 ESAEITMNTH TSPLGATTQG TSTLDTSSTT SLTMTHSTIS QGFSHSQMST
7951 LMRRGPEDVS WMSPPLLEKT RPSFSLMSSP ATTSPSPVSS TLPESISSSP
8001 LPVTSLLTSG LAKTTDMLHK SSEPVTNSPA NLSSTSVEIL ATSEVTTDTE
8051 KTHPSSNRTV TDVGTSSSGH ESTSFVLADS QTSKVTSPMV ITSTMEDTSV

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

8101 STSTPGFFET SRIQTEPTSS LTLGLRKTSS SEGTSLATEM STVLSGVPTG

8151 ATAEVSRTEV TSSSRTSISG FAQLTVSPET STETITRLPT SSIMTESAEM

8201 MIKTQTDPPG STPESTHTVD ISTTPNWVET HSTVTQRFSH SEMTTLVSRS

8251 PGDMLWPSQS SVEETSSASS LLSLPATTSP SPVSSTLVED FPSASLPVTS

8301 LLTPGLVITT DRMGISREPG TSSTSNLSST SHERLTTLED TVDTEAMQPS

8351 THTAVTNVRT SISGHESQSS VLSDSETPKA TSSMGTTYTM GETSVSISTS

8401 DFFETSRVQI EPTSSLTSGL RETSSSERIS SATEGSTVLS EVPSGATTEV

8451 SRTEVISSRG TSMSGPDQFT ISPDISTEAI TRLSTSPIMT ESAESAITIE

8501 TGSPGATSEG TLTLDTSTTT FWSGTHSTAS PGFSHSEMTT LMSRTPGDVP

8551 WPSLPSVEEA SSVSSSLSSP AMTSTSFFST LPESISSSPH PVTALLTLGP

8601 VKTTDMLRTS SEPETSSPPN LSSTSAEILA TSEVTKDREK IHPSSNTPVV

8651 NVGTVIYKHL SPSSVLADLV TTKPTSPMAT TSTLGNTSVS TSTPAFPETM

8701 MTQPTSSLTS GLREISTSQE TSSATERSAS LSGMPTGATT KVSRTEALSL

8751 GRTSTPGPAQ STISPEISTE TITRISTPLT TTGSAEMTIT PKTGHSGASS

8801 QGTFTLDTSS RASWPGTHSA ATHRSPHSGM TTPMSRGPED VSWPSRPSVE

8851 KTSPPSSLVS LSAVTSPSPL YSTPSESSHS SPLRVTSLFT PVMMKTTDML

8901 DTSLEPVTTS PPSMNITSDE SLATSKATME TEAIQLSENT AVTQMGTISA

8951 RQEFYSSYPG LPEPSKVTSP VVTSSTIKDI VSTTIPASSE ITRIEMESTS

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)

(SEQ ID NO: 310)

9001 TLTPTPRETS TSQEIHSATK PSTVPYKALT SATIEDSMTQ VMSSSRGPSP

9051 DQSTMSQDIS TEVITRLSTS PIKAESTEMT ITTQTGSPGA TSRGTLTLDT

9101 STTFMSGTHS TASQGFSHSQ MTALMSRTPG DVPWLSHPSV EEASSASFSL

9151 SSPVMTSSSP VSSTLPDSIH SSSLPVTSLL TSGLVKTTEL LGTSSEPETS

9201 SPPNLSSTSA EILATTEVTT DTEKLEMTNV VTSGYTHESP SSVLADSVTT

9251 KATSSMGITY PTGDTNVLTS TPAFSDTSRI QTKSKLSLTP GLMETSISEE

Contig 36

9301 TSSATEKSTV LSSVPTGATT EVSRTEAISS SRTSIPGPAQ STMSSDTSME

9351 TITRISTPLT RKESTDMAIT PKTGPSGATS QGTFTLDSSS TASWPGTHSA

9401 TTQRFPQSVV TTPMSRGPED VSWPSPLSVE KNSPPSSLVS SSSVTSPSPL

9451 YSTPSGSSHS SPVPVTSLFT SIMMKATDML DASLEPETTS APNMNITSDE

9501 SLAASKATTE TEAIHVFENT AASHVETTSA TEELYSSSPG FSEPTKVISP

9551 VVTSSSIRDN MVSTTMPGSS GITRIEIESM SSLTPGLRET RTSQDITSST

9601 ETSTVLYKMP SGATPEVSRT EVMPSSRTSI PGPAQSTMSL DISDEVVTRL

9651 STSPIMTESA EITITTQTGY SLATSQVTLP LGTSMTFLSG THSTMSQGLS

9701 HSEMTNLMSR GPESLSWTSP RFVETTRSSS SLTSLPLTTS LSPVSSTLLD

9751 SSPSSPLPVT SLILPGLVKT TEVLDTSSEP KTSSSPNLSS TSVEIPATSE

9801 IMTDTEKIHP SSNTAVAKVR TSSSVHESHS SVLADSETTI TIPSMGITSA

9851 VDDTTVFTSN PAFSETRRIP TEPTFSLTPG FRETSTSEET TSITETSAVL

Table 25 (continued)

Amino Terminal Extension of the CA125 Gene (Protein Sequence)
(SEQ ID NO: 310)

9901 YGVPTSATTE VSMTEIMSSN RIHIPDSDQS TMSPDIITEV ITRLSSSSMM

9951 SESTQMTITT QKSSPGATAQ STLTWPQQQP PWQGPTQLFL LDFYTSEMTT

10001 LMSRSPENPS WKSSLFVEKT SSSSSLLSLP VTTSPSVSST LPQSIPSSSF

10051 SVTSLLTPGM VKTTDTSTEP GTSLSPNLSG TSVEILAASE VTTDTEKIHP

10101 SSSMAVTNVG TTSSGHELYS SVSIHSEPSK ATYPVGTPSS MAETSISTSM

10151 PANFETTGFE AEPFSHLTSG FRKTNMSLDT SSVTPTNTPS SPGSTHLLQS

10201 SKTDFTSSAK TSSPDWPPAS QYTEIPVDII TPFNASPSIT ESTGITSFPE

10251 SRFTMSVTES THHLSTDLLP SAETISTGTV MPSLSEAMTS FATTGVPRAI

10301 SGSGSPFSRT ESGPGDATLS TIAESLPSST PVPFSSSTFT TTDSSTIPAL

10351 HEITSSSATP YRVDTSLGTE SSTTEGRLVM VSTLDTSSQP GRTSSTPILD

10401 TRMTESVELG TVTSAYQVPS LSTRLTRTDG I

Table 26

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

contig62

```
          o       oo            o                   o
    1   MLKPSGLPGS SSPTRSLMTG SRSTKATPEM DSGLTGATLS PKTSTGAIVV
        o                 o                 o    o  o
   51   TEHTLPFTSP DKTLASPTSS VVGRTTQSLG VMSSALPEST SRGMTHSEQR
          o o       o             oo       oo  x       o
  101   TSPSLSPQVN GTPSRNYPAT SMVSGLSSPR TRTSSTEGNF TKEASTYTLT
          oo   o       o ooo o   oo                o
  151   VETTSGPVTE KYTVPTETST TEGDSTETPW DTRYIPVKIT SPMKTFADST
                o      oo   o  o   o
  201   ASKENAPVSM TPAETTVTDS HTPGRTNPSF GTLYSSFLDL SPKGTPNSRG
                   o     o         o  oo
  251   ETSLELILST TGYPFSSPEP GSAGHSRIST SAPLSSSASV LDNKISETSI
          o  o   o                                      o  o
  301   FSGQSLTSPL SPGVPEARAS TMPNSAIPFS MTLSNAETSA ERVRSTISSL
         o o                                             o
  351   GTPSISTKQT AETILTFHAF AETMDIPSTH IAKTLASEWL GSPGTLGGTS
        oo  oooo o oo  o        o          x        oo
  401   TSALTTTSPS TTLVSEETNT HHSTSGKETE GTLNTSMTPL ETSAPGEESE
          o                    o   o   o      o o      o oo
  451   MTATLVPTLG FTTLDSKIRS PSQVSSSHPT RELRTTGSTS GRQSSSTAAH
                o   ooo  oo o o       o    o    o  o  o
  501   GSSDILRATT SSTSKASSWT SESTAQQFSE PQHTQWVETS PSMKTERPPA
        ooo     oo                                   oo   o
  551   STSVAAPITT SVPSVVSGFT TLKTSSTKGI WLEETSADTL IGESTAGPTT
                       oo              o                  o
  601   HQFAVPTGIS MTGGSSTRGS QGTTHLLTRA TASSETSADL TLATNGVPVS
             o o    oo        o o   o
  651   VSPAVSKTAA GSSPPGGTKP SYTMVSSVIP ETSSLQSSAF REGTSLGLTP
          o    oo             oo                        oo
  701   LNTRHPFSSP EPDSAGHTKI STSIPLLSSA SVLEDKVSAT STFSHHKATS
        o oo o   o o    o                      x o    o  o o
  751   SITTGTPEIS TKTKPSSAVL SSMTLSNAAT SPERVRNATS PLTHPSPSGE
                  o  oo        o    o  oo o oo     o      o
  801   ETAGSVLTLS TSAETTDSPN IHPTGTLTSE SSESPSTLSL PSVSGVKTTF
        oooo oo    o       oo   o              o  o oo  o    o
  851   SSSTPSTHLF TSGEETEETS NPSVSQPETS VSRVRTTLAS TSVPTPVFPT
```

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

```
          o o                    o oo  ox oo o
 901  MDTWPTRSAQ FSSSHLVSEL RATSSTSVTN STGSALPKIS HLTGTATMSQ
           x        oo        o    o   o  ooo ooo     o
 951  TNRDTFNDSA APQSTTWPET SPRFKTGLPS ATTTVSTSAT SLSATVMVSK
       o   o        o      oo   oo  o           o
1001  FTSPATSSME ATSIREPSTT ILTTETTNGP GSMAVASTNI PIGKGYITEG
                 oo                    o   o o      ooo
1051  RLDTSHLPIG TTASSETSMD FTMAKESVSM SVSPSQSMDA AGSSTPGRTS
                                      oo  o    o o   o
1101  QFVDTFSDDV YHLTSREITI PRDGTSSALT PQMTATHPPS PDPGSARSTW
          ooo oo  o   o ooo   o   o                      oo o
1151  LGILSSSPSS PTPKVTMSST FSTQRVTTSM IMDTVETSRW NMPNLPSTTS
         o   o       oo      o o  o     o        o     oo o
1201  LTPSNIPTSG AIGKSTLVPL DTPSPATSLE ASEGGLPTLS TYPESTNTPS
              o    oo x
1251  IHLGAHASSE SPSTINLTMA SVVKPGSYTP LTFPSIETHI HVSTARMAYS
      o  o           o oo    oo  oo      o o    o
1301  SGSSPEMTAP GETNTGSTWD PTTYITTTDP KDTSSAQVST PHSVRTLRTT
          o o o      o o    o   x      o   o
1351  ENHPKTESAT PAAYSGSPKI SSSPNLTSPA TKAWTITDTT EHSTQLHYTK
                   o     o    o  o  o
1401  LAEKSSGFET QSAPGPVSVV IPTSPTIGSS TLELTSDVPG EPLVLAPSEQ
                   o                 oo o    oo        oo     o
1451  TTITLPMATW LSTSLTEEMA STDLDISSPS SPMSTFAIFP PMSTPSHELS
                                          o   o
1501  KSEADTSAIR NTDSTTLDQH LGIRSLGRTG DLTTVPITPL TTTWTSVIEH
                   o   o  o o     oo   o  o
1551  STQAQDTLSA TMSPTHVTQS LKDQTSIPAS ASPSHLTEVY PELGTQGRSS
       o                     o   oo     x oo  o
1601  SEATTFWKPS TDTLSREIET GPTNIQSTPP MDNTTTGSSS SGVTLGIAHL
       o        o                        o
1651  PIGTSSPAET STNMALERRS STATVSMAGT MGLLVTSAPG RSISQSLGRV
              o    o  o                  o             oo
1701  SSVLSESTTE GVTDSSKGSS PRLNTQGNTA LSSSLEPSYA EGSQMSTSIP
       ooo oo                          o  o  o   o     o
1751  LTSSPTTPDV EFIGGSTFWT KEVTTVMTSD ISKSSARTES SSATLMSTAL
```

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

```
                          o  o o   o        o   x
1801  GSTENTGKEK LRTASMDLPS PTPSMEVTPW ISLTLSNAPN TTDSLDLSHG
                  o                x              x o
1851  VHTSSAGTLA TDRSLNTGVT RASRLENGSD TSSKSLSMGN STHTSMTDTE
       o  oo       oo        o oo                        o
1901  KSEVSSSIHP RPETSAPGAE TTLTSTPGNR AISLTLPFSS IPVEEVISTG
            o    o o  o    o    o      oo        o
1951  ITSGPDINSA PMTHSPITPP TIVWTSTGTI EQSTQPLHAV SSEKVSVQTQ
      o     o           o  oo  oo o   oo                .
2001  STPYVNSVAV SASPTHENSV SSGSSTSSPY SSASLESLDS TISRRNAITS
          oo   ooo  o o o    o   o   o  ooooo
2051  WLWDLTTSLP TTTWPSTSLS EALSSGHSGV SNPSSTTTEF PLFSAASTSA
             o       o              o   o          oo
2101  AKQRNPETET HGPQNTAAST LNTDASSVTG LSETPVGASI SSEVPLPMAI
                   oo   o       o        o    o
2151  TSRSDVSGLT SESTANPSLG TASSAGTKLT RTISLPTSES LVSFRMNKDP
                  o     o     o      o         o  o       o
2201  WTVSIPLGSH PTTNTETSIP VNSAGPPGLS TVASDVIDTP SDGAESIPTV
      o o o  o   oo o             o          o  o        oo
2251  SFSPSPDTEV TTISHFPEKT THSFRTISSL THELTSRVTP IPGDWMSSAM
      oo  o    o        o o o   ooo     o       o     x
2301  STKPTGASPS ITLGERRTIT SAAPTTSPIV LTASFTETST VSLDNETTVK
                           x       o     o o    o  o  o
2351  TSDILDARKT NELPSDSSSS SDLINTSIAS STMDVTKTAS ISPTSISGMT
       ooo    oo       o oo  o o oo o                  o oo
2401  ASSSPSLFSS DRPQVPTSTT ETNTATSPSV SSNTYSLDGG SNVGGTPSTL
         o                          o    o o      o  o    oo
2451  PPFTITHPVE TSSALLAWSR PVRTFSTMVS TDTASGENPT SSNSVVTSVP
                                        o
2501  APGTWTSVGS TTDLPAMGFL KTSPAGEAHS LLASTIEPAT AFTPHLSAAV
       o    o        o        oo  o oo  oo                 o
2551  VTGSSATSEA SLLTTSESKA IHSSPQTPTT PTSGANWETS ATPESLLVVT
                           o oo  o     o       o   o    o
2601  ETSDTTLTSK ILVTDTILFS TVSTPPSKFP STGTLSGASF PTLLPDTPAI
          o  o o   o          o    o  o         o
2651  PLTATEPTSS LATSFDSTPL VTIASDSLGT VPETTLTMSE TSNGDALVLK
```

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

```
                          o       ooo  o        x      o     o
2701  TVSNPDRSIP GITIQGVTES PLHPSSTSPS KIVAPRNTTY EGSITVALST
            o
2751  LPAGTTGSLV FSQSSENSET TALVDSSAGL ERASVMPLTT GSQGMASSGG
        o                 o        o      o     o  o
2801  IRSGSTHSTG TKTFSSLPLT MNPGEVTAMS EITTNRLTAT QSTAPKGIPV
                    o o o o        oo    o              o
2851  KPTSAESGLL TPVSASSSPS KAFASLTTAP PTWGIPQSTL TFEFSEVPSL
      o o  o                    o o   o
2901  DTKSASLPTP GQSLNTIPDS DASTASSSLS KSPEKNPRAR MMTSTKAISA
        o   o       o   o
2951  SSFQSTGFTE TPEGSASPSM AGHEPRVPTS GTGDPRYASE SMSYPDPSKA
         ooo                      oo                  o o
3001  SSAMTSTSLA SKLTTLFSTG QAARSGSSSS PISLSTEKET SFLSPTASTS
                                    o    oo  x          o   o
3051  RKTSLFLGPS MARQPNILVH LQTSALTLSP TSTLNMSQEE PPELTSSQTI
                   o o o o o . oo    oo  o  o             oo
3101  AEEEGTTAET QTLTFTPSET PTSLLPVSSP TEPTARRKSS PETWASSISV
      o              o           xoo         o o o   oo  o
3151  PAKTSLVETT DGTLVTTIKM SSQAAQGNST QPAPAEETGT SPAGTSPGSP
            o o             o .          oo      o
3201  EMSTTLKIMS SKEPSISPEI RSTVRNSPWK TPETTVPMET TVEPVTLQST
          oo o    o oo  o  o o     o       o o
3251  ALGSGSTSIS HLPTGTTSPT KSPTENMLAT ERVSLSPSPP EAWTNLYSGT
            o           o
3301  PGGTRQSLAT MSSVSLESPT ARSITGTGQQ SSPELVSKTT GMEFSMWHGS
                    o                                 o o
3351  TGGTTGDTHV SLSTSSNILE DPVTSPNSVS SLTDKSKHKT ETWVSTTAIP
      o                        o o
3401  STVLNNKIMA AEQQTSRSVD EAYSSTSSWS DQTSGSDITL GASPDVTNTL
         o     o                    o  o o
3451  YITSTAQTTS LVSLPSGDQG ITSLTNPSGG KTSSASSVTS PSIGLETLRA
      x           o      o           oo  o   oo o  o  o o
3501  NVSAVKSDIA PTAGHLSQTS SPAEVSILDV TTAPTPGIST TITTMGTNSI
      oooo        oo  oo  o    oooo    oo  oo     o
3551  STTTPNPEVG MSTMDSTPAT ERRTTSTEHP STWSSTAASD SWTVTDMTSN
```

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

```
                 o  oo       o     o              o  o
3601  LKVARSPGTI STMHTTSFLA SSTELDSMST PHGRITVIGT SLVTPSSDAS
        o    o   o o o oo  oo   o                 ooo o ooo
3651  AVKTETSTSE RTLSPSDTTA STPISTFSRV QRMSISVPDI LSTSWTPSST
           o              o                              o o
3701  EAEDVPVSMV PTDHASTKTD PNTPLSTFLF DSLSTLDWDT GRSLSSATAT
      oo     oo                          o  o
3751  TSAPQGATTP QELTLETMIS PATSQLPFSI GHITSAVTPA AMARSSGVTF
      o    oo      ooo   oo oo                   o
3801  SRPDPTSKKA EQTSTQLPTT TSAHPGQVPR SAATTLDVIP HTAKTPDATF
             o                 oo                       o
3851  QRQGQTALTT EARATSDSWN EKEKSTPSAP WITEMMNSVS EDTIKEVTSS
                                                       oo
3901  SSVLKDPEYA GHKLGIWDDF IPKFGKAAHM RELPLLSPPQ DKEAIHPSTN
        o   o        oo     o  o        o              o
3951  TVETTGWVTS SEHASHSTIP AHSASSKLTS PVVTTSTREQ AIVSMSTTTW
        o                            o  o  o  oo
4001  PESTRARTEP NSFLTIELRD VSPYMDTSST TQTSIISSPG STAITKGHRT
                          o                              oo
4051  EITSYKRISS SFLAQSMRSS DSPSEAITRL SNFPAMTESG GMILAMQTSP
        oo o  o    o o o o       o                      o
4101  PGATSISAPT LDTSATASWT GTPLATTQRF TYSEKTTLFS KGREDTSQPS
  o         ooo oo      oo          o    o ooo    o    o
4151  PPCVEETSSS SSVVPIHATT SPSNILLTSQ GHSPSSTPPV TSVFLSETSG
                       o    x  o
4201  LGKTTDMSRI SLEPGTSLPP NLSSTAGEAL STYEASRDTK AIHHSADTAV
        ooo   o        o   o                  o     o
4251  TNMEATSSEY SPIPGHTKPS KATSPLVTSH IMGDITSSTS VFGSSETTEI
                          o   o        o     o        o  o
4301  ETVSSVNQGL QERSTSQVAS SATETSTVIT HVSSGDATTH VTKTQATFSS
       oo o                   oo  o o   o oo  o oo  o  o   o
4351  GTSISSPHQF ITSTNTFTDV STNPSTSLIM TESSGVTITT QTGPTGAATQ
           ooo     o                      o       o
4401  GPYLLDTSTM PYLTETPLAV TPDFMQSEKT TLISKGPKDV TWTSPPSVAE
      oo  o       oo    oo       ooo     o             x
4451  TSYPSSLTPF LVTTIPPATS TLQGQHTSSP VSATSVLTSG LVKTTDMLNT
```

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

```
         o                        o     o
4501  SMEPVTNSPQ NLNNPSNEIL ATLAATTDIE TIHPSINKAV TNMGTASSAH
            oo   oo oo      oo                        o
4551  VLHSTLPVSS EPSTATSPMV PASSMGDALA SISIPGSETT DIEGEPTSSL
          x      x          x                          o
4601  TAGRKENSTL QEMNSTTESN IILSNVSVGA ITEATKMEVP SFDATFIPTP
       o               o     o oo    oo o  o    o        o
4651  AQSTKFPDIF SVASSRLSNS PPMTISTHMT TTQTGSSGAT SKIPLALDTS
        o  o     o                        o         oo o
4701  TLETSAGTPS VVTEGFAHSK ITTAMNNDVK DVSQTNPPFQ DEASSPSSQA
        o               oo oo     o                      o
4751  PVLVTTLPSS VAFTPQWHST SSPVSMSSVL TSSLVKTAGK VDTSLETVTS
                    o   o     oo            o        oo o
4801  SPQSMSNTLD DISVTSAATT DIETTHPSIN TVVTNVGTTG SAFESHSTVS
                                      o  o  o    oooo o
4851  AYPEPSKSHI LPMLPPPPWK TPQFPRSIPK SSKTTRTETE TTSSLTPKLR
            oo oo  oo                    oooooo o      o
4901  ETSISQEITS STETSTVPYK ELTGATTEVS RTDVTSSSST SFPGPDQSTV
        o       o o  o        oo        o      o   o  o
4951  SLDISTETNT RLSTSPIMTE SAEITITTQT GPHGATSQDT FTMDPSNTTP
                                      o       oo o  o  oo
5001  QAGIHSAMTH GFSQLDVTTL MSRIPQDVSW TSPPSVDKTS SPSSFLSSPA
       oo o  o                                    o  x o
5051  MTTPSLISST LPEDKLSSPM TSLLTSGLVK ITDILRTRLE PVTSSLPNFS
                                       x              o o
5101  STSDKILATS KDSKDTKEIF PSINTEETNV KANNSGHESH SPALADSETP
        o    oo o      ooo      oo                      ooo
5151  KATTQMVITT TVGDPAPSTS MPVHGSSETT NIKREPTYFL TPRLRETSTS
        o  o       o          oo                    oo
5201  QESSFPTDTS FLLSKVPTGT ITEVSSTGVI SSSKISTPDH DKSTVPPDTF
                     o        oo  o      o oo       o  o
5251  TGEIPRVFTS SIKTKSAEMT ITTQASPPES ASHSTLPLDT STTLSQGGTH
      o                       x    oo       oo oo   oo   oo o
5301  STVSQGFPYS EVTTLMGMGP GNVSWMTTPP VEETSSVSSL MSSPAMTSPS
        oooo  o   oo    o    o     o      ooo     ooo  x oo
5351  PVSSTSPQSI PSSPLPVTAL PTSVLVTTTD VLGTTSPESV TSSPPNLSSI
```

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

```
          o                                                    o
5401  THERPATYKD TAHTEAAMHH STNTAVTNVG TSGSGHKSQS SVLADSETSK
        o o      oo oooo  x   o      o  o           ooo  o
5451  ATPLMSTAST LGDTSVSTST PNISQTNQIQ TEPTASLSPR LRESSTSEKT
      oooo       o        o          o           oo       o
5501  SSTTETNTAF SYVPTGAITQ ASRTEISSSR TSISDLDRST IAPDISTGMI
            o  o     oo  ooo   o
5551  TRLFTSPIMT KSAEMTVTTQ TTTPGATSQG ILPWDTSTTL FQGGTHSTVS
                           oo        oo  o  o o    o o  ooo
5601  QGFPHSEITT LRSRTPGDVS WMTTPPVEET SSGFSLMSPS MTSPSPVSST
      o  o  oo                        oo o    ooo   x oo
5651  SPESIPSSPL PVTALLTSVL VTTTNVLGTT SPEPVTSSPP NLSSPTQERL
                                          o        oo  o
5701  TTYKDTAHTE AMHASMHTNT AVANVGTSIS GHESQSSVPA DSHTSKATSP
                     o                  o                  o
5751  MGITFAMGDT SVYTSTPAFF ETRIQSESTS SLIPGLRDTR TSEEINTVTE
       oo  o   o o oo    o     o  o       o               o
5801  TSTVLSEVPT TTTTEVSRTE VITSSRTTIS GPDHSKMSPY ISTETITRLS
                  ox       o          o  o o          o
5851  TFPFVTGSTE MAITNQTGPI GTISQATLTL DTSSTASWEG THSPVTQRFP
                  o                ooo o o     o      o
5901  HSEETTTMSR STKGVSWQSP PSVEETSSPS SPVPLPAITS HSSLYSAVSG
      oo oo                                 o
5951  SSPTSALPVT SLLTSGRRKT IDMLDTHSEL VTSSLPSASS FSGEILTSEA
                                             o        o
6001  STNTETIHFS ENTAETNMGT TNSMHKLHSS VSIHSQPSGH TPPKVTGSMM
           oooo                              x  oo
6051  EDAIVSTSTP GSPETKNVDR DSTSPLTPEL KEDSTALVMN STTESNTVFS
            o                      oo       o   o oo o o
6101  SVSLDAATEV SRAEVTYYDP TFMPASAQST KSPDISPEAS SSHSNSPPLT
                  o  o               o   oo  o    o
6151  ISTHKTIATQ TGPSGVTSLG QLTLDTSTIA TSAGTPSART QDFVDSETTS
                                 o        ooo o  oo       ooo
6201  VMNNDLNDVL KTSPFSAEEA NSLSSQAPLL VTTSPSPVTS TLQEHSTSSL
       o oo  o o                  o             o    oo   o
6251  VSVTSVPTPT LAKITDMDTN LEPVTRSPQN LRNTLATSEA TTDTHTMHPS
```

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

```
                  o                                    ooo       oo
6301  INTAMANVGT TSSPNEFYFT VSPDSDPYKA TSAVVITSTS GDSIVSTSMP
                                                           o
6351  RSSAMKKIES ETTFSLIFRL RETSTSQKIG SSSDTSTVFD KAFTAATTEV
            oo  o    o   o       oo
6401  SRTELTSSSR TSIQGTEKPT MSPDTSTRSV TMLSTFAGLT KSEERTIATQ
            o        oo  o o                          o      o
6451  TGPHRATSQG TLTWDTSITT SQAGTHSAMT HGFSQLDLST LTSRVPEYIS
       oo        ooo    o     oo o   o o   o  oo      o  o
6501  GTSPPSVEKT SSSSSLLSLP AITSPSPVPT TLPESRPSSP VHLTSLPTSG
                             o    o
6551  LVKTTDMLAS VASLPPNLGS TSHKIPTTSE DIKDTEKMYP STNIAVTNVG
              o       o       o                oo
6601  TTTSEKESYS SVPAYSEPPK VTSPMVTSFN IRDTIVSTSM PGSSEITRIE
                                                      o    o
6651  MESTFSLAHG LKGTSTSQDP IVSTEKSAVL HKLTTGATET SRTEVASSRR
      oo      oo       oo                  x       o       o
6701  TSIPGPDHST ESPDISTEVI PSLPISLGIT ESSNMTIITR TGPPLGSTSQ
            o oo oo          o                        o
6751  GTFTLDTPTT SSRAGTHSMA TQEFPHSEMT TVMNKDPEIL SWTIPPSIEK
       o ooo   o    oo   oo o   o  oo  o  oo
6801  TSFSSSLMPS PAMTSPPVSS TLPKTIHTTP SPMTSLLTPS LVMTTDTLGT
      o   oooo   x ooo           o         o oo   o   ooo
6851  SPEPTTSSPP NLSSTSHEIL TTDEDTTAIE AMHPSTSTAA TNVETTSSGH
                             ooo    oo  ooo   o
6901  GSQSSVLADS EKTKATAPMD TTSTMGHTTV STSMSVSSET TKIKRESTYS
              o    x           o              o     o  o
6951  LTPGLRETSI SQNASFSTDT SIVLSEVPTG TTAEVSRTEV TSSGRTSIPG
         oo       oo              o o       o o
7001  PSQSTVLPEI STRTMTRLFA SPTMTESAEM TIPTQTGPSG STSQDTLTLD
      o oo                           o                   o
7051  TSTTKSQAKT HSTLTQRFPH SEMTTLMSRG PGDMSWQSSP SLENPSSLPS
        o   ooo     ooo   o  ooo    oo   oo   o
7101  LLSLPATTSP PPISSTLPVT ISSSPLPVTS LLTSSPVTTT DMLHTSPELV
      ooo                      o     o                o      o
7151  TSSPPKLSHT SDERLTTGKD TTNTEAVHPS TNTAASNVEI PSSGHESPSS
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Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

```
          o   o      o      o    o
7201  ALADSETSKA TSPMFITSTQ EDTTVAISTP HFLETSRIQK ESISSLSPKL
                         o              o  o o    oo o o  oo
7251  RETGSSVETS SAIETSAVLS EVSVGATTEI SRTEVTSSSR TSISGSAIST
          o                    o     o  o    ooo  oo     ooo
7301  MLPEISTTRK IIKFPTSPIL AISSEMTIKT QTSPPGSTSE STFTLDTSTT
       o      o                                   oo      o
7351  PSLVITHSTM TQRLPHSEIT TLVSRGAGDV PRPSSLPVEE TSPPSSQLSL
      o   o o  o o     o  o o o  o                  o    ooo
7401  SAMISPSPVS STLPASSHSS SASVTSLLTP GQVKTTEVLD ASAEPETSSP
       o oo o      o   o                      oo       oo
7451  PSLSSTSVEI LATSEVTTDT EKIHPFSNTA VTKVGTSSSG HESPSSVLPD
         o               oo  oo                        o
7501  SETTKATSAM GTISIMGDTS VSTLTPALSM TRKIQSEPAS SLTTRLRETS
      oo   o  o                 o
7551  TSEETSLATE ANTVLSKVST GATTEVSRTE AISFSRTSMS GPEQSTMSQD
       o              o        oo o  o   o  o        oo
7601  ISIGTIPRIS ASSVLTESAK MTITTQTGPS ESTLESTLNL NTATTPSWVE
                        o                   oo  o o  o    oo
7651  THSIVIQGFP HPEMTTSMGR GPGGVSWPSP PFVKETSPPS SPLSLPAVTS
           o         o      o  oo    o       oo    oooooo oo
7701  PHPVSTTFLA HIPPSPLPVT SLLTSGPATT TDILGTSTEP GTSSSSSLST
                        o      o          oo
7751  TSHERLTTYK DTAHTEAVHP STNTGGTNVA TTSSGYKSQS SVLADSSPMC
      o o    oo   o o                              o  o
7801  TTSTMGDTSV LTSTPAFLET RRIQTELASS LTPGLRESSG SEGTSSGTKM
       o  o   o    o        oo       oo      oo o     o    o
7851  STVLSKVPTG ATTEISKEDV TSIPGPAQST ISPDTSTRTV SWFSTSPVMT
                       o    o   ooooo o       o
7901  ESAEITMNTH TSPLGATTQG TSTLDTSSTT SLTMTHSTIS QGFSHSQMST
                            o o  oo   ooo o  oo        o o
7951  LMRRGPEDVS WMSPPLLEKT RPSFSLMSSP ATTSPSPVSS TLPESISSSP
                           o   o o   x  o         oo  o
8001  LPVTSLLTSG LAKTTDMLHK SSEPVTNSPA NLSSTSVEIL ATSEVTTDTE
       o    x       oo                  o   o      oo    oo
8051  KTHPSSNRTV TDVGTSSSGH ESTSFVLADS QTSKVTSPMV ITSTMEDTSV
```

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

```
      oooo              o              o     o      oo  o
8101  STSTPGFFET SRIQTEPTSS LTLGLRKTSS SEGTSLATEM STVLSGVPTG
       o     o   o o            o       o   o   o o   o
8151  ATAEVSRTEV TSSSRTSISG FAQLTVSPET STETITRLPT SSIMTESAEM
        o     oo  oo o    ooo           o
8201  MIKTQTDPPG STPESTHTVD ISTTPNWVET HSTVTQRFSH SEMTTLVSRS
                  o oo   o   ooo  o   o
8251  PGDMLWPSQS SVEETSSASS LLSLPATTSP SPVSSTLVED FPSASLPVTS
                    o      ooo x  o                   o     o
8301  LLTPGLVITT DRMGISREPG TSSTSNLSST SHERLTTLED TVDTEAMQPS
                       o      o      o o             o  oo
8351  THTAVTNVRT SISGHESQSS VLSDSETPKA TSSMGTTYTM GETSVSISTS
                    o                    o      o       o
8401  DFFETSRVQI EPTSSLTSGL RETSSSERIS SATEGSTVLS EVPSGATTEV
          o    o o     o        o    o   o   o        o
8451  SRTEVISSRG TSMSGPDQFT ISPDISTEAI TRLSTSPIMT ESAESAITIE
      o o              oo o        oo o                 o o
8501  TGSPGATSEG TLTLDTSTTT FWSGTHSTAS PGFSHSEMTT LMSRTPGDVP
                  o o o oo   ooo   o       o o
8551  WPSLPSVEEA SSVSSSLSSP AMTSTSFFST LPESISSSPH PVTALLTLGP
            oo o   ooo  x  ooo       o
8601  VKTTDMLRTS SEPETSSPPN LSSTSAEILA TSEVTKDREK IHPSSNTPVV
                         o   o    o oo   xoo o ooo
8651  NVGTVIYKHL SPSSVLADLV TTKPTSPMAT TSTLGNTSVS TSTPAFPETM
       o  oo   o       oo    o   o  o o   o       o
8701  MTQPTSSLTS GLREISTSQE TSSATERSAS LSGMPTGATT KVSRTEALSL
        ooo      oo o    o    o  oo    oo o   o o      o
8751  GRTSTPGPAQ STISPEISTE TITRISTPLT TTGSAEMTIT PKTGHSGASS
                   o          o          o
8801  QGTFTLDTSS RASWPGTHSA ATHRSPHSGM TTPMSRGPED VSWPSRPSVE
       oo   o  o  o  oo o    oo o  o   o
8851  KTSPPSSLVS LSAVTSPSPL YSTPSESSHS SPLRVTSLFT PVMMKTTDML
        o    ooo     x  o      o   o
8901  DTSLEPVTTS PPSMNITSDE SLATSKATME TEAIQLSENT AVTQMGTISA
                     o   o    o o       ooo    o
8951  RQEFYSSYPG LPEPSKVTSP VVTSSTIKDI VSTTIPASSE ITRIEMESTS
```

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

```
      o o o   oo oo    o o   oo                        oo
9001  TLTPTPRETS TSQEIHSATK PSTVPYKALT SATIEDSMTQ VMSSSRGPSP
        oo       o       o        o     oo o o    o
9051  DQSTMSQDIS TEVITRLSTS PIKAESTEMT ITTQTGSPGA TSRGTLTLDT
       o         o                                  o
9101  STTFMSGTHS TASQGFSHSQ MTALMSRTPG DVPWLSHPSV EEASSASFSL
      oo    ooo  ooo        o                      oo   oo
9151  SSPVMTSSSP VSSTLPDSIH SSSLPVTSLL TSGLVKTTEL LGTSSEPETS
      o  x oooo     oo  o                          o       o
9201  SPPNLSSTSA EILATTEVTT DTEKLEMTNV VTSGYTHESP SSVLADSVTT
        o o             o  o                          o o
9251  KATSSMGITY PTGDTNVLTS TPAFSDTSRI QTKSKLSLTP GLMETSISEE
      oo  o  oo   oo  o  oo     o   oo   oo        oo  o
9301  TSSATEKSTV LSSVPTGATT EVSRTEAISS SRTSIPGPAQ STMSSDTSME
                   o         o  o             o   o o     o
9351  TITRISTPLT RKESTDMAIT PKTGPSGATS QGTFTLDSSS TASWPGTHSA
       o         o  o                        o  o ooo oo o
9401  TTQRFPQSVV TTPMSRGPED VSWPSPLSVE KNSPPSSLVS SSSVTSPSPL
       oo o oo o o                          oo     x
9451  YSTPSGSSHS SPVPVTSLFT SIMMKATDML DASLEPETTS APNMNITSDE
            o                      o   o    ooo    o
9501  SLAASKATTE TEAIHVFENT AASHVETTSA TEELYSSSPG FSEPTKVISP
        o  o       oo     o           o                o oo
9551  VVTSSSIRDN MVSTTMPGSS GITRIEIESM SSLTPGLRET RTSQDITSST
         o          o     o     o  oo       o
9601  ETSTVLYKMP SGATPEVSRT EVMPSSRTSI PGPAQSTMSL DISDEVVTRL
           o                    o                    o
9651  STSPIMTESA EITITTQTGY SLATSQVTLP LGTSMTFLSG THSTMSQGLS
                                 o   o o oo     o  o   o
9701  HSEMTNLMSR GPESLSWTSP RFVETTRSSS SLTSLPLTTS LSPVSSTLLD
       o o       o                 oo     ooo x oo oo     oo
9751  SSPSSPLPVT SLILPGLVKT TEVLDTSSEP KTSSSPNLSS TSVEIPATSE
                                 o        o                o  oo
9801  IMTDTEKIHP SSNTAVAKVR TSSSVHESHS SVLADSETTI TIPSMGITSA
            o                  o   o         ooo  o o
9851  VDDTTVFTSN PAFSETRRIP TEPTFSLTPG FRETSTSEET TSITETSAVL
```

Table 26 (continued)

Serine/Threonine O-Glycosylation Pattern for the CA125 Amino Terminal Extension

```
        oo oo                          o o      o
 9901   YGVPTSATTE VSMTEIMSSN RIHIPDSDQS TMSPDIITEV ITRLSSSSMM
        o oo     o   oo   o   o
 9951   SESTQMTITT QKSSPGATAQ STLTWPQQQP PWQGPTQLFL LDFYTSEMTT
                                 o  o    ooo o ooo        oo
10001   LMSRSPENPS WKSSLFVEKT SSSSSLLSLP VTTSPSVSST LPQSIPSSSF
        o                 oo     o o x               o
10051   SVTSLLTPGM VKTTDTSTEP GTSLSPNLSG TSVEILAASE VTTDTEKIHP
                  o                    o   o    o  o     o ooo
10101   SSSMAVTNVG TTSSGHELYS SVSIHSEPSK ATYPVGTPSS MAETSISTSM
                                  x    o oo o o o o o  o    o
10151   PANFETTGFE AEPFSHLTSG FRKTNMSLDT SSVTPTNTPS SPGSTHLLQS
             o o   o o      o   o                  o  o   o
10201   SKTDFTSSAK TSSPDWPPAS QYTEIPVDII TPFNASPSIT ESTGITSFPE
        o  o   o              o  o o  o    o o        oo
10251   SRFTMSVTES THHLSTDLLP SAETISTGTV MPSLSEAMTS FATTGVPRAI
          o        o       o o      ooo     oooo o oo ooo
10301   SGSGSPFSRT ESGPGDATLS TIAESLPSST PVPFSSSTFT TTDSSTIPAL
           oooo         o  o                    o     ooo
10351   HEITSSSATP YRVDTSLGTE SSTTEGRLVM VSTLDTSSQP GRTSSTPILD
           o                 o
10401   TRMTESVELG TVTSAYQVPS LSTRLTRTDG I
```

WE CLAIM:

1. A CA125 molecule, comprising:

(a) an extracellular amino terminal domain, comprising 5 genomic exons, wherein exon 1 comprises amino acids #1-33 of SEQ ID NO: 299, exon 2 comprises amino acids #34-1593 of SEQ ID NO: 299, exon 3 comprises amino acids #1594-1605 of SEQ ID NO: 299, exon 4 comprises amino acids #1606-1617 of SEQ ID NO: 299, and exon 5 comprises amino acids #1618-1637 of SEQ ID NO: 299;

(b) an amino terminal extension, comprising 4 genomic exons, wherein exon 1 comprises amino acids #1-3157 of SEQ ID NO: 310, exon 2 comprises amino acids #3158-3193 of SEQ ID NO: 310, exon 3 comprises amino acids #3194-9277 of SEQ ID NO: 310, and exon 4 comprises amino acids #9278-10,427 of SEQ ID NO: 310;

(c) a multiple repeat domain, wherein each repeat unit comprises 5 genomic exons, wherein exon 1 comprises amino acids #1-42 in any of SEQ ID NOS: 164 through 194; exon 2 comprises amino acids #43-65 in any of SEQ ID NOS: 195 through 221; exon 3 comprises amino acids #66-123 in any of SEQ ID NOS: 222 through 249; exon 4 comprises amino acids #124-135 in any of SEQ ID NOS: 250 through 277; and exon 5 comprises amino acids #136-156 in any of SEQ ID NOS: 278 through 298; and

(d) a carboxy terminal domain comprising a transmembrane anchor with a short cytoplasmic domain, and further comprising 9 genomic exons, wherein exon 1 comprises amino acids #1-11 of SEQ ID NO: 300; exon 2 comprises amino acids #12-33 of SEQ ID NO: 300; exon 3 comprises amino acids #34-82 of SEQ ID NO: 300; exon 4 comprises amino acids #83-133 of SEQ ID NO: 300; exon 5 comprises amino acids #134-156 of SEQ ID NO: 300; exon 6 comprises amino acids #157-212 of SEQ ID NO: 300; exon 7 comprises amino acids #213-225 of SEQ ID NO: 300; exon 8 comprises amino acids #226-253 of SEQ ID NO: 300; and exon 9 comprises amino acids #254-284 of SEQ ID NO: 300.

2. The CA125 molecule according to claim 1, wherein the N-glycosylation sites of the amino terminal domain marked (x) in Figure 8B are encoded at positions #81, #271, #320, #624, #795, #834, #938, and #1,165 in SEQ ID NO: 299.

3. The CA125 molecule according to claim 1, wherein the serine and threonine O-glycosylation pattern for the amino terminal domain is marked (o) in SEQ ID NO: 299 in Figure 8B.

4. The CA125 molecule according to claim 1, wherein the N-glycosylation sites of the amino terminal extension marked (x) in Table 26 are encoded at positions #139, #434, #787, #930, #957, #1266, #1375, #1633, #1840, #1877, #1890, #2345, #2375, #2737, #3085, #3178, #3501, #4221, #4499, #4607, #4614, #4625, #5048, #5133, #5322, #5396, #5422, #5691, #5865, #6090, #6734, #6861, #6963, #8031, #8057, #8326, #8620, #8686, #8915, #9204, #9495, #9787, #10, 077, and #10, 175.

5. The CA125 molecule according to claim 1, wherein the serine and threonine O-glycosylation pattern for the amino terminal extension is marked (o) in Table 26.

6. The CA125 molecule according to claim 1, wherein exon 2 in the repeat domain comprises at least 31 different copies; exon 2 comprises at least 27 different copies; exon 3 comprises at least 28 different copies; exon 4 comprises at least 28 different copies, and exon 5 comprises at least 21 different copies.

7. The CA125 molecule according to claim 1, wherein the repeat domain comprises 156 amino acid repeat units which comprise epitope binding sites.

8. The CA125 molecule according to claim 7, wherein the epitope binding sites are located in the C-enclosure at amino acids #59-79 (marked C-C) in SEQ ID NO: 150 in Figure 5.

9. The CA125 molecule according to claim 7, wherein the 156 amino acid repeat unit comprises O-glycosylation sites at positions #128, #129, #132, #133, #134, #135, #139, #145, #146, #148, #150, #151, and #156 in SEQ ID NO: 150 in Figure 5C.

10. The CA125 molecule according to claim 7, wherein the 156 amino acid repeat unit comprises N-glycosylation sites at positions #33 and #49 in SEQ ID NO: 150 in Figure 5C.

11. The CA125 molecule according to claim 7, wherein the 156 amino acid repeat unit comprises at least one conserved methionine (designated M) at position #24 in SEQ ID NO: 150 in Figure 5C.

12. The CA125 molecule according to claim 1, wherein the transmembrane domain of the carboxy terminal domain is located at positions #230-252 (underlined) in SEQ ID NO: 300 of Figure 9B.

13. The CA125 molecule according to claim 1, wherein the cytoplasmic domain of the carboxy terminal domain comprises a highly basic sequence adjacent to the transmembrane at positions #256-260 in SEQ ID NO: 300 of Figure 9B, serine and threonine phosporylation sites at positions #254, #255, and #276 in SEQ ID NO: 300 in Figure 9B, and tyrosine phosphorylation sites at positions #264, #273, and #274 in SEQ ID NO: 300 of Figure 9B.

14. The CA125 molecule according to claim 7, wherein at least 45 repeat units are present in the repeat domain of the CA125 molecule.

15. A CA125 molecule, comprising an amino terminal domain comprising amino acids #1-1,638 in SEQ ID NO: 162, a repeat domain comprising amino acids #1,643-11,438 in SEQ ID NO: 162, and a carboxy terminal domain comprising amino acids #11,439-11,722 in SEQ ID NO: 162.

16. A repeat domain of the CA125 molecule comprising SEQ ID NO: 146 in Table 16.

17. The repeat domain according to claim 16, further comprising 63 individual repeat units.

18. The repeat domain according to claim 17, wherein each repeat unit comprises at least 156 amino acids.

19. The repeat domain according to claim 18, wherein each repeat unit comprises epitope binding sites located in the C-enclosure at amino acids #59-79 (underlined) in SEQ ID NO: 146.

20. The repeat domain according to claim 18, wherein each repeat unit comprises O-glycosylation sites at positions #128, #129, #132, #133, #134, #135, #139, #145, #146, #148, #150, #151, and #156 in SEQ ID NO: 146.

21. The repeat domain according to claim 18, wherein each repeat unit comprises N-glycosylation sites at positions #33 and #49 in SEQ ID NO: 146.

22. An isolated nucleic acid of the CA125 gene, comprising a nucleotide sequence selected from the group consisting of:

(a) the nucleotide sequences set forth in SEQ ID NOS: 49, 67, 81, 83-145, 147, 150, and 152;

(b) a nucleotide sequence having at least 70% sequence identity to any one of the sequences in (a);

(c) a degenerate variant of any one of (a) to (b); and

(d) a fragment of any one of (a) to (c).

23. An isolated nucleic acid of the CA125 gene, comprising a sequence that encodes a polypeptide with the amino acid sequence selected from the group consisting of:

(a) the amino acid sequences set forth in SEQ ID NOS: 11-47, 50-80, 82, 146, 148, 149, 151, and 153-158;

(b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a);

(c) a conservative variant of any one of (a) to (b); and

(d) a fragment of any one of (a) to (c).

24. A vector comprising the nucleic acid of claim 22.

25. The vector according to claim 24, wherein the vector is a cloning vector, a shuttle vector, or an expression vector.

26. A cultured cell comprising the vector of claim 24.

27. A cultured cell transfected with the vector of claim 24, or a progeny of the cell, wherein the cell expresses the polypeptide.

28. A method of expressing CA125 antigen in a cell, comprising the steps of:

(a) providing at least one nucleic acid comprising a nucleotide sequence selected from the group consisting of:

(i) the nucleotide sequences set forth in SEQ ID NOS: 49, 67, 81, 83-145, 147, 150, and 152;

(ii) a nucleotide sequence having at least 70% sequence identity to any one of the sequences in (i);

(iii) a degenerate variant of any one of (i) to (ii); and

(iv) a fragment of any one of (i) to (iii).

(b) providing cells comprising an mRNA encoding the CA125 antigen; and

(c) introducing the nucleic acid into the cells, wherein the CA125 antigen is expressed in the cells.

29. A purified polypeptide of the CA125 gene, comprising an amino acid sequence selected from the group consisting of:

(a) the amino acid sequences set forth in SEQ ID NOS: 11-48, 50, 68-80, 82, 146, 148, 149, 150, 151, and 153-158;

(b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a);

(c) a conservative variant of any one of (a) to (b); and

(d) a fragment of any one of (a) to (c).

30. A purified antibody that selectively binds to an epitope in the receptor-binding domain of CA125 protein, wherein the epitope is within the amino acid sequence selected from the group consisting of:

(a) the amino acid sequences set forth in SEQ ID NOS: 11-48, 50, 68-80, 146, 151, and 153-158;

(b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a);

(c) a conservative variant of any one of (a) to (b); and

(d) a fragment of any one of (a) to (c).

31. The antibody according to claim 30 that binds selectively to carcinoma cells selected from the group consisting of the ovaries, colon, liver, and pancreas.

32. A diagnostic for detecting and monitoring the presence of CA125 antigen, comprising recombinant CA125 comprising at least one repeat unit of the CA125 repeat domain including epitope binding sites selected from the group consisting of amino acid sequences set forth in SEQ ID NOS: 11-48, 50, 68-80, 82, 146, 150, 151, 153-161, and 162 (amino acids #1,643-11,438).

33. The diagnostic according to claim 32, wherein the epitope binding sites are located in the C-enclosure at amino acids #59-79 in SEQ ID NO: 150, and comprise the underlined amino acids in SEQ ID NO: 146 and SEQ ID NO: 162.

34. A therapeutic vaccine to treat mammals with elevated CA125 antigen levels or at risk of developing a disease or disease recurrence associated with elevated CA125 antigen levels, comprising recombinant CA125 repeat domains including epitope binding sites, wherein the repeat domains are selected from the group of amino acid sequences consisting of SEQ ID NOS: 11-48, 50, 68-80, 82, 146, 148, 149, 150, 151, 153-161, and 162 (amino acids #1,643-11,438), and amino acids #175-284 of SEQ ID NO: 300.

35. The therapeutic vaccine according to claim 34, wherein the mammals include animals and humans.

36. An antisense oligonucleotide that inhibits the expression of CA 125 encloded by:

(a) the nucleotide sequences set forth in SEQ ID NOS: 49, 67, 81, 83-145, 147, 150 and 152;

(b) a nucleotide sequence having at least 70% sequence identity to any one of the sequences in (a);

(c) a degenerate variant of any one of (a) to (b); and

(d) a fragment of any one of (a) to (c).

Cyanogen Bromide (CNBr) Cleavage

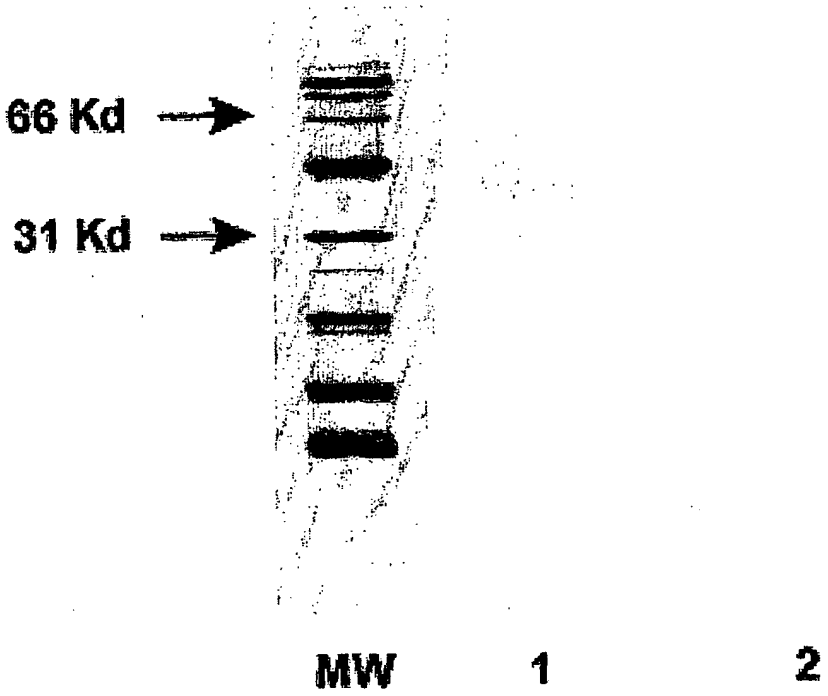
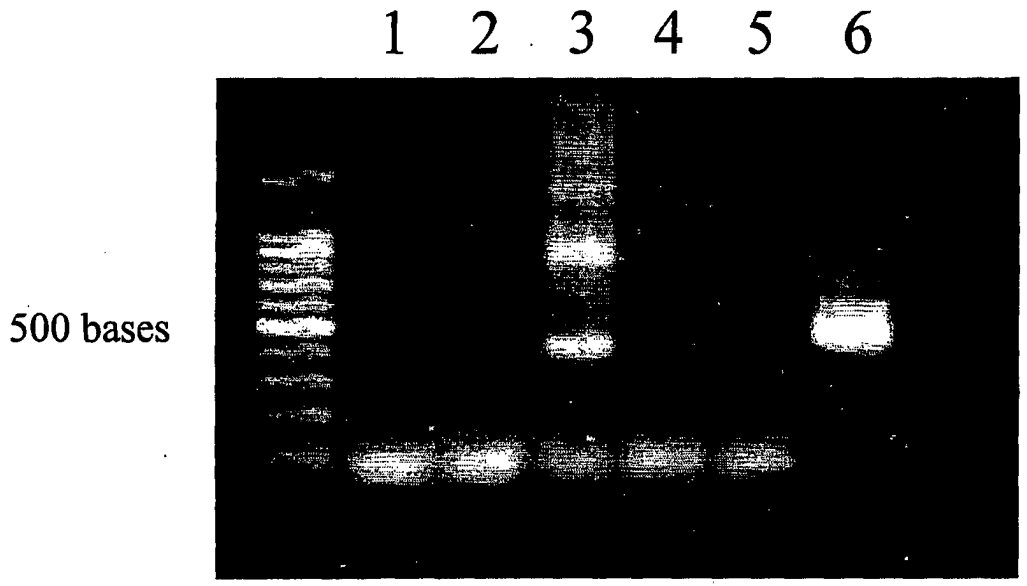


Figure 1

A



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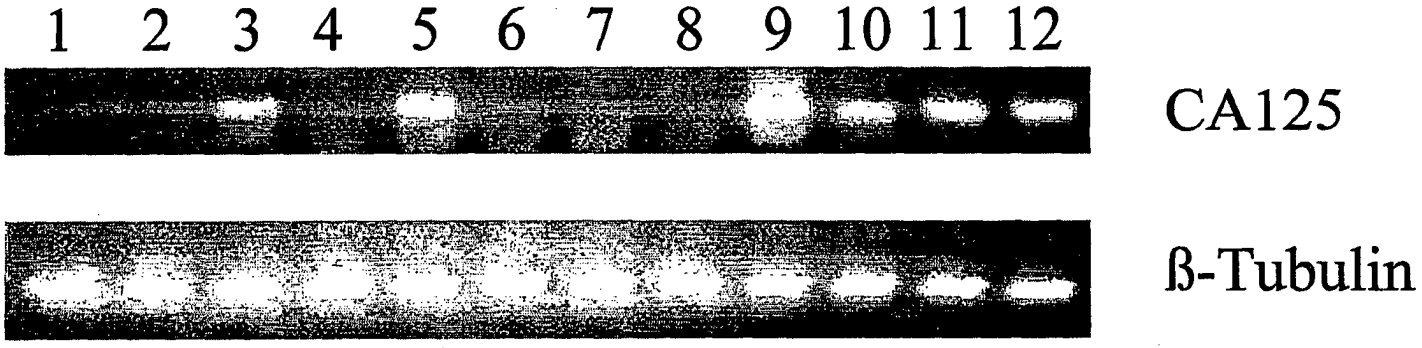
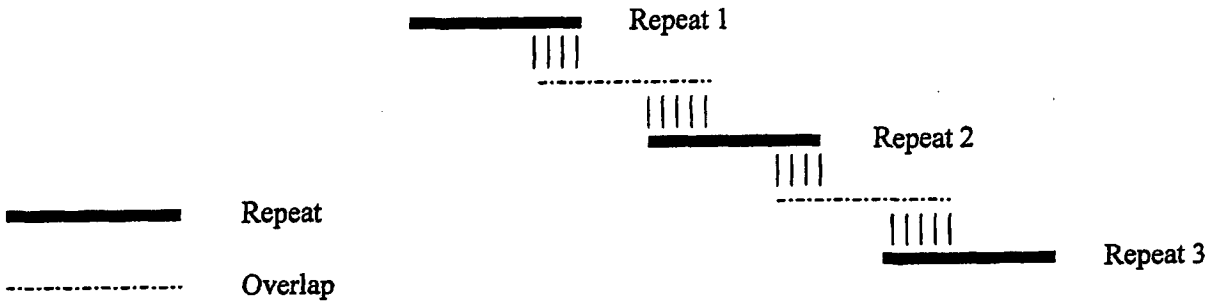


Figure 2

A Strategy for Placing Repeat Sequences in Contiguous Order Using Overlap Sequence Allignment



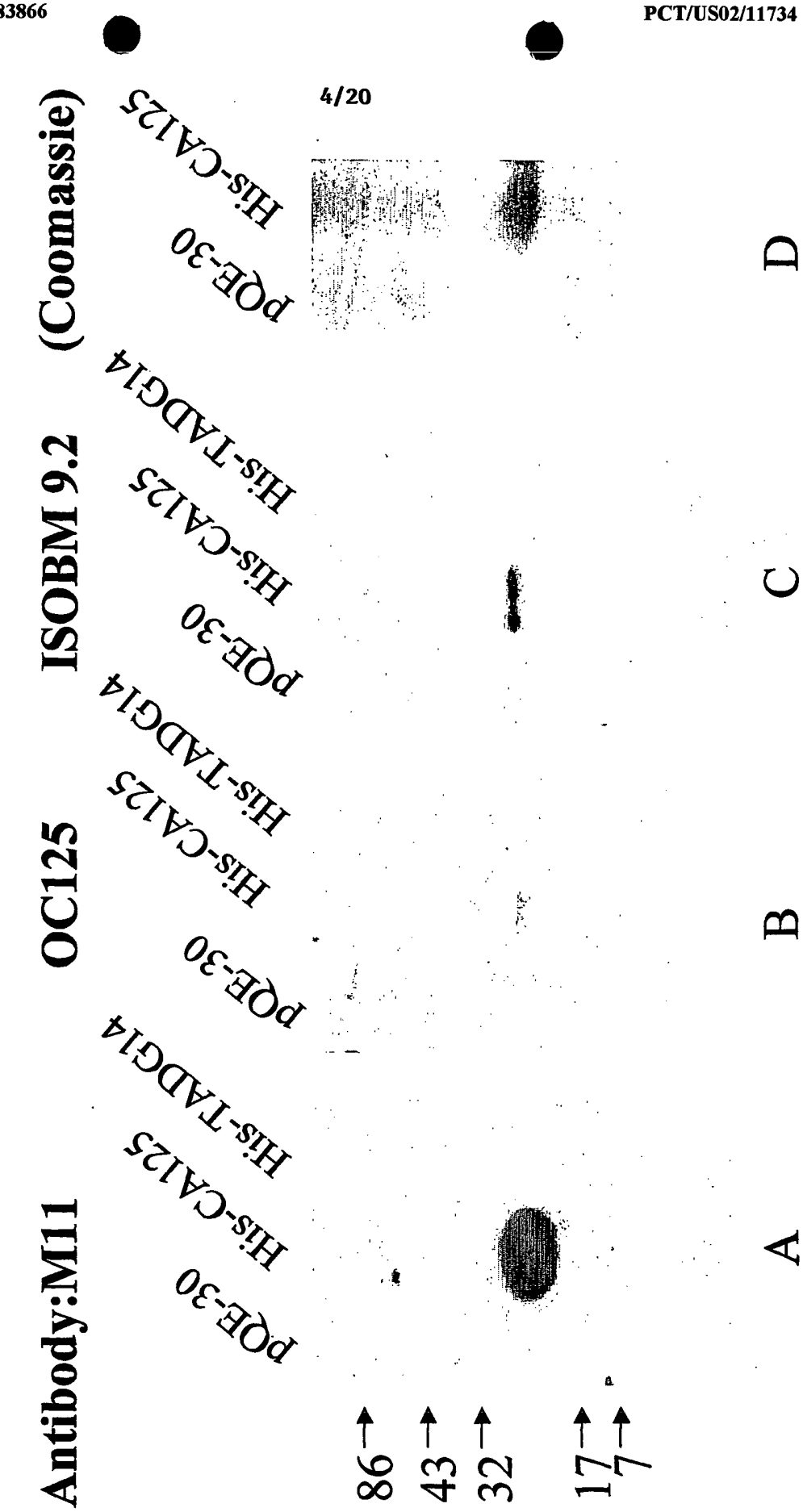

```
(SEQ ID NO: 158)
  1 ATVPEMVPFTLNFTITNLQYEEDMRHPGSRKFNATERELQGLLKPLFRNSSLEYLYSGCRLASLRPEKDSSAMAVDAICTHRPDPEDLGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNGFTHRSSMPTTSTPGTSTVDVGTSGTPSSSPSPT  156
157 AAGPLLMPFTLNFTITNLQYEEDMARTGSRKFNTMESVLQGLLKPLFKNTSVGPLYSGCRLTLLRPEKDGAATGVDAICTHRLDPKSPGLNREQLYWELSKLTNDIEELGPYTLDRNSLYVNGFTHQSSVSTTSTPGTSTVDLRTSGTPSSLSSPTIM 314
315 AAGPLLVPFTLNFTITNLQYGEDMGHPGSRKFNTTERVLQGLLGPIFKNTSVGPLYSGCRLTSLRSEKDGAATGVDAICIHHLDPKSPGLNRERLYWELSQLTNGIKELGPYTLDRNSLYVNGFTHRTSVPTSSTPGTSTVDLGTSGTPFSLPSPA 470
471 TAGPLLVLFTLNFTITNLKYEEDMHRPGSRKFNTTERVLQTLLGPMFKNTSVGLLYSGCRLTLLRSEKDGAATGVDAICTHRLDPKSPGLDREQLYWELSQLTNGIKELGPYTLDRNSLYVNGFTHWIPVPTSSTPGTSTVDLG.SGTPSSLPSPT  625
626 AAGPLLVPFTLNFTITNLQYEEDMHHPGSRKFNTTERVLQGLLGPMFKNTSVGLLYSGCRLTLLRSEKDGAATGVDAICTHRLDPKSPGVDREQLYWELSQLTNGIKELGPYTLDRNSLYVNGFTHQTSAPNTSTPGTSTVDLGTSGTPSSLPSPT  781

(SEQ ID NO: 159)
  1 SAGPLLVPFTLNFTITNLQYEEDMHHPGSRKFNTTERVLQGLLGPMFKNTSVGLLYSGCRLTLLRPEKNGAATGMDAICSHRLDPKSPGLNREQLYWELSQLTHGIKELGPYTLDRNSLYVNGFTHRSSVAPTSTPGTSTVDLGTSGTPSSLPSPT  156
157 TAVPLLVPFTLNFTITNLQYGEDMRHPGSRKFNTTERVLQGLLGPLFKNSSVGPLYSGCRLISLRSEKDGAATGVDAICTHHLNPQSPGLDREQLYWQLSQMTNGIKELGPYTLDRNSLYVNGFTHRSSGLTTSTPWTSTVDLGTSGTPSPVPSPT  312
313 TAGPLLVPFTLNFTITNLQYEEDMHRPGSRKFNATERVLQGLLSPIFKNSSVGPLYSGCRLTSLRPEKDGAATGMDAVCLYHPNPKRPGLDREQLYWELSQLTHNITELGPYSLDRDSLYVNGFTHQNSVPTTSTPGTSTVYWATTGTPSSFPGHT  468
469 EPGPLLIPFTFNFTITNLHYEENMQHPGSRKFNTTERVLQGLLKPLFKNTSVGPLYSGCRLTSLRPEKDGAATGMDAVCLYHPNPKRPGLDREQLYCELSQLTHNITELGPYSLDRDSLYVNGFTHQNSVPTTSTPGTSTVYWATTGTPSSFPGHT  624
625 EPGPLLIPFTFNFTITNLHYEENMQHPGSRKFNTTERVLQGLLKPLFKNTSVGPLYSGCRLTLLRPEKHEAATGVDTICTHRVDPIGPGLDRERLYWELSQLTNSITELGPYTLDRDSLYVNGFNPRSSVPTTSTPGTSTVHLATSGTPSSLPGHT  780

(SEQ ID NO: 160)
  1 TAGPLLVPFTLNFTITNLQYEEDMHRPGSRRFNTTERVLQGLLTPLFKNTSVGPLYSGCRLTLLRPEKQEAATGVDTICTHRVDPIGPGLDRERLYWELSQLTNSITELGPYTLDRDSLYVNGFNPWSSVPTTSTPGTSTVHLATSGTPSSLPGHT  156
157 APVPLLIPFTLNFTITDLHYEENMQHPGSRKFNTTERVLQGLLKPLFKSTSVGPLYSGCRLTLLRPEKHGAATGVDAICTLRLDPTGPGLDRERLYWELSQLTNSVTELGPYTLDRDSLYVNGFTHRSSVPTTSIPGTSAVHLETSGTPASLPGHT  312
313 APGPLLVPFTLNFTITNLQYEEDMRHPGSRKFSTTERVLQGLLKPLFKNTSVSSLYSGCRLTLLRPEKDGAATRVDAVCTHRPDPKSPGLDRERLYWKLSQLTHGITELGPYTLDRHSLYVNGFTHQSSMTTTRTPDTSTMHLATSRTPASLSGPT  468
469 TASPLLVLFTINFTITNQRYEENMHHPGSRKFNTTERVLQGLLRPVFKNTSVGPLYSGCRLTLLRPKKDGAATKVDAICTYRPDPKSPGLDREQLYWELSQLTHSITELGPYTQDRDSLYVNGFTHRSSVPTTSIPGTSAVHLETSGTPASLPGHT  624

(SEQ ID NO: 161)
  1 ATGPVLLPFTLNFTITNLQYEEDMHRPGSRKFNTTERVLQGLLMPLFKNTSVSSLYSGCRLTLLRPEKDGAATRVDAVCTHRPDPKSPGLDRERLYWKLSQLTHGITELGPYTLDRHSLYVNGFTHQSSMTTTRTPDTSTMHLATSRTPASLSGPT  156
157 TASPLLVLFTINFTITNLRYEENMHHPGSRKFNTTERVLQGLLRPVFKNTSVGPLYSGCRLTLLRPKKDGAATKVDAICTYRPDPKSPGLDREQLYWELSQLTHSITELGPYTQDRDSLYNVGFTQRSSVPTTSVPGTPTVDLGTSGTPVSKPGPS  312
313 AASPLLVLFTLNGTITNLRYEENMQHPGSRKFNTTERVLQGLLRSLFKSTSVGPLYSGCRLTLLRPEKDGTATGVDAICTHHPDPKSPRLDREQLYWELSQLTHNITELGHYALDNDSLFVNGFTHRSSVSTTSTPGTPTVYLGASKTPASIFGPS  468
```

Figure 3 (SEQ ID NOS: 158, 159, 160, and 161)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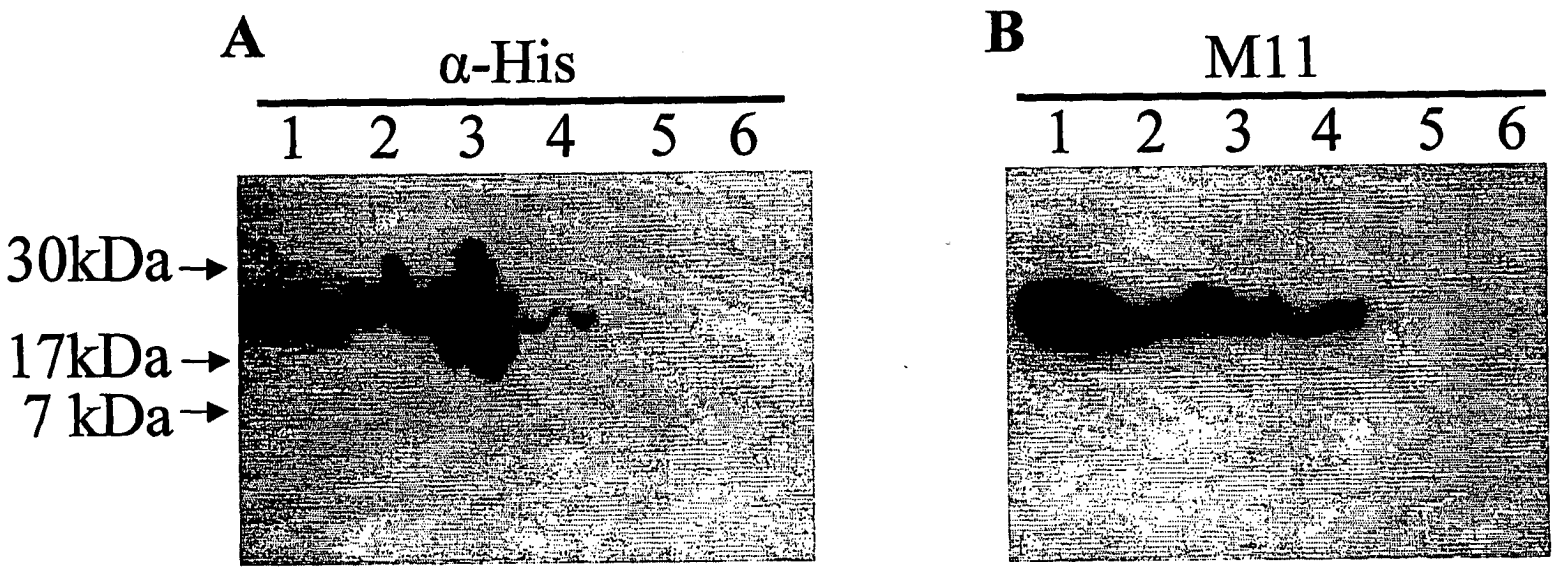
OC125
ISOBM 9.2
(Coomassie)
pQE-30
His-CA125
pQE-30
His-CA125
His-TADG14
pQE-30
His-CA125
His-TADG14
pQE-30
His-CA125
His-TADG14
pQE-30
His-CA125
His-TADG14
86
43
32
17
7
A
B
C
D

Figure 4



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                                          OO   OOOO   O       OO O O
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     O    O
151  SLPKLT
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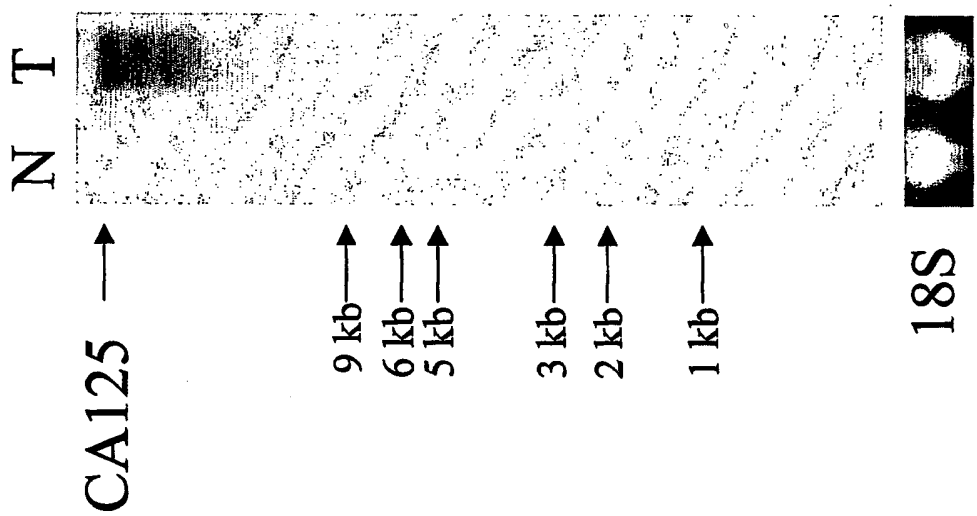
Figure 5 (SEQ ID NO: 150)



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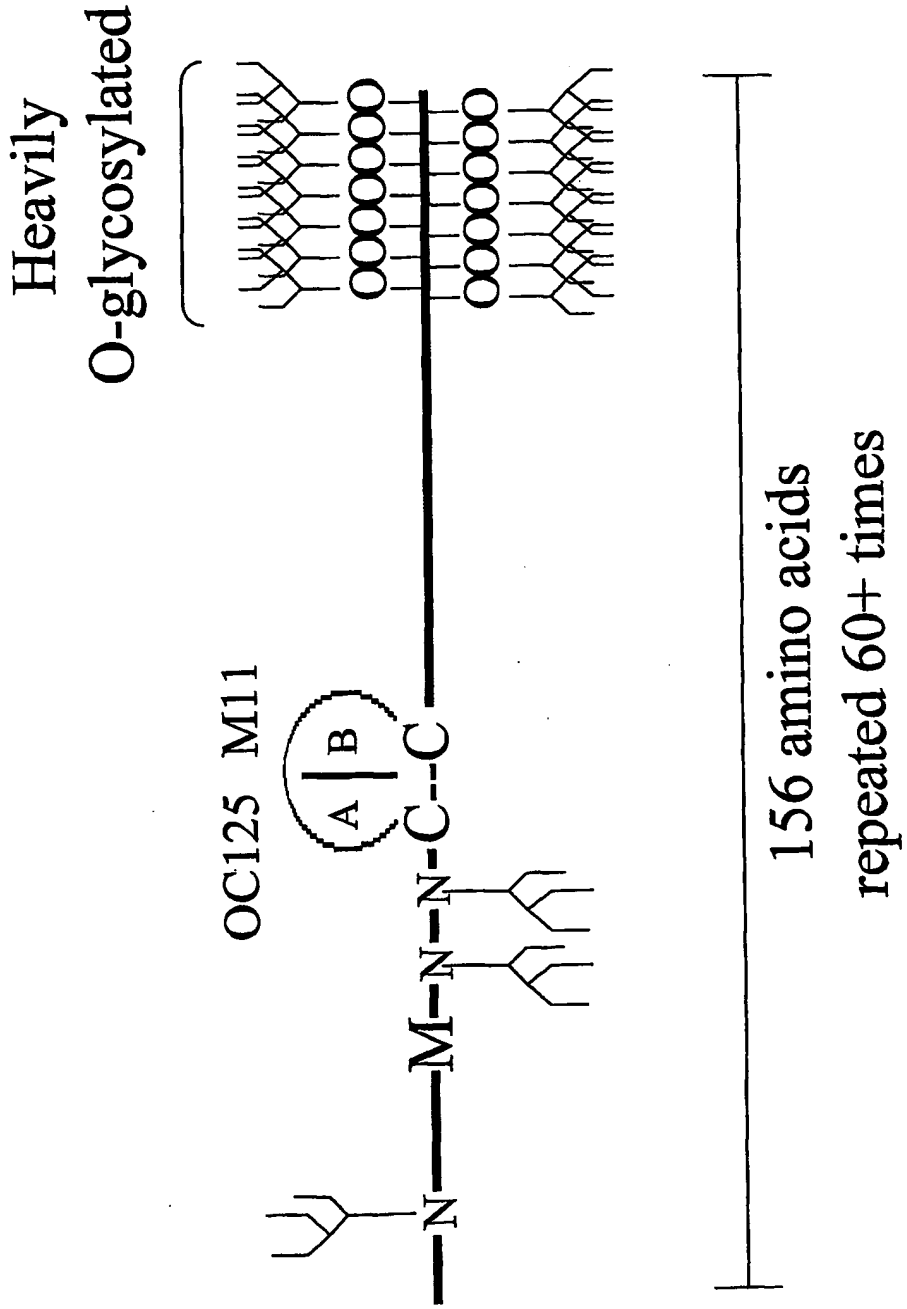
Heavily
O-glycosylated
OC125 M11
A
B
C
C
N
N
N
M
N
156 amino acids
repeated 60+ times

Figure 7A

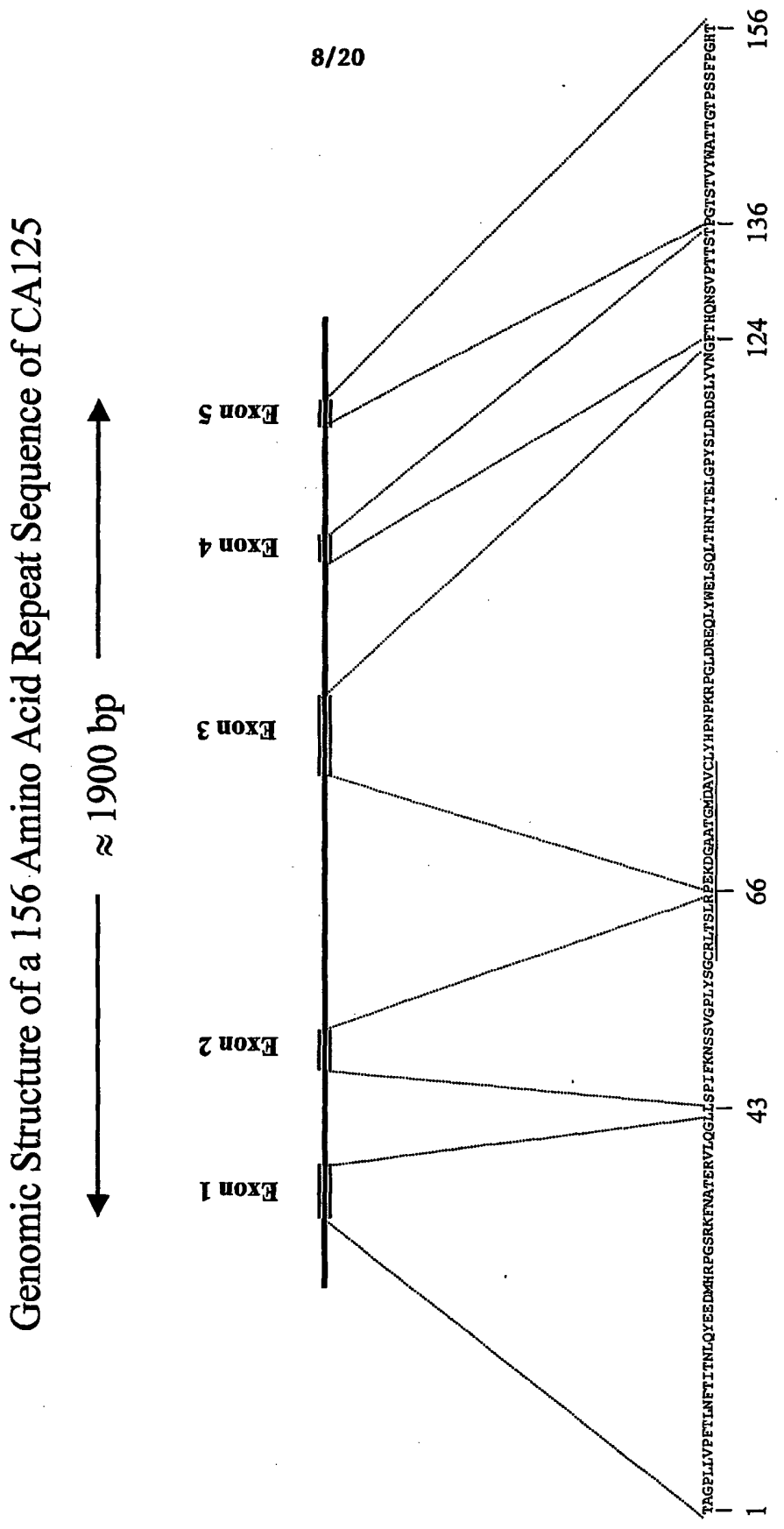

Figure 7B (SEQ ID NO: 163)

Exon 1

1 42

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APGPLLVPFTLNFTITNLQYEEDMRHPGSRKFSTTERVLQGL (SEQ ID NO: 167)
APGPLLVPFTLNFTITNLQYEEDMRHPGSRKFNTTERVLQGL (SEQ ID NO: 168)
APGPLLVPFTLNFTITNLQYEVDMRHPGSRKFNTTERVLQGL (SEQ ID NO: 169)
SAGPLLVPFTLNFTITNLQYEEDMRHPGSRKFNTTERVLQGL (SEQ ID NO: 170)
AAGPLLMPFTLNFTITNLQYEEDMRRTGSRKFNTMESVLQGL (SEQ ID NO: 171)
TASPLLVLFTINCTITNLQYEEDMRRTGSRKFNTMESVLQGL (SEQ ID NO: 172)
AAGPLLVPFTLNFTITNLQYGEDMGHPGSRKFNTTERVLQGL (SEQ ID NO: 173)
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TGVVSEEPFTLNFTINNLRYMADMGQPGSLKFNITDNVMKHL (SEQ ID NO: 193)
AMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLL (SEQ ID NO: 194)

Figure 7C

Exon 2

43 65

LKPLFRNSSLEYLYSGCRLASLR (SEQ ID NO: 195)
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LKPLFKNTSVGPLYSGCRLTLLR (SEQ ID NO: 197)
LKPLFKSTSVGPLYSGCRLTLLR (SEQ ID NO: 198)
LKPLFKSTSVGPLYSSCRLTLLR (SEQ ID NO: 199)
LKPLFKNTSVGPLYSGCRLTSLR (SEQ ID NO: 200)
LGPIFKNTSVGPLYSGCRLTSLR (SEQ ID NO: 201)
LGPMFKNTSVGLLYSGCRLTLLR (SEQ ID NO: 202)
LGPMFKNTSVGPLYSGCRLTLLR (SEQ ID NO: 203)
LGPMFKNTSVGPLYSGCRLTSLR (SEQ ID NO: 204)
LGPLFKNSSVGPLYSGCRLISLR (SEQ ID NO: 205)
LGPLFKNSSVDPLYSGCRLTSLR (SEQ ID NO: 206)
LSPIFKNSSVGPLYSGCRLTSLR (SEQ ID NO: 207)
LSPIFKNTSVGPLYSGCRLTLLR (SEQ ID NO: 208)
LSPLFQRSSLGARYTGCRVIALR (SEQ ID NO: 209)
LRPLFKNTSVSSLYSGCRLTLLR (SEQ ID NO: 210)
LRPLFKNTSVGPLYSGSRLTLLR (SEQ ID NO: 211)
LRPLFKNTSIGPLYSSCRLTLLR (SEQ ID NO: 212)
LRPLFKSTSVGPLYSGCRLTLLR (SEQ ID NO: 213)
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LRSLFKSTSVGPLYSGCRLTLLR (SEQ ID NO: 216)
LRSLFKSTSVGPLYSGCRLTSLR (SEQ ID NO: 217)
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LTPLFRNTSVSSLYSGCRLTLLR (SEQ ID NO: 219)
LMPLFKNTSVSSLYSGCRLTLLR (SEQ ID NO: 220)
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Figure 7C

Exon 3

66 123

PEKDSSAMAVDAICTHRPDPEDLGLDRERLYWELSNLTNGIQELGPYTLDRNSLYVNG (SEQ ID NO: 222)

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PKKDGAATGVDAICTHRLDPKSPGLNREQLYWELSKLTNDIEELGPYTLDRNSLYVNG (SEQ ID NO: 224)

PEKDGTATGVDAICTHHPDPKSPRLDREQLYWELSQLTHNITELGHYALDNDSLFVNG (SEQ ID NO: 225)

PEKDGEATGVDAICTHRPDPTGPGLDREQLYLELSQLTHSITELGPYTLDRDSLYVNG (SEQ ID NO: 226)

PEKDGAATGMDAVCLYHPNPKRPGLDREQLYWELSQLTHNITELGPYSLDRDSLYVNG (SEQ ID NO: 227)

PEKDGAATGMDAVCLYHPNPKRPGLDREQLYCELSQLTHNITELGPYSLDRDSLYVNG (SEQ ID NO: 228)

PEKDGAATRVDAACTYRPDPKSPGLDREQLYWELSQLTHSITELGPYTLDRVSLYVNG (SEQ ID NO: 229)

PKKDGAATKVDAICTYRPDPKSPGLDREQLYWELSQLTHSITELGPYTQDRDSLYVNG (SEQ ID NO: 230)

PKKDGAATKVDAICTYRPDPKSPGLDREQLYWELSQLTHSITELGPYTQDRDSLYNVG (SEQ ID NO: 231)

PEKDGAATRVDAVCTHRPDPKSPGLDRERLYWKLSQLTHGITELGPYTLDRHSLYVNG (SEQ ID NO: 232)

PEKDGVATRVDAICTHRPDPKIPGLDRQQLYWELSQLTHSITELGPYTLDRDSLYVNG (SEQ ID NO: 233)

SEKDGAATGVDAICIHHLDPKSPGLNRERLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 234)

SEKDGAATGVDAICTHRLDPKSPGLDREQLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 235)

SEKDGAATGVDAICTHRLDPKSPGVDREQLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 236)

SEKDGAATGVDAICTHRVDPKSPGVDREQLYWELSQLTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 237)

SEKDGAATGVDAICTHHLNPQSPGLDREQLYWQLSQMTNGIKELGPYTLDRNSLYVNG (SEQ ID NO: 238)

PEKRGAATGVDTICTHRLDPLNPGLDREQLYWELSKLTRGIIELGPYLLDRGSLYVNG (SEQ ID NO: 239)

PEKNGAATGMDAICSHRLDPKSPGLNREQLYWELSQLTHGIKELGPYTLDRNSLYVNG (SEQ ID NO: 240)

PEKNGAATGMDAICSHRLDPKSPGLDREQLYWELSQLTHGIKELGPYTLDRNSLYVNG (SEQ ID NO: 241)

PEKHGAATGVDAICTLRLDPTGPGLDRERLYWELSQLTNSVTELGPYTLDRDSLYVNG (SEQ ID NO: 242)

PEKHGAATGVDAICTLRLDPTGPGLDRERLYWELSQLTNSITELGPYTLDRDSLYVNG (SEQ ID NO: 243)

PEKHEAATGVDTICTHRVDPIGPGLDRERLYWELSQLTNSITELGPYTLDRDSLYVNG (SEQ ID NO: 244)

PEKQEAATGVDTICTHRVDPIGPGLDRERLYWELSQLTNSITELGPYTLDRDSLYVNG (SEQ ID NO: 245)

PEKQEAATGVDTICTHRVDPIGPGLDRERLYWELSQLTNSITELGPYTLDRDSLYVDG (SEQ ID NO: 246)

PEKDKAATRVDAICTHHPDPQSPGLNREQLYWELSQLTHGITELGPYTLDRDSLYVDG (SEQ ID NO: 247)

SVKNGAETRVDLLCTYLQPLSGPGLPIKQVFHELSQQTHGITRLGPYSLDKDSLYLNG (SEQ ID NO: 248)

PEKDGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTHGVTQLGFYVLDRDSLFING (SEQ ID NO: 249)

Figure 7C

Exon 4

124 135

FTHRSSMPTTST (SEQ ID NO: 250)
FTHRSSMPTTSI (SEQ ID NO: 251)
FTHRTSVPTSST (SEQ ID NO: 252)
FTHRTSVPTTST (SEQ ID NO: 253)
FTHRSSVPTTSS (SEQ ID NO: 254)
FTHRSSVSTTST (SEQ ID NO: 255)
FTHRSSVAPTST (SEQ ID NO: 256)
FTHRSSGLTTST (SEQ ID NO: 257)
FTHRSFGLTTST (SEQ ID NO: 258)
FTHRSSFLTTST (SEQ ID NO: 259)
FTHRNFVPITST (SEQ ID NO: 260)
FTHRSSVPTTSI (SEQ ID NO: 261)
FTHQSSVSTTST (SEQ ID NO: 262)
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FTHQTFAPNTST (SEQ ID NO: 264)
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FNPRSSVPTTST (SEQ ID NO: 271)
FNPWSSVPTTST (SEQ ID NO: 272)
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FTQRSSVPTTST (SEQ ID NO: 274)
FTQRSSVPTTSV (SEQ ID NO: 275)
YNEPGLDEPPTT (SEQ ID NO: 276)
YAPQNLSIRGEY (SEQ ID NO: 277)

Exon 5

136 156

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PGTSTVHLGTSETPSSLPRPI (SEQ ID NO: 292)
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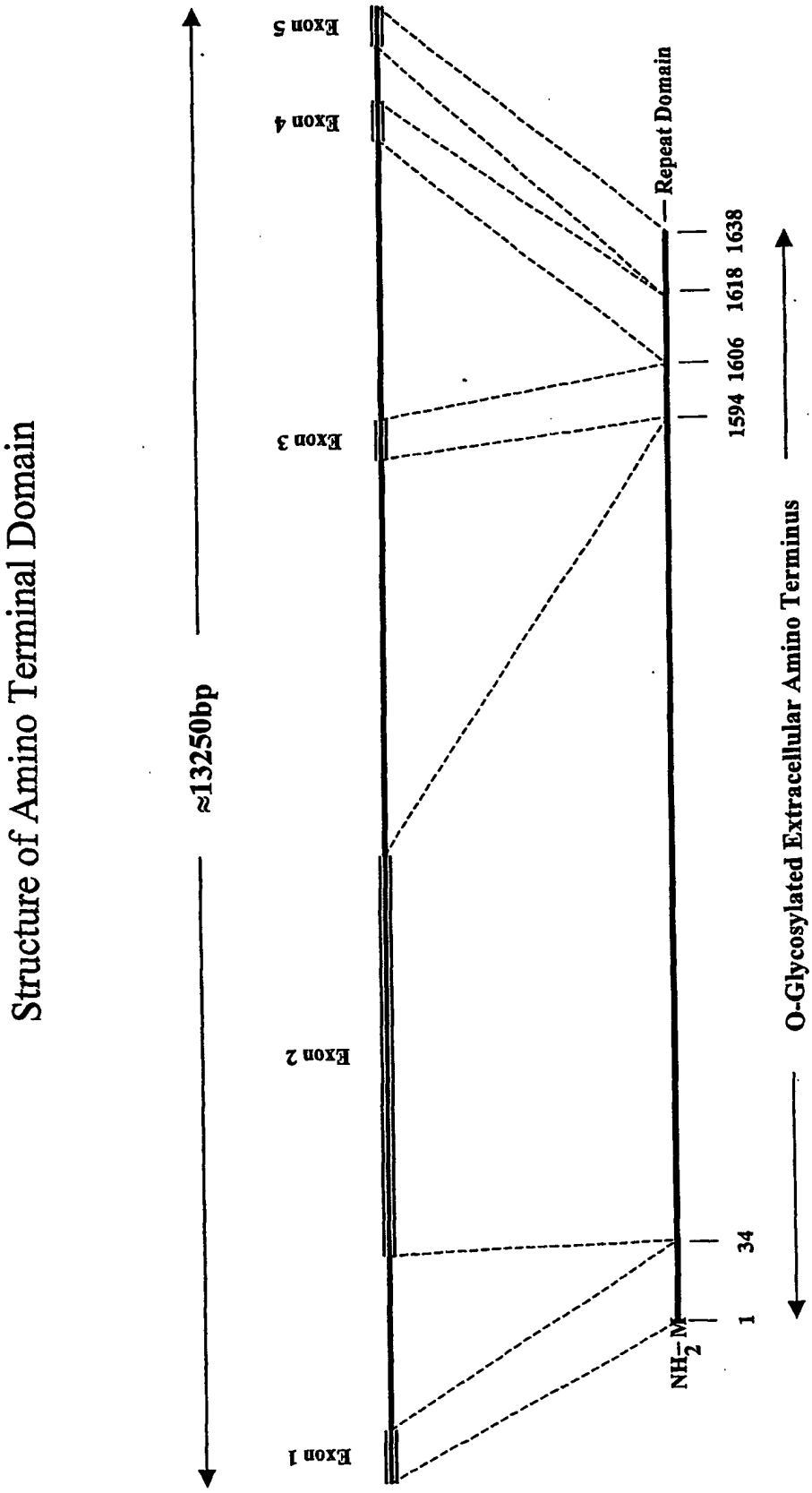
Figure 7C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Exon 4
Exon 3
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Repeat Domain
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1594
34
1
NH2-M
O-Glycosylated Extracellular Amino Terminus

Figure 8A

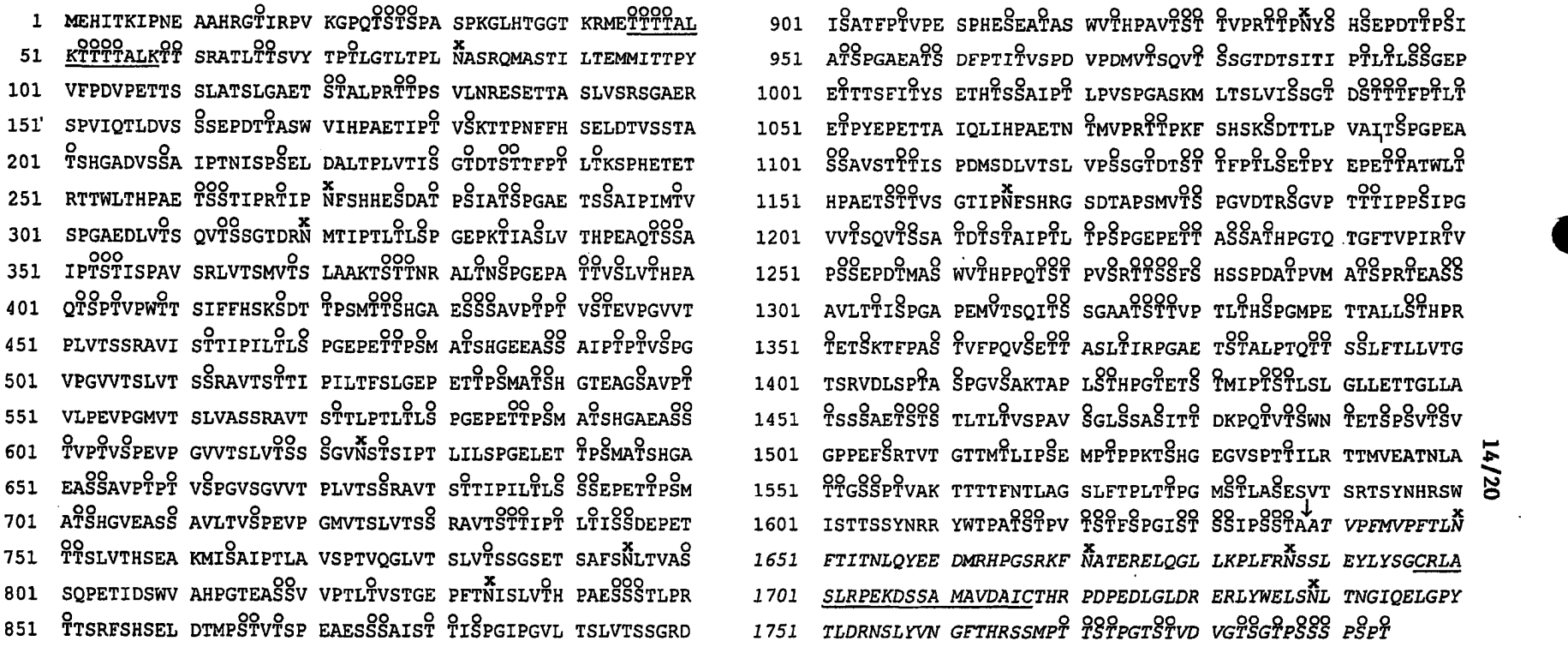
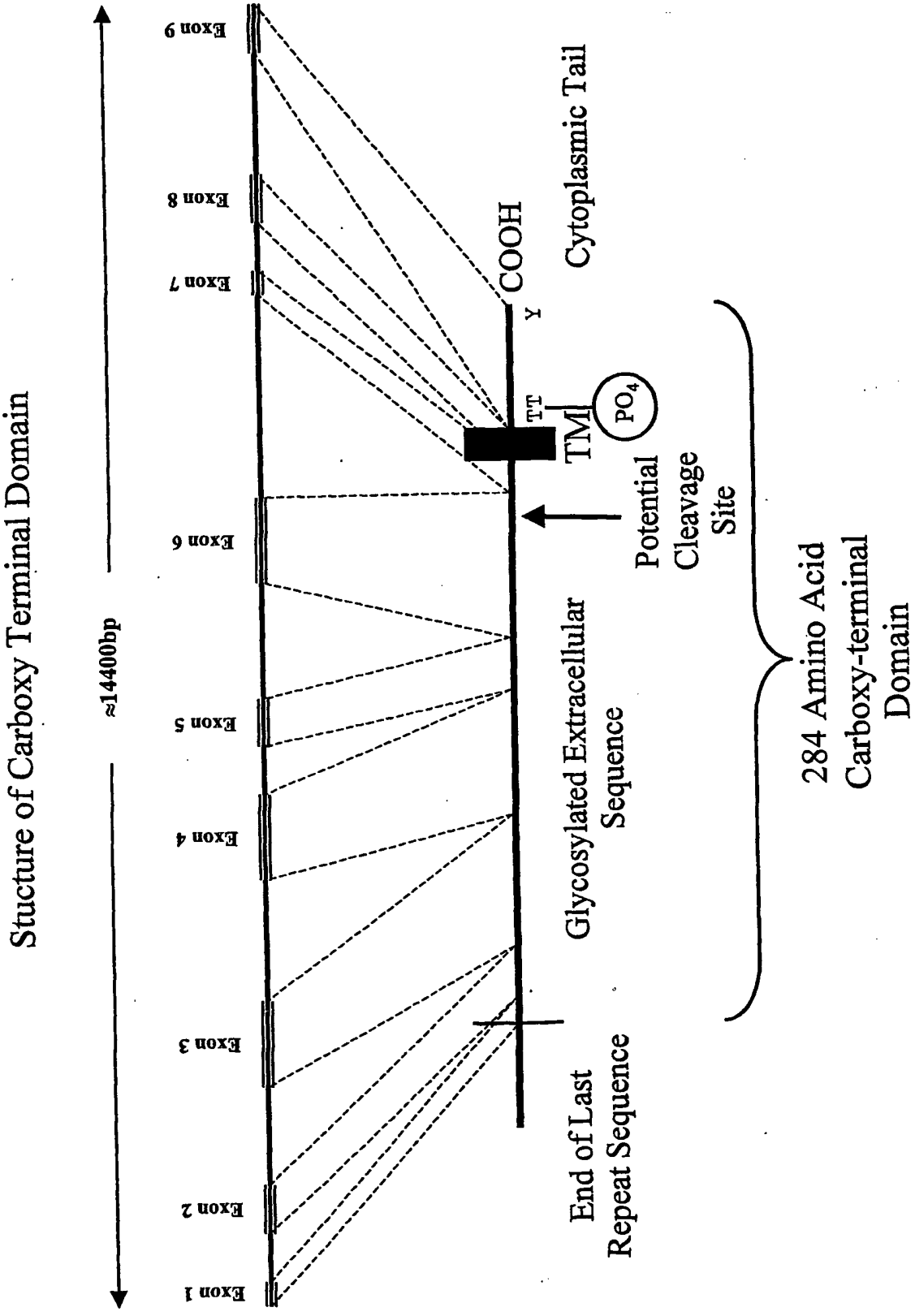


Figure 8B (SEQ ID NO: 299)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Exon 9
Exon 8
Exon 7
Exon 6
Exon 5
Exon 4
Exon 3
Exon 2
Exon 1
COOH
Y
Cytoplasmic Tail
TM
TT
PO4
Potential Cleavage Site
Glycosylated Extracellular Sequence
End of Last Repeat Sequence
284 Amino Acid Carboxy-terminal Domain

Figure 9A

Figure 9B (SEQ ID NO: 300)

Proposed Structure of CA125

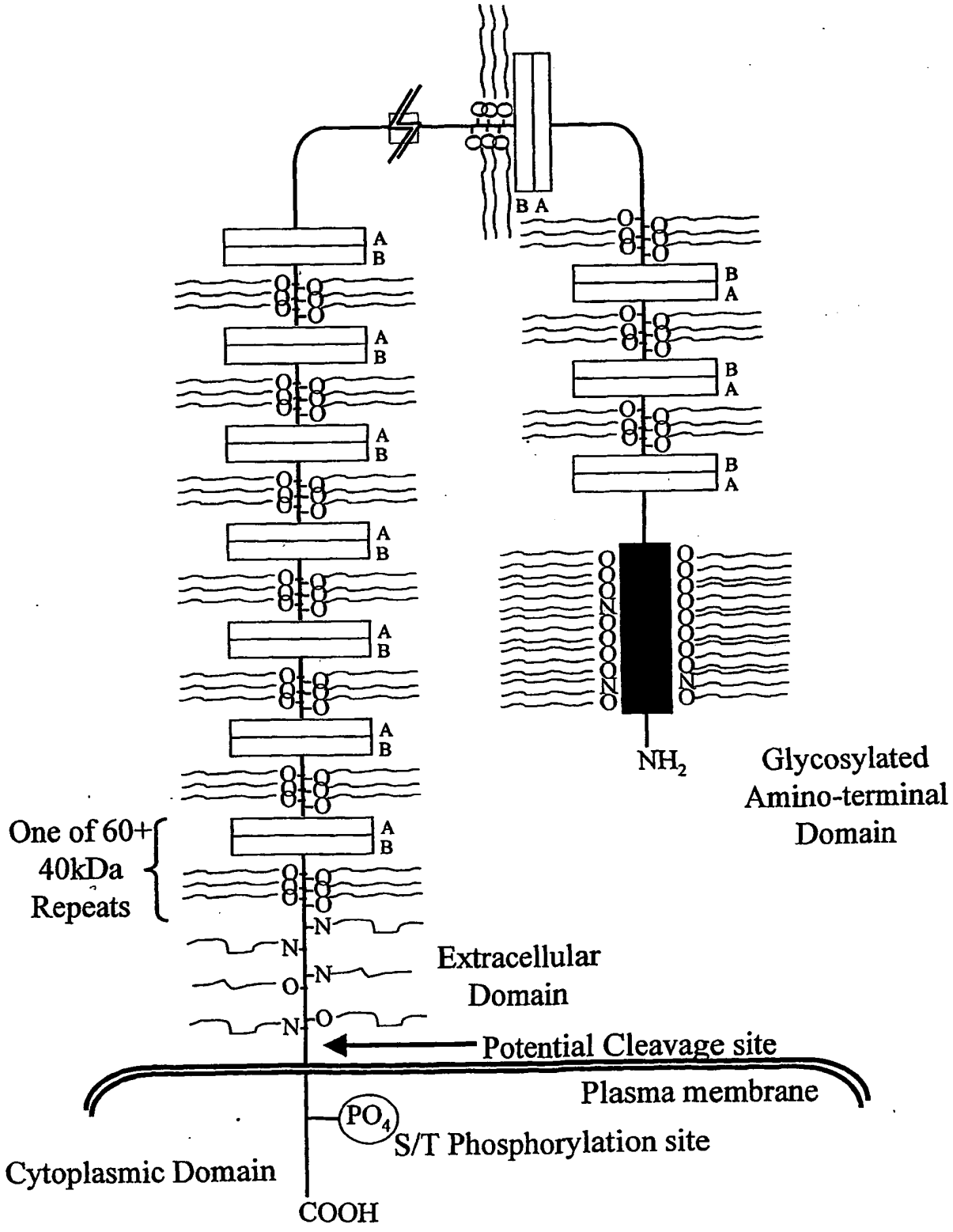
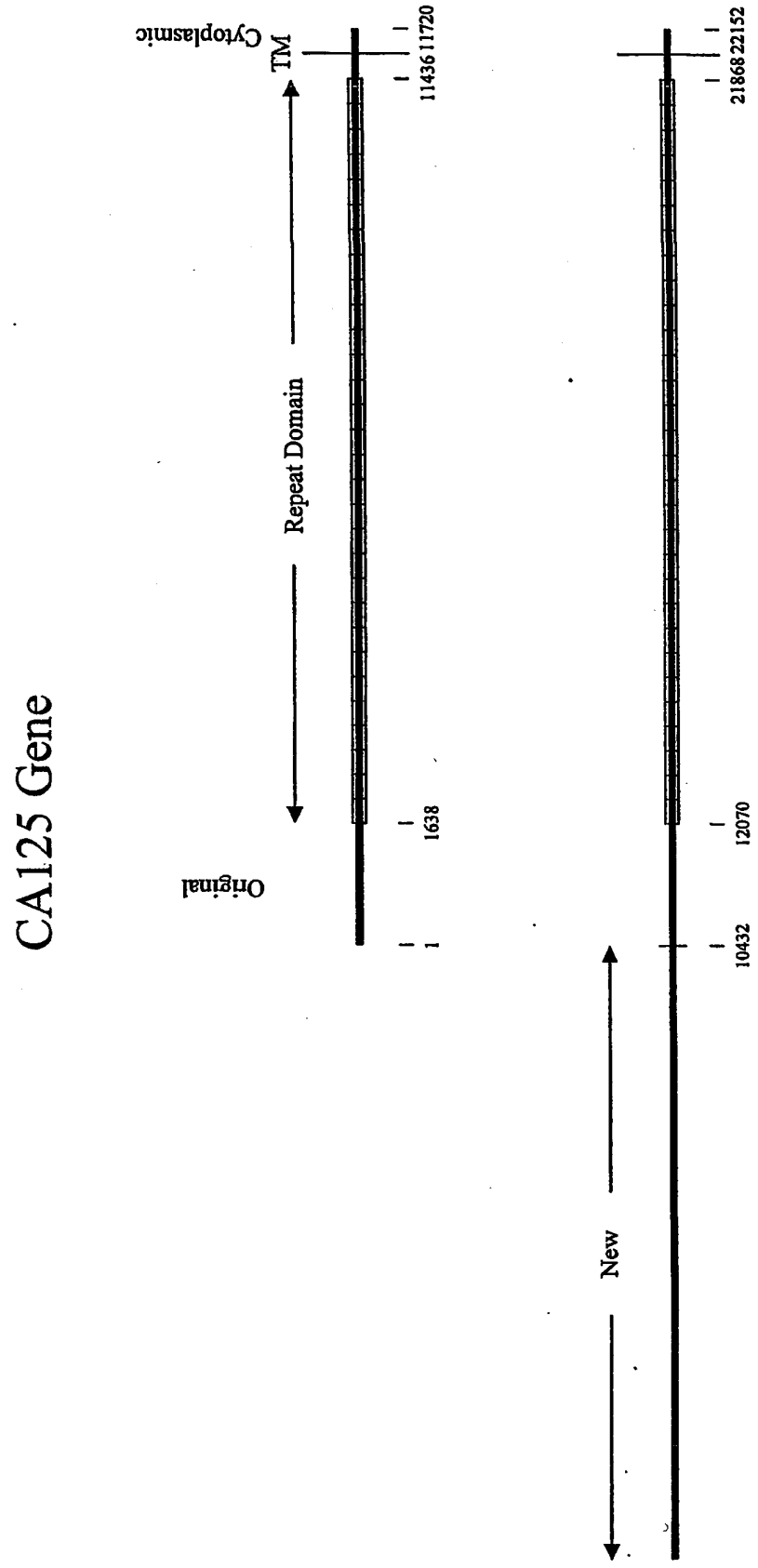


Figure 10


CA125 Gene
Original
Repeat Domain
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Cytoplasmic
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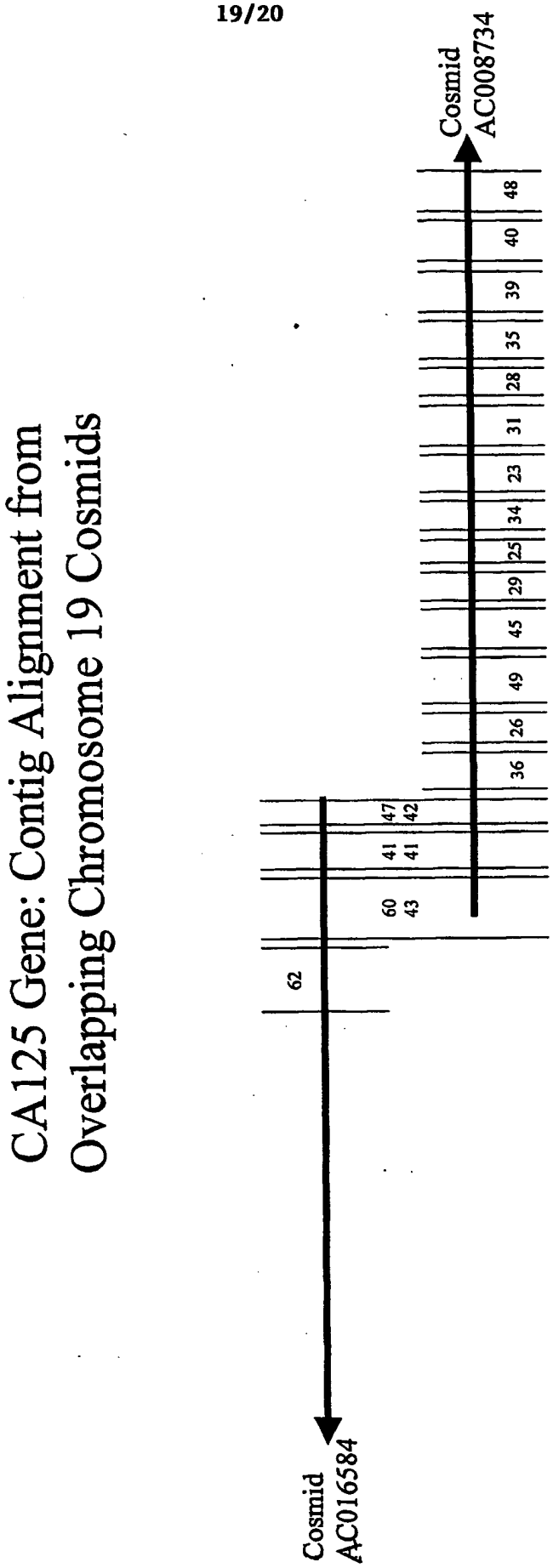
1638
10432
11436 11720
New
12070
21868 22152

Figure 11


CA125 Gene: Contig Alignment from Overlapping Chromosome 19 Cosmids
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42
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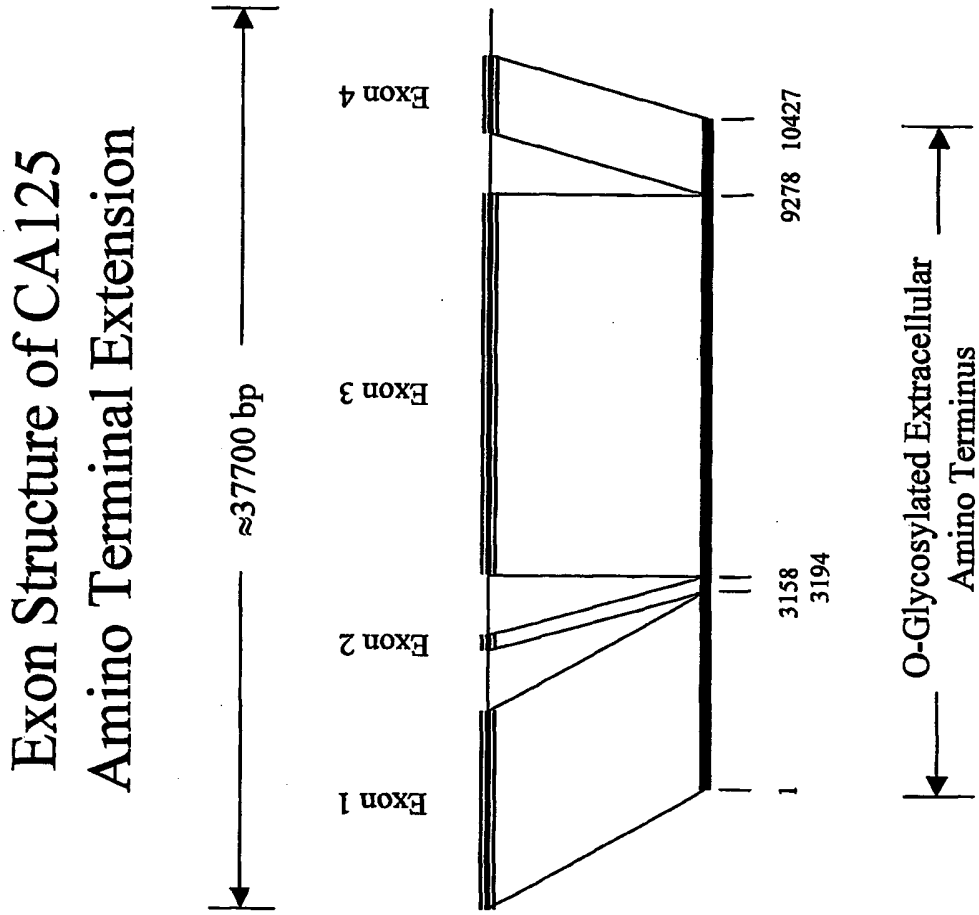
60
43
62
Cosmid AC016584

Figure 12


Exon Structure of CA125
Amino Terminal Extension
≈37700 bp
Exon 4
Exon 3
Exon 2
Exon 1
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9278
10427
O-Glycosylated Extracellular
Amino Terminus

Figure 13

SEQUENCE LISTING

<110> The Board of Trustees of the University of Arkansas

<120> Repeat Sequences of the CA125 Gene and Their Use for Diagnostic and Therapeutic Interventions

<130> 40715-268163

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<150> US 60/299,380

<151> 2001-06-19

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ggt ctg ctc agg cct gtg ttc aag aac acc agt gtt ggc cct ctg tac      96
Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr
            20                  25                  30

tct ggc tgc aga ctg acc ttg ctc agg ccc aag aag gat ggg gca gcc     144
Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala
        35                  40                  45

acc aaa gtg gat gcc atc tgc acc tac cgc cct gat ccc aaa agc cct     192
Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro
    50                  55                  60

gga ctg gac aga gag cag cta tac tgg gag ctg agc cag ggt gat gca     240
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Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
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Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ala Leu Asp
65 70 75 80

Asn Asp Ser Leu Phe Val Asn Gly Phe Thr His Arg Ser Ser Val Ser
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Pro Phe Thr
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35 40 45

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50 55 60

Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg His Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr
85 90 95

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115 120 125

Pro Phe
130

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20 25 30

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35 40 45

Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly
100 105 110

Thr Pro Ser Ser Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu
115 120 125

Leu Ile Pro Phe
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20 25 30

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35 40 45

Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Ala
85 90 95

Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
100 105 110

Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Val Pro Leu Leu Ile
115 120 125

Pro Phe
130

<210> 15

<211> 130

<212> PRT

<213> Homo sapiens

<400> 15

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys Asn Ser Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu
20 25 30

Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His His Leu
35 40 45

Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu
50 55 60

Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu
85 90 95

Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
100 105 110

Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Phe Leu Ile
115 120 125

Pro Phe
130

<210> 16

<211> 130

<212> PRT

<213> Homo sapiens

<400> 16

Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Ser Thr Ser
1 5 10 15

Ala Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu
35 40 45

Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
85 90 95

Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly
100 105 110

Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Ile
115 120 125

Pro Phe
130

<210> 17

<211> 130

<212> PRT

<213> Homo sapiens

<400> 17

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
85 90 95

Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly
100 105 110

Thr Pro Ala Ser Leu Pro Gly His Ile Val Pro Gly Pro Leu Leu Ile
115 120 125

Pro Phe
130

<210> 18

<211> 131

<212> PRT

<213> Homo sapiens

<400> 18

Glu Arg Val Leu Gln Gly Leu Leu Thr Pro Leu Phe Lys Asn Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val
35 40 45

Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asp Gly Phe Asn Pro Trp Ser Ser Val Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly
100 105 110

Thr Pro Ser Pro Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile
115 120 125

Pro Phe Thr
130

<210> 19

<211> 131

<212> PRT

<213> Homo sapiens

<400> 19

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
65 70 75 80

Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro
85 90 95

Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu
100 105 110

Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Val
115 120 125

Pro Phe Thr
130

<210> 20

<211> 130

<212> PRT

<213> Homo sapiens

<400> 20

Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu
20 25 30

Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
35 40 45

Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly
100 105 110

Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile
115 120 125

Pro Phe
130

<210> 21

<211> 131

<212> PRT

<213> Homo sapiens

<400> 21

Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser
1 5 10 15

Ile Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Asp Lys Ala Ala Thr Arg Val Asp Ala Ile Cys Thr His His Pro
35 40 45

Asp Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asp Gly Phe Thr His Trp Ser Pro Ile Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Ile Val Asn Leu Gly Thr Ser Gly
100 105 110

Ile Pro Pro Ser Leu Pro Glu Thr Thr Ala Thr Gly Pro Leu Leu Ile
115 120 125

Pro Phe Thr
130

<210> 22

<211> 282

<212> PRT

<213> Homo sapiens

<400> 22

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser
1 5 10 15

Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu
20 25 30

```
Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro
        35                  40                  45

Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
    50                  55                  60

Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp
65                  70                  75                  80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro
                85                  90                  95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly
            100                 105                 110

Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Met
        115                 120                 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
    130                 135                 140

Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu
145                 150                 155                 160

Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
                165                 170                 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
            180                 185                 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
        195                 200                 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
    210                 215                 220

His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
225                 230                 235                 240
```

Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr
245 250 255

Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser
260 265 270

Phe Pro Gly His Thr Glu Pro Gly Pro Leu
275 280

<210> 23

<211> 286

<212> PRT

<213> Homo sapiens

<400> 23

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser
1 5 10 15

Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu
20 25 30

Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro
35 40 45

Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
50 55 60

Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu
85 90 95

Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
100 105 110

Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Ile
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
130 135 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala
180 185 190

Ala Thr Arg Val Asp Ala Val Cys Thr Gln Arg Pro Asp Pro Lys Ser
195 200 205

Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr
210 215 220

His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu
225 230 235 240

Tyr Val Asn Gly Leu Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr
245 250 255

Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser
260 265 270

Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Ile Pro Phe
275 280 285

<210> 24

<211> 250

<212> PRT

<213> Homo sapiens

<400> 24

```
Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
1               5                  10                  15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
            20                  25                  30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
        35                  40                  45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
    50                  55                  60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
65                  70                  75                  80

Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Thr Ser Val Pro
                85                  90                  95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
            100                 105                 110

Thr Pro Phe Ser Leu Pro Ser Pro Ala Thr Ala Gly Pro Leu Leu Val
        115                 120                 125

Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp
    130                 135                 140

Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145                 150                 155                 160

Gln Thr Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu
                165                 170                 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala
            180                 185                 190

Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
        195                 200                 205

Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
    210                 215                 220
```

Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Trp Ile Pro
245 250

<210> 25

<211> 286

<212> PRT

<213> Homo sapiens

<400> 25

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
65 70 75 80

Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro
85 90 95

Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu
100 105 110

Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Ile
115 120 125

Pro Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
130 135 140

Met His His Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Gly Pro Leu Phe Lys Asn Ser Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu Lys Asp Gly Ala
180 185 190

Ala Thr Gly Val Asp Ala Ile Cys Thr His His Leu Asn Pro Gln Ser
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser Gln Met Thr
210 215 220

Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu Thr Thr Ser Thr
245 250 255

Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro
260 265 270

Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Ile Pro Phe
275 280 285

<210> 26

<211> 286

<212> PRT

<213> Homo sapiens

<400> 26

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
65 70 75 80

Arg Gly Ser Leu Tyr Val Asn Gly Phe Ser Arg Gln Ser Ser Met Thr
85 90 95

Thr Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg
100 105 110

Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Ile
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
130 135 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Asn Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Lys Pro Glu Lys Asp Gly Ala
180 185 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

His Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Ala Pro Thr Ser Thr
245 250 255

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser
260 265 270

Leu Pro Ser Pro Thr Thr Ala Val Pro Leu Leu Ile Pro Phe
275 280 285

<210> 27

<211> 286

<212> PRT

<213> Homo sapiens

<400> 27

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
85 90 95

Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Phe Gly
100 105 110

Thr Pro Ala Ser Leu His Gly His Thr Ala Pro Gly Pro Val Leu Val
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
130 135 140

Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala
180 185 190

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
210 215 220

Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr
245 250 255

Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser
260 265 270

Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Ile Pro Phe
275 280 285

<210> 28

<211> 286

<212> PRT

<213> Homo sapiens

<400> 28

```
Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
1               5                  10                  15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
            20                  25                  30

Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu
        35                  40                  45

Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
    50                  55                  60

Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65                  70                  75                  80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
                85                  90                  95

Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly
            100                 105                 110

Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Val
        115                 120                 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
    130                 135                 140

Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145                 150                 155                 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu
                165                 170                 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala
            180                 185                 190

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn
        195                 200                 205
```

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Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
    210                 215                 220

Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu
225                 230                 235                 240

Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr
                245                 250                 255

Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser
            260                 265                 270

Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Ile Pro Phe
        275                 280                 285
```

<210> 29

<211> 281

<212> PRT

<213> *Homo sapiens*

<400> 29

```
Glu Arg Val Leu Gln Gly Leu Leu Thr Pro Leu Phe Lys Asn Thr Ser
1               5                   10                  15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
            20                  25                  30

Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val
        35                  40                  45

Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
    50                  55                  60

Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65                  70                  75                  80
```

Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Trp Ser Ser Val Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly
100 105 110

Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
130 135 140

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala
180 185 190

Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
195 200 205

Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr
245 250 255

Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu
260 265 270

Pro Ser Pro Thr Thr Ala Gly Pro Leu
275 280

<210> 30

<211> 217

<212> PRT

<213> Homo sapiens

<400> 30

```
Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser
1               5                  10                  15

Ile Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr Leu Leu Arg Pro Glu
            20                  25                  30

Lys Asp Lys Ala Ala Thr Arg Val Asp Ala Ile Cys Thr His His Pro
        35                  40                  45

Asp Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu
    50                  55                  60

Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65                  70                  75                  80

Arg Asp Ser Leu Tyr Val Asp Gly Phe Thr His Trp Ser Pro Ile Pro
                85                  90                  95

Thr Thr Ser Thr Pro Gly Thr Ser Ile Val Asn Leu Gly Thr Ser Gly
            100                 105                 110

Ile Pro Pro Ser Leu Pro Glu Thr Thr Ala Thr Gly Pro Leu Leu Ile
        115                 120                 125

Pro Phe Thr Pro Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
    130                 135                 140

Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu
145                 150                 155                 160

Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
                165                 170                 175
```

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
180 185 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr
210 215

<210> 31

<211> 286

<212> PRT

<213> Homo sapiens

<400> 31

Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys
20 25 30

Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro
35 40 45

Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro
85 90 95

Thr Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly
100 105 110

Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser Pro Leu Leu Val
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
130 135 140

Met His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
180 185 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr
245 250 255

Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser
260 265 270

Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Ile Pro Phe
275 280 285

<210> 32

<211> 288

<212> PRT

<213> Homo sapiens

<400> 32

```
Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser
1               5                  10                  15

Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys
            20                  25                  30

Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro
        35                  40                  45

Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
    50                  55                  60

Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65                  70                  75                  80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro
                85                  90                  95

Thr Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly
            100                 105                 110

Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser Pro Leu Leu Ile
        115                 120                 125

Pro Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
    130                 135                 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu
145                 150                 155                 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
                165                 170                 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala
            180                 185                 190

Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
        195                 200                 205

Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
    210                 215                 220
```

```
Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
225                 230                 235                 240

Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr
                245                 250                 255

Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser
            260                 265                 270

Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Ile Pro Phe
        275                 280                 285
```

<210> 33

<211> 284

<212> PRT

<213> Homo sapiens

<400> 33

```
Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
1               5                   10                  15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
            20                  25                  30

Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
        35                  40                  45

Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Cys Glu Leu
    50                  55                  60

Ser Gln Leu Thr His Asp Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp
65                  70                  75                  80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro
                85                  90                  95
```

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly
100 105 110

Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile
115 120 125

Pro Phe Thr Phe Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
130 135 140

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Glu Ala
180 185 190

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val Asp Pro Ile Gly
195 200 205

Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

Asn Ser Ile His Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Asn Pro Arg Ser Ser Val Pro Thr Thr Ser Thr
245 250 255

Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser
260 265 270

Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile
275 280

<210> 34

<211> 288

<212> PRT

<213> Homo sapiens

<400> 34

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Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Ser Lys Asn Ser Ser
1               5                  10                  15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu
            20                  25                  30

Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
        35                  40                  45

Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
    50                  55                  60

Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp
65                  70                  75                  80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro
                85                  90                  95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly
            100                 105                 110

Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile
        115                 120                 125

Pro Phe Thr Val Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
    130                 135                 140

Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145                 150                 155                 160

Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu
                165                 170                 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala
            180                 185                 190
```

Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
210 215 220

Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr
245 250 255

Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser
260 265 270

Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Ile Pro Phe
275 280 285

<210> 35

<211> 274

<212> PRT

<213> Homo sapiens

<400> 35

Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser
1 5 10 15

Val Gly Ser Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val Cys Thr His Arg Pro
35 40 45

Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu
50 55 60

Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg His Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr
85 90 95

Thr Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg
100 105 110

Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Val
115 120 125

Leu Phe Thr Ile Asn Phe Thr Ile Thr Asn Gln Arg Tyr Glu Glu Asn
130 135 140

Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala
180 185 190

Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Gln Asp Arg Asp Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile
245 250 255

Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser
260 265 270

Leu Pro

<210> 36

<211> 386

<212> PRT

<213> Homo sapiens

<400> 36

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser
1 5 10 15

Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
65 70 75 80

Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro
85 90 95

Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu
100 105 110

Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Val
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Ala
130 135 140

Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala
180 185 190

Ala Thr Arg Val Asp Ala Ala Cys Thr Tyr Arg Pro Asp Pro Lys Ser
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Val Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Asn Pro Arg Ser Ser Val Pro Thr Thr Ser Thr
245 250 255

Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser
260 265 270

Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu
275 280 285

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro
290 295 300

Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu
305 310 315 320

Arg Pro Leu Phe Lys Asn Thr Ser Ile Gly Pro Leu Tyr Ser Ser Cys
325 330 335

Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Lys Ala Ala Thr Arg Val
340 345 350

Asp Ala Ile Cys Thr His His Pro Asp Pro Gln Ser Pro Gly Leu Asn
355 360 365

Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Thr
370 375 380

Glu Leu
385

<210> 37

<211> 438

<212> PRT

<213> Homo sapiens

<400> 37

Glu Arg Val Leu His Gly Leu Leu Thr Pro Leu Phe Lys Asn Thr Arg
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val
35 40 45

Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Trp Ser Ser Val Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly
100 105 110

Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
130 135 140

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145 150 155 160

```
Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
                165                 170                 175

Tyr Ser Gly Cys Arg Leu Thr Leu Phe Lys Pro Glu Lys His Glu Ala
            180                 185                 190

Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly
        195                 200                 205

Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr
    210                 215                 220

Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
225                 230                 235                 240

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile
                245                 250                 255

Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser
            260                 265                 270

Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu
        275                 280                 285

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr
    290                 295                 300

Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu
305                 310                 315                 320

Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
                325                 330                 335

Arg Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val
            340                 345                 350

Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp
        355                 360                 365
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Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Arg Gly Ile Ile
370 375 380

Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu Tyr Val Asn Gly
385 390 395 400

Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr Pro Gly Thr Ser
405 410 415

Thr Val His Leu Gly Thr Ser Glu Ile His Pro Ser Leu Pro Arg Pro
420 425 430

Ile Val Pro Gly Pro Leu
435

<210> 38

<211> 420

<212> PRT

<213> Homo sapiens

<400> 38

Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys
1 5 10 15

Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn
20 25 30

Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser
35 40 45

Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg
50 55 60

Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr
65 70 75 80

Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr
85 90 95

```
Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro
            100                 105                 110

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met
        115                 120                 125

Gly His Pro Gly Ser Arg Lys Phe Asn Ile Thr Glu Ser Val Leu Gln
    130                 135                 140

Gly Leu Leu Thr Pro Leu Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr
145                 150                 155                 160

Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala
                165                 170                 175

Thr Gly Val Asp Ala Ile Cys Thr His His Leu Asn Pro Gln Ser Pro
            180                 185                 190

Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser Gln Met Thr Asn
        195                 200                 205

Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr
    210                 215                 220

Val Asn Gly Phe Thr His Arg Ser Leu Gly Leu Thr Thr Ser Thr Pro
225                 230                 235                 240

Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val
                245                 250                 255

Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn
            260                 265                 270

Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His Pro Gly
        275                 280                 285

Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu Gln Gly Leu Leu Arg
    290                 295                 300
```

Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
305 310 315 320

Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp
325 330 335

Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg
340 345 350

Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu
355 360 365

Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe
370 375 380

Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Pro Thr
385 390 395 400

Val Asp Leu Gly Thr Ser Gly Thr Pro Val Ser Lys Pro Gly Pro Ser
405 410 415

Ala Ala Ser Pro
420

<210> 39

<211> 439

<212> PRT

<213> Homo sapiens

<400> 39

Glu Arg Val Leu Gln Gly Pro Leu Ser Pro Ile Phe Lys Asn Ser Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu
20 25 30

Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
35 40 45

```
Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
    50                  55                  60

Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp
65                  70                  75                  80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro
                85                  90                  95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly
            100                 105                 110

Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile
        115                 120                 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
    130                 135                 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Thr Glu Arg Val Leu
145                 150                 155                 160

Gln Gly Leu Leu Asn Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
                165                 170                 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
            180                 185                 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
        195                 200                 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Cys Glu Leu Ser Gln Leu Thr
    210                 215                 220

His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
225                 230                 235                 240

Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr
                245                 250                 255
```

Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser
260 265 270

Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu
275 280 285

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr
290 295 300

Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu
305 310 315 320

Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
325 330 335

Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val
340 345 350

Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp
355 360 365

Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr
370 375 380

Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
385 390 395 400

Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser
405 410 415

Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His
420 425 430

Thr Ala Pro Gly Pro Leu Leu
435

<210> 40

<211> 424

<212> PRT

<213> Homo sapiens

<400> 40

```
Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
1               5                  10                  15

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Tyr Thr His
            20                  25                  30

Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp
        35                  40                  45

Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
    50                  55                  60

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr Ser
65                  70                  75                  80

Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr
                85                  90                  95

Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly Pro Leu
            100                 105                 110

Leu Ile Pro Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu
        115                 120                 125

Glu Asn Met His His Pro Gly Ser Arg Lys Phe Asn Thr Met Glu Arg
    130                 135                 140

Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly
145                 150                 155                 160

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp
                165                 170                 175

Gly Val Ala Thr Arg Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro
            180                 185                 190
```

Lys Ile Pro Gly Leu Asp Arg Gln Gln Leu Tyr Trp Glu Leu Ser Gln
195 200 205

Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp
210 215 220

Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr
225 230 235 240

Ser Thr Pro Gly Thr Phe Thr Val Gln Pro Glu Thr Ser Glu Thr Pro
245 250 255

Ser Ser Leu Pro Gly Pro Thr Ala Thr Gly Pro Val Leu Leu Pro Phe
260 265 270

Thr Leu Asn Phe Thr Ile Ile Asn Leu Gln Tyr Glu Glu Asp Met His
275 280 285

Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
290 295 300

Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser
305 310 315 320

Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr
325 330 335

Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly
340 345 350

Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser
355 360 365

Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val
370 375 380

Asn Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly
385 390 395 400

Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro
405 410 415

Gly His Thr Ala Pro Val Pro Leu
420

<210> 41

<211> 418

<212> PRT

<213> Homo sapiens

<400> 41

Thr Leu Leu Arg Pro Lys Lys Asp Gly Val Ala Thr Gly Val Asp Ala
1 5 10 15

Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu
20 25 30

Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu
35 40 45

Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr
50 55 60

His Gln Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Ser Thr Val
65 70 75 80

Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser Leu Ser Ser Pro Thr Ile
85 90 95

Met Ala Ala Gly Pro Leu Leu Ile Pro Phe Thr Ile Asn Phe Thr Ile
100 105 110

Thr Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys
115 120 125

Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu Met Pro Leu Phe
130 135 140

Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys Arg Leu Thr Leu
145 150 155 160

Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val Cys
165 170 175

Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg Leu
180 185 190

Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro
195 200 205

Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg
210 215 220

Ser Ser Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val
225 230 235 240

Gly Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly
245 250 255

Pro Leu Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln
260 265 270

Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met
275 280 285

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
290 295 300

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
305 310 315 320

Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu
325 330 335

Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
340 345 350

Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp
355 360 365

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
370 375 380

Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly
385 390 395 400

Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Ile
405 410 415

Pro Phe

<210> 42

<211> 443

<212> PRT

<213> Homo sapiens

<400> 42

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Asp Gly Val Ala Thr Arg Val Asp Ala Ile Cys Thr His Arg Pro
35 40 45

Asp Pro Lys Ile Pro Gly Leu Asp Arg Gln Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Phe Thr Val Gln Pro Glu Thr Ser Glu
100 105 110

Thr Pro Ser Ser Leu Pro Gly Pro Thr Ala Thr Gly Pro Val Leu Leu
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Ile Asn Leu Gln Tyr Glu Glu Asp
130 135 140

Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Met Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Gln Glu Ala
180 185 190

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp Pro Ser Glu
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Ser Gly Val Leu Cys Pro Pro Pro Ser
245 250 255

Ile Leu Gly Ile Phe Thr Val Gln Pro Glu Thr Phe Glu Thr Pro Ser
260 265 270

Ser Leu Pro Gly Pro Thr Ala Thr Gly Pro Val Leu Leu Pro Phe Thr
275 280 285

Leu Asn Phe Thr Ile Ile Asn Leu Gln Tyr Glu Glu Asp Met His Arg
290 295 300

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
305 310 315 320

Leu Met Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
325 330 335

Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Gln Glu Ala Ala Thr Gly
340 345 350

Val Asp Thr Ile Cys Thr His Arg Val Asp Pro Ile Gly Pro Gly Leu
355 360 365

Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile
370 375 380

Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
385 390 395 400

Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr
405 410 415

Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly
420 425 430

His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe
435 440

<210> 43

<211> 442

<212> PRT

<213> Homo sapiens

<400> 43

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser
1 5 10 15

Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu
20 25 30

Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro
35 40 45

Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
50 55 60

Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly
100 105 110

Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Met
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
130 135 140

Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Ser Val Leu
145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala
180 185 190

Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
195 200 205

Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
210 215 220

Asn Asp Ile Glu Glu Val Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Ser Phe Val Ala Pro Thr Ser Thr
245 250 255

Leu Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser
260 265 270

Leu Pro Ser Pro Thr Thr Gly Val Pro Leu Leu Ile Pro Phe Thr Leu
275 280 285

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His Pro
290 295 300

Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu Gln Gly Leu Leu
305 310 315 320

Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys
325 330 335

Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val
340 345 350

Val Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp
355 360 365

Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr
370 375 380

Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly
385 390 395 400

Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser
405 410 415

Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro
420 425 430

Thr Thr Ala Ser Pro Leu Leu Ile Pro Phe
435 440

<210> 44

<211> 442

<212> PRT

<213> Homo sapiens

<400> 44

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
65 70 75 80

Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro
85 90 95

Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu
100 105 110

Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Ile
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
130 135 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Ser Ser
180 185 190

Thr Met Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp
195 200 205

Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr
210 215 220

Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Ser Phe Met Pro Thr Thr Ser Thr
245 250 255

Leu Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser
260 265 270

Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Met Pro Phe Thr Leu
275 280 285

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr
290 295 300

Gly Ser Arg Lys Phe Asn Thr Met Glu Ser Val Leu Gln Gly Leu Leu
305 310 315 320

Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
325 330 335

Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Gly Val
340 345 350

Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn
355 360 365

Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu
370 375 380

Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
385 390 395 400

Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Ser
405 410 415

Thr Val Asp Pro Arg Thr Ser Gly Thr Pro Ser Ser Leu Ser Ser Pro
420 425 430

Thr Ile Met Ala Ala Gly Pro Leu Leu Ile
435 440

<210> 45

<211> 379

<212> PRT

<213> Homo sapiens

<400> 45

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser
1 5 10 15

Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser His Arg Leu
35 40 45

Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Ala
85 90 95

Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
100 105 110

Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Val Pro Leu Leu Ile
115 120 125

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Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp
    130                 135                 140

Met His Cys Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145                 150                 155                 160

Gln Ser Leu Phe Gly Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu
                165                 170                 175

Tyr Ser Gly Cys Arg Leu Thr Leu Phe Arg Ser Glu Lys Asp Gly Ala
            180                 185                 190

Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
        195                 200                 205

Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
    210                 215                 220

Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
225                 230                 235                 240

Tyr Val Asn Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr Ser Thr
                245                 250                 255

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser
            260                 265                 270

Leu Pro Ser Pro Thr Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu
        275                 280                 285

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr
    290                 295                 300

Gly Ser Arg Lys Phe Asn Thr Met Glu Ser Val Leu Gln Gly Leu Leu
305                 310                 315                 320

Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
                325                 330                 335
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Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val
340 345 350

Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn
355 360 365

Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu
370 375

<210> 46

<211> 439

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(439)

<223> Any "X" = any amino acid

<400> 46

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu
35 40 45

Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
85 90 95

Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly
100 105 110

Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Ile
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
130 135 140

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu
145 150 155 160

Gln Gly Cys Leu Val Pro Cys Ser Arg Asn Thr Asn Val Gly Leu Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
180 185 190

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
195 200 205

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
210 215 220

Xaa Xaa Xaa Xaa Xaa Xaa Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Ala Pro Thr Ser Thr
245 250 255

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser
260 265 270

Leu Pro Ser Pro Thr Thr Val Pro Leu Leu Val Pro Phe Thr Leu Asn
275 280 285

Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Arg His Pro Gly
290 295 300

Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly
305 310 315 320

Pro Leu Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
325 330 335

Leu Ile Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp
340 345 350

Ala Ile Cys Thr His His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg
355 360 365

Glu Gln Leu Tyr Trp Gln Leu Ser Gln Val Thr Asn Gly Ile Lys Glu
370 375 380

Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe
385 390 395 400

Thr His Arg Ser Ser Gly Leu Thr Thr Ser Thr Pro Trp Thr Ser Thr
405 410 415

Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val Pro Ser Pro Thr
420 425 430

Thr Ala Gly Pro Leu Leu Ile
435

<210> 47

<211> 1366

<212> PRT

<213> Homo sapiens

<400> 47

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser
1 5 10 15

Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu
20 25 30

Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro
35 40 45

Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
50 55 60

Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly
100 105 110

Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Met
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
130 135 140

Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu
145 150 155 160

Gln Gly Pro Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
180 185 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr
245 250 255

Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser
260 265 270

Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu
275 280 285

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His Pro
290 295 300

Gly Ser Arg Lys Phe Asn Ile Thr Glu Arg Val Leu Gln Gly Leu Leu
305 310 315 320

Asn Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys
325 330 335

Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Met
340 345 350

Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp
355 360 365

Arg Glu Gln Leu Tyr Cys Glu Leu Ser Gln Leu Thr His Asn Ile Thr
370 375 380

Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
385 390 395 400

Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser
405 410 415

Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His
420 425 430

Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile
435 440 445

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Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys
    450                 455                 460

Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe
465                 470                 475                 480

Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
                485                 490                 495

Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys
            500                 505                 510

Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu
        515                 520                 525

Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro
    530                 535                 540

Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg
545                 550                 555                 560

Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu
                565                 570                 575

Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly
            580                 585                 590

Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln
        595                 600                 605

Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr
    610                 615                 620

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
625                 630                 635                 640

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
                645                 650                 655

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
            660                 665                 670
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Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
675 680 685

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
690 695 700

Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro
705 710 715 720

Ile Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu
725 730 735

Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Ile
740 745 750

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
755 760 765

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Thr Glu Arg Val Leu
770 775 780

Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu
785 790 795 800

Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser
805 810 815

Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp
820 825 830

Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr
835 840 845

Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
850 855 860

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr
865 870 875 880

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Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser
                885                 890                 895

Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Met Pro Phe Thr Leu
            900                 905                 910

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr
        915                 920                 925

Gly Ser Arg Lys Phe Asn Thr Met Glu Ser Val Leu Gln Gly Leu Leu
    930                 935                 940

Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
945                 950                 955                 960

Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Gly Val
                965                 970                 975

Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn
            980                 985                 990

Arg Glu Gln Leu Tyr Trp Glu Leu  Ser Lys Leu Thr Asn  Asp Ile Glu
        995                 1000                1005

Glu Val  Gly Pro Tyr Thr Leu  Asp Arg Asn Ser Leu  Tyr Val Asn
    1010                1015                1020

Gly Phe  Thr His Arg Ser Phe  Val Ala Pro Thr Ser  Thr Leu Gly
    1025                1030                1035

Thr Ser  Thr Val Asp Leu Gly  Thr Ser Gly Thr Pro  Ser Ser Leu
    1040                1045                1050

Pro Ser  Pro Thr Thr Gly Val  Pro Leu Leu Ile Pro  Phe Thr Leu
    1055                1060                1065

Asn Phe  Thr Ile Thr Asn Leu  Gln Tyr Glu Glu Asn  Met Gly His
    1070                1075                1080

Pro Gly  Ser Arg Lys Phe Asn  Ile Met Glu Arg Val  Leu Gln Gly
    1085                1090                1095
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Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Ser Leu Tyr
1100 1105 1110

Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala
1115 1120 1125

Ala Thr Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys
1130 1135 1140

Ser Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln
1145 1150 1155

Leu Thr His Gly Ile Ile Glu Leu Gly Pro Tyr Thr Leu Asp Arg
1160 1165 1170

His Ser Phe Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr
1175 1180 1185

Thr Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser
1190 1195 1200

Arg Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu
1205 1210 1215

Leu Val Leu Phe Thr Ile Asn Phe Thr Ile Thr Asn Gln Arg Tyr
1220 1225 1230

Glu Glu Asn Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr
1235 1240 1245

Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr
1250 1255 1260

Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
1265 1270 1275

Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr
1280 1285 1290

Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu
1295 1300 1305

Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly
1310 1315 1320

Pro Tyr Thr Gln Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr
1325 1330 1335

His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala
1340 1345 1350

Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro
1355 1360 1365

<210> 48

<211> 1148

<212> PRT

<213> Homo sapiens

<400> 48

Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys
1 5 10 15

Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val
20 25 30

Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp
35 40 45

Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly Ile Ile
50 55 60

Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Phe Tyr Val Asn Gly
65 70 75 80

Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser
85 90 95

Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro
100 105 110

Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile
115 120 125

Thr Asn Gln Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys
130 135 140

Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe
145 150 155 160

Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
165 170 175

Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys
180 185 190

Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu
195 200 205

Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro
210 215 220

Tyr Thr Gln Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg
225 230 235 240

Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu
245 250 255

Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly Pro Ser Ala Ala Ser
260 265 270

Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg
275 280 285

Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr
290 295 300

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Glu Arg Val Leu Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser
305                 310                 315                 320

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
                325                 330                 335

Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile Cys Thr His His Pro
            340                 345                 350

Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
        355                 360                 365

Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly His Tyr Ala Leu Asp
    370                 375                 380

Asn Asp Ser Leu Phe Val Asn Gly Phe Thr His Arg Ser Ser Val Ser
385                 390                 395                 400

Thr Thr Ser Thr Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys
                405                 410                 415

Thr Pro Ala Ser Ile Phe Gly Pro Ser Ala Ala Ser His Leu Leu Ile
            420                 425                 430

Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
        435                 440                 445

Met Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln
    450                 455                 460

Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr
465                 470                 475                 480

Ser Gly Ser Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Glu Ala
                485                 490                 495

Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Thr Gly Pro
            500                 505                 510

Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu Ser Gln Leu Thr His
        515                 520                 525
```

Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr
530 535 540

Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr Gly
545 550 555 560

Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn Asn Leu
565 570 575

Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe Asn Ile
580 585 590

Thr Asp Asn Val Met Lys His Leu Leu Ser Pro Leu Phe Gln Arg Ser
595 600 605

Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val Ile Ala Leu Arg Ser
610 615 620

Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr Leu
625 630 635 640

Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His Glu
645 650 655

Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser Leu
660 665 670

Asp Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Leu Asp
675 680 685

Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr Phe Leu Pro Pro Leu
690 695 700

Ser Glu Ala Thr Thr Ala Met Gly Tyr His Leu Lys Thr Leu Thr Leu
705 710 715 720

Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly
725 730 735

Ser Ala Thr Phe Asn Ser Thr Glu Gly Val Leu Gln His Leu Leu Arg
740 745 750

Pro Leu Phe Gln Lys Ser Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln
755 760 765

Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp
770 775 780

Thr Thr Cys Thr Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile
785 790 795 800

Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Val Thr Gln
805 810 815

Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr
820 825 830

Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile Asn Phe His
835 840 845

Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr
850 855 860

Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys
865 870 875 880

Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu
885 890 895

Thr Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn
900 905 910

Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn
915 920 925

Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His
930 935 940

Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser
945 950 955 960

Thr Gln His Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser
965 970 975

Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg
980 985 990

Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys
995 1000 1005

Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro
1010 1015 1020

Asn Arg His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro
1025 1030 1035

Leu Ala Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu
1040 1045 1050

Arg Met Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp
1055 1060 1065

Arg Ser Ser Val Leu Val Asp Gly Tyr Ser Pro Asn Arg Asn Glu
1070 1075 1080

Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu
1085 1090 1095

Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys
1100 1105 1110

Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr
1115 1120 1125

Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp
1130 1135 1140

Leu Glu Asp Leu Gln
1145

<210> 49

<211> 6833

<212> DNA

<213> Homo sapiens

<400> 49

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tattcaggct gcagactagc ctcactcagg ccagagaagg atagctcagc catggcagtg 120

gatgccatct gcacacatcg ccctgaccct gaagacctcg gactggacag agagcgactg 180

tactgggagc tgagcaatct gacaaatggc atccaggagc tgggccccta caccctggac 240

cggaacagtc tctatgtcaa tggtttcacc catcgaagct ctatgcccac caccagcact 300

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ctctaccacc ctaatcccaa aagacctggg ctggacagag agcagctgta ctgggagcta 660

agccagctga cccacaacat cactgagctg ggcccctaca gcctggacag ggacagtctc 720

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cacaacatca ctgagctggg cccctacagc ttggacaggg acagtcttta tgtcaatggt 1200

ttcacccatc agaactctgt gcccaccacc agtactcctg ggacctccac agtgtactgg 1260

gcaaccactg ggactccatc ctccttcccc ggccacacag agcctggccc tctcctgata 1320

ccattcaccc tcaacttcac catcaccaac ctgcagtacg aggaggacat gcgtcgcact 1380

ggctccagga agttcaacac catggagagg gttctgcagg gtctgctcaa gcccttgttc 1440

aagagcacca gcgttggccc tctgtactct ggctgcagac tgaccttgct cagacctgag 1500

aaacatgggg cagccactgg agtggacgcc atctgcaccc tccgccttga tcccactggt 1560

cctggactgg acagagagcg gctatactgg gagctgagcc agctgaccaa cagcgttaca 1620

gagctgggcc cctacaccct ggacagggac agtctctatg tcaatggctt cacccatcgg 1680

agctctgtgc caaccaccag tattcctggg acctctgcag tgcacctgga aacctctggg 1740

actccagcct ccctccctgg ccacacagcc cctggccctc tcctggtgcc attcaccctc 1800

aacttcacta tcaccaacct gcagtatgag gaggacatgc gtcaccctgg ttccaggaag 1860

ttcaacacca cggagagagt cctgcagggt ctgctcaagc ccttgttcaa gagcaccagt 1920

gttggccctc tgtactctgg ctgcagactg accttgctca ggcctgaaaa acgtggggca 1980

gccaccggcg tggacaccat ctgcactcac cgccttgacc ctctaaaccc tggactggac 2040

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35 40 45

Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
50 55 60

Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly
100 105 110

Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Met
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
130 135 140

Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu
145 150 155 160

Gln Gly Pro Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
180 185 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr
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Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser
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Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu
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Gly Ser Arg Lys Phe Asn Ile Thr Glu Arg Val Leu Gln Gly Leu Leu
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Asn Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys
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Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Met
            340                 345                 350

Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp
        355                 360                 365

Arg Glu Gln Leu Tyr Cys Glu Leu Ser Gln Leu Thr His Asn Ile Thr
    370                 375                 380

Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
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Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser
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Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His
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Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile
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Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys
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Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe
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Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys
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Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro
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Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg
545                 550                 555                 560

Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu
                565                 570                 575

Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly
            580                 585                 590

Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln
        595                 600                 605

Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr
    610                 615                 620

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
625                 630                 635                 640

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
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Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
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Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
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Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
    690                 695                 700

Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro
705                 710                 715                 720
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725 730 735

Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Ile
740 745 750

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
755 760 765

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Thr Glu Arg Val Leu
770 775 780

Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu
785 790 795 800

Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser
805 810 815

Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp
820 825 830

Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr
835 840 845

Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
850 855 860

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr
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Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser
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Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Met Pro Phe Thr Leu
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Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr
915 920 925

Gly Ser Arg Lys Phe Asn Thr Met Glu Ser Val Leu Gln Gly Leu Leu
930 935 940

Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
945 950 955 960

Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Gly Val
965 970 975

Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn
980 985 990

Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu
995 1000 1005

Glu Val Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
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Gly Phe Thr His Arg Ser Phe Val Ala Pro Thr Ser Thr Leu Gly
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Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu
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Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu Gln Gly
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Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Ser Leu Tyr
1100 1105 1110

Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala
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Ala Thr Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys
1130 1135 1140

Ser Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln
1145 1150 1155

Leu Thr His Gly Ile Ile Glu Leu Gly Pro Tyr Thr Leu Asp Arg
1160 1165 1170

His Ser Phe Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr
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Thr Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser
1190 1195 1200

Arg Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu
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Leu Val Leu Phe Thr Ile Asn Phe Thr Ile Thr Asn Gln Arg Tyr
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Glu Glu Asn Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr
1235 1240 1245

Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr
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Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
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Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr
1280 1285 1290

Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu
1295 1300 1305

Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly
1310 1315 1320

Pro Tyr Thr Gln Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr
1325 1330 1335

His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala
1340 1345 1350

Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly Pro
1355 1360 1365

Ser Ala Ala Ser Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr
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Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Gln His Pro Gly Ser
1385 1390 1395

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg
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Ser Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
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Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly
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Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His
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Asn Ile Thr Glu Leu Gly His Tyr Ala Leu Asp Asn Asp Ser Leu
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Phe Val Asn Gly Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser
1490 1495 1500

Thr Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro
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Ala Ser Ile Phe Gly Pro Ser Ala Ala Ser His Leu Leu Ile Leu
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Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
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Met Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
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Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro
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Leu Tyr Ser Gly Ser Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp
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Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro Asp
1595 1600 1605

Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu Glu Leu
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Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu
1625 1630 1635

Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser
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Val Pro Thr Thr Ser Thr Gly Val Val Ser Glu Glu Pro Phe Thr
1655 1660 1665

Leu Asn Phe Thr Ile Asn Asn Leu Arg Tyr Met Ala Asp Met Gly
1670 1675 1680

Gln Pro Gly Ser Leu Lys Phe Asn Ile Thr Asp Asn Val Met Lys
1685 1690 1695

His Leu Leu Ser Pro Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg
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Tyr Thr Gly Cys Arg Val Ile Ala Leu Arg Ser Val Lys Asn Gly
1715 1720 1725

Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr Leu Gln Pro Leu
1730 1735 1740

Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His Glu Leu Ser
1745 1750 1755

Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser Leu Asp
1760 1765 1770

Lys Asp Ser Leu Tyr Leu Asn Gly Tyr Asn Glu Pro Gly Leu Asp
1775 1780 1785

Glu Pro Pro Thr Thr Pro Lys Pro Ala Thr Thr Phe Leu Pro Pro
1790 1795 1800

Leu Ser Glu Ala Thr Thr Ala Met Gly Tyr His Leu Lys Thr Leu
1805 1810 1815

Thr Leu Asn Phe Thr Ile Ser Asn Leu Gln Tyr Ser Pro Asp Met
1820 1825 1830

Gly Lys Gly Ser Ala Thr Phe Asn Ser Thr Glu Gly Val Leu Gln
1835 1840 1845

His Leu Leu Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro Phe
1850 1855 1860

Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly
1865 1870 1875

Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro
1880 1885 1890

Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser
1895 1900 1905

Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp
1910 1915 1920

Arg Asp Ser Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser
1925 1930 1935

Ile Arg Gly Glu Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn
1940 1945 1950

Leu Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu
1955 1960 1965

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1970 1975 1980

Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr Met
1985 1990 1995

Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu
2000 2005 2010

Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn
2015 2020 2025

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His Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser
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Ser Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu
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Cys Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg Val Ala Ile
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<213> Homo sapien

<400> 67
atgagaggat cgcatcacca tcaccatcac ggatccatgg gccacacaga gcctggccct 60

ctcctgatac cattcacttt caactttacc atcaccaacc tgcattatga ggaaaacatg 120

caacaccctg gttccaggaa gttcaacacc acggagaggg ttctgcaggg tctgctcaag 180

cccttgttca agaacaccag tgttggccct ctgtactctg gctgcagact gaccttgctc 240

agacctgaga agcatgaggc agccactgga gtggacacca tctgtaccca ccgcgttgat 300

cccatcggac ctggactgga cagagagcgg ctatactggg agctgagcca gctgaccaac 360

agcatcacag agctgggacc ctacaccctg gacagggaca gtctctatgt caatggcttc 420

aaccctcgga gctctgtgcc aaccaccagc actcctggga cctccacagt gcacctggca 480

acctctggga ctccatcctc cctgcct 507

<210> 68

<211> 169

<212> PRT

<213> Homo sapiens

<400> 68

Met Arg Gly Ser His His His His His His Gly Ser Met Gly His Thr
1 5 10 15

Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr
20 25 30

Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
35 40 45

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys
50 55 60

Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
65 70 75 80

Arg Pro Glu Lys His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr
85 90 95

His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr
100 105 110

Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr
115 120 125

Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Arg Ser
130 135 140

Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala
145 150 155 160

Thr Ser Gly Thr Pro Ser Ser Leu Pro
165

<210> 69

<211> 909

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(909)

<223> Any "X" = any amino acid

<400> 69

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser
1 5 10 15

Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys
20 25 30

Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro
35 40 45

Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro
85 90 95

Thr Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly
100 105 110

Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser Pro Leu Leu Ile
115 120 125

Pro Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
130 135 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala
180 185 190

Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
195 200 205

Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
210 215 220

Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr
245 250 255

```
Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser
            260                 265                 270

Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Ile Pro Phe
        275                 280                 285

Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met His
    290                 295                 300

His Pro Gly Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu Gln Gly
305                 310                 315                 320

Leu Leu Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser
                325                 330                 335

Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr
            340                 345                 350

Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly
        355                 360                 365

Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His Gly
    370                 375                 380

Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val
385                 390                 395                 400

Asn Gly Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr Pro Gly
                405                 410                 415

Thr Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser Ser Pro
            420                 425                 430

Ser Pro Thr Thr Ala Gly Pro Leu Leu Met Pro Phe Thr Leu Asn Phe
        435                 440                 445

Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser
    450                 455                 460

Arg Lys Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu Lys Pro
465                 470                 475                 480
```

Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu
485 490 495

Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala
500 505 510

Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu
515 520 525

Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu Leu
530 535 540

Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr
545 550 555 560

His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala Val
565 570 575

His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr Ala
580 585 590

Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
595 600 605

Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn
610 615 620

Thr Met Glu Arg Val Leu Gln Gly Cys Leu Val Pro Cys Ser Arg Asn
625 630 635 640

Thr Asn Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
645 650 655

Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa Xaa
660 665 670

Xaa Xaa Asp Pro Xaa Xaa Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp
675 680 685

Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Thr
690 695 700

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser
705 710 715 720

Val Ala Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr
725 730 735

Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Val Pro Leu Leu
740 745 750

Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu
755 760 765

Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
770 775 780

Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys Asn Ser Ser Val Gly Pro
785 790 795 800

Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu Lys Asp Gly
805 810 815

Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His His Leu Asn Pro Gln
820 825 830

Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser Gln Val
835 840 845

Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser
850 855 860

Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu Thr Thr Ser
865 870 875 880

Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser
885 890 895

Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Ile
900 905

<210> 70

<211> 525

<212> PRT

<213> Homo sapiens

<400> 70

Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu
1 5 10 15

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala
20 25 30

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn
35 40 45

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
50 55 60

Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu
65 70 75 80

Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr
85 90 95

Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser
100 105 110

Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Val Pro Phe Thr Leu
115 120 125

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Ala Met Arg His Pro
130 135 140

Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu
145 150 155 160

Arg Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys
165 170 175

Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val
180 185 190

Asp Ala Ala Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp
195 200 205

Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr
210 215 220

Glu Leu Gly Pro Tyr Thr Leu Asp Arg Val Ser Leu Tyr Val Asn Gly
225 230 235 240

Phe Asn Pro Arg Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser
245 250 255

Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His
260 265 270

Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile
275 280 285

Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys
290 295 300

Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe
305 310 315 320

Lys Asn Thr Ser Ile Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr Leu
325 330 335

Leu Arg Pro Glu Lys Asp Lys Ala Ala Thr Arg Val Asp Ala Ile Cys
340 345 350

Thr His His Pro Asp Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln Leu
355 360 365

Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro
370 375 380

Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asp Gly Phe Thr His Trp
385 390 395 400

Ser Pro Ile Pro Thr Thr Ser Thr Pro Gly Thr Ser Ile Val Asn Leu
405 410 415

Gly Thr Ser Gly Ile Pro Pro Ser Leu Pro Glu Thr Thr Ala Thr Gly
420 425 430

Pro Leu Leu Ile Pro Phe Thr Pro Asn Phe Thr Ile Thr Asn Leu Gln
435 440 445

Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met
450 455 460

Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser
465 470 475 480

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu
485 490 495

Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
500 505 510

Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr
515 520 525

<210> 71

<211> 594

<212> PRT

<213> Homo sapiens

<400> 71

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Asp Gly Val Ala Thr Arg Val Asp Ala Ile Cys Thr His Arg Pro
35 40 45

Asp Pro Lys Ile Pro Gly Leu Asp Arg Gln Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Phe Thr Val Gln Pro Glu Thr Ser Glu
100 105 110

Thr Pro Ser Ser Leu Pro Gly Pro Thr Ala Thr Gly Pro Val Leu Leu
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Ile Asn Leu Gln Tyr Glu Glu Asp
130 135 140

Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Met Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Gln Glu Ala
180 185 190

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp Pro Ser Glu
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Ser Gly Val Leu Cys Pro Pro Pro Ser
245 250 255

Ile Leu Gly Ile Phe Thr Val Gln Pro Glu Thr Phe Glu Thr Pro Ser
260 265 270

Ser Leu Pro Gly Pro Thr Ala Thr Gly Pro Val Leu Leu Pro Phe Thr
275 280 285

Leu Asn Phe Thr Ile Ile Asn Leu Gln Tyr Glu Glu Asp Met His Arg
290 295 300

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
305 310 315 320

Leu Thr Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
325 330 335

Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Gln Glu Ala Ala Thr Gly
340 345 350

Val Asp Thr Ile Cys Thr His Arg Val Asp Pro Ile Gly Pro Gly Leu
355 360 365

Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile
370 375 380

Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
385 390 395 400

Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr
405 410 415

Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly
420 425 430

His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr
435 440 445

```
Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg
    450                 455                 460

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu
465                 470                 475                 480

Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
                485                 490                 495

Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile
            500                 505                 510

Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln
        515                 520                 525

Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly
    530                 535                 540

Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His
545                 550                 555                 560

Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr Ser Thr Val Asp
                565                 570                 575

Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Gly
            580                 585                 590

Pro Leu
```

<210> 72

<211> 424

<212> PRT

<213> Homo sapiens

<400> 72

```
Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
1               5                   10                  15
```

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Tyr Thr His
20 25 30

Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp
35 40 45

Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
50 55 60

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr Ser
65 70 75 80

Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr
85 90 95

Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly Pro Leu
100 105 110

Leu Ile Pro Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu
115 120 125

Glu Asn Met His His Pro Gly Ser Arg Lys Phe Asn Thr Met Glu Arg
130 135 140

Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly
145 150 155 160

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp
165 170 175

Gly Val Ala Thr Arg Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro
180 185 190

Lys Ile Pro Gly Leu Asp Arg Gln Gln Leu Tyr Trp Glu Leu Ser Gln
195 200 205

Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp
210 215 220

```
Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro Thr Thr
225                 230                 235                 240

Ser Thr Pro Gly Thr Phe Thr Val Gln Pro Glu Thr Ser Glu Thr Pro
                245                 250                 255

Ser Ser Leu Pro Gly Pro Thr Ala Thr Gly Pro Val Leu Leu Pro Phe
            260                 265                 270

Thr Leu Asn Phe Thr Ile Ile Asn Leu Gln Tyr Glu Glu Asp Met His
        275                 280                 285

Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
    290                 295                 300

Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser
305                 310                 315                 320

Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr
                325                 330                 335

Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly
            340                 345                 350

Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser
        355                 360                 365

Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val
    370                 375                 380

Asn Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly
385                 390                 395                 400

Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro
                405                 410                 415

Gly His Thr Ala Pro Val Pro Leu
            420
```

<210> 73

<211> 286

<212> PRT

<213> Homo sapiens

<400> 73

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro
85 90 95

Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly
100 105 110

Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Val
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
130 135 140

Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala
180 185 190

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
210 215 220

Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr
245 250 255

Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser
260 265 270

Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Ile Pro Phe
275 280 285

<210> 74

<211> 286

<212> PRT

<213> Homo sapiens

<400> 74

Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys
20 25 30

Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro
35 40 45

Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro
85 90 95

Thr Thr Ser Ile Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly
100 105 110

Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser Pro Leu Leu Val
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
130 135 140

Met His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
180 185 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
195 200 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
210 215 220

His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
225 230 235 240

Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr
245 250 255

Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser
260 265 270

Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Ile Pro Phe
275 280 285

<210> 75

<211> 286

<212> PRT

<213> Homo sapiens

<400> 75

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
35 40 45

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp
65 70 75 80

Arg Gly Ser Leu Tyr Val Asn Gly Phe Ser Arg Gln Ser Ser Met Thr
85 90 95

Thr Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg
100 105 110

Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Ile
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
130 135 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu
145 150 155 160

```
Gln Gly Leu Leu Asn Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu
                165                 170                 175

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Lys Pro Glu Lys Asp Gly Ala
            180                 185                 190

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg
        195                 200                 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
    210                 215                 220

His Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
225                 230                 235                 240

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Ala Pro Thr Ser Thr
                245                 250                 255

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser
            260                 265                 270

Leu Pro Ser Pro Thr Thr Ala Val Pro Leu Leu Ile Pro Phe
        275                 280                 285
```

<210> 76

<211> 286

<212> PRT

<213> Homo sapiens

<400> 76

```
Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser
1               5                   10                  15

Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu
            20                  25                  30
```

Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro
35 40 45

Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
50 55 60

Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu
85 90 95

Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
100 105 110

Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Ile
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn
130 135 140

Met Gly His Pro Gly Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala
180 185 190

Ala Thr Arg Val Asp Ala Val Cys Thr Gln Arg Pro Asp Pro Lys Ser
195 200 205

Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr
210 215 220

His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu
225 230 235 240

Tyr Val Asn Gly Leu Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr
245 250 255

Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser
260 265 270

Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Ile Pro Phe
275 280 285

<210> 77

<211> 288

<212> PRT

<213> Homo sapiens

<400> 77

Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Ser Lys Asn Ser Ser
1 5 10 15

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu
20 25 30

Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
35 40 45

Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly
100 105 110

Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile
115 120 125

```
Pro Phe Thr Val Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn
    130                 135                 140

Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145                 150                 155                 160

Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu
                165                 170                 175

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala
            180                 185                 190

Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser
        195                 200                 205

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr
    210                 215                 220

Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
225                 230                 235                 240

Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr
                245                 250                 255

Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser
            260                 265                 270

Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Ile Pro Phe
        275                 280                 285
```

<210> 78

<211> 597

<212> PRT

<213> Homo sapiens

<400> 78

```
Glu Arg Val Leu His Gly Leu Leu Thr Pro Leu Phe Lys Asn Thr Arg
1               5                   10                  15
```

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu
20 25 30

Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val
35 40 45

Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
50 55 60

Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp
65 70 75 80

Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Trp Ser Ser Val Pro
85 90 95

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly
100 105 110

Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile
115 120 125

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
130 135 140

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
145 150 155 160

Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
165 170 175

Tyr Ser Gly Cys Arg Leu Thr Leu Phe Lys Pro Glu Lys His Glu Ala
180 185 190

Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly
195 200 205

Pro Gly Leu Asp Arg Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn
210 215 220

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Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr
225                 230                 235                 240

Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro
                245                 250                 255

Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu
            260                 265                 270

Pro Gly His Thr Ala Pro Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn
        275                 280                 285

Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly
    290                 295                 300

Ser Arg Lys Phe Asn Thr Met Glu Arg Val Leu Gln Gly Leu Leu Lys
305                 310                 315                 320

Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
                325                 330                 335

Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp
            340                 345                 350

Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg
        355                 360                 365

Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Arg Gly Ile Ile Glu
    370                 375                 380

Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu Tyr Val Asn Gly Phe
385                 390                 395                 400

Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr Pro Gly Thr Ser Thr
                405                 410                 415

Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser Leu Pro Arg Pro Ile
            420                 425                 430

Val Pro Gly Pro Leu Leu Ile Pro Phe Thr Ile Asn Phe Thr Ile Thr
        435                 440                 445
```

Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys Phe
450 455 460

Asn Ile Met Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys
465 470 475 480

Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu
485 490 495

Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr
500 505 510

His His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr
515 520 525

Trp Gln Leu Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr
530 535 540

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
545 550 555 560

Ser Gly Leu Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly
565 570 575

Thr Ser Gly Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro
580 585 590

Leu Leu Ile Pro Phe
595

<210> 79

<211> 420

<212> PRT

<213> Homo sapiens

<400> 79

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Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys
1               5                  10                  15

Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn
            20                  25                  30

Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser
        35                  40                  45

Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg
    50                  55                  60

Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr
65                  70                  75                  80

Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr
                85                  90                  95

Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro
            100                 105                 110

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met
        115                 120                 125

Gly His Pro Gly Ser Arg Lys Phe Asn Ile Thr Glu Ser Val Leu Gln
    130                 135                 140

Gly Leu Leu Thr Pro Leu Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr
145                 150                 155                 160

Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala
                165                 170                 175

Thr Gly Val Asp Ala Ile Cys Thr His His Leu Asn Pro Gln Ser Pro
            180                 185                 190

Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser Gln Met Thr Asn
        195                 200                 205

Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr
    210                 215                 220
```

```
Val Asn Gly Phe Thr His Arg Ser Leu Gly Leu Thr Thr Ser Thr Pro
225                 230                 235                 240

Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val
                245                 250                 255

Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn
            260                 265                 270

Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His Pro Gly
        275                 280                 285

Ser Arg Lys Phe Asn Ile Met Glu Arg Val Leu Gln Gly Leu Leu Arg
    290                 295                 300

Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
305                 310                 315                 320

Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp
                325                 330                 335

Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg
            340                 345                 350

Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu
        355                 360                 365

Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe
    370                 375                 380

Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Pro Thr
385                 390                 395                 400

Val Asp Leu Gly Thr Ser Gly Thr Pro Val Ser Lys Pro Gly Pro Ser
                405                 410                 415

Ala Ala Ser Pro
            420
```

<210> 80

<211> 479

<212> PRT

<213> Homo sapiens

<400> 80

Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu
1 5 10 15

Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr
20 25 30

His Gln Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Ser Thr Val
35 40 45

Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser Leu Ser Ser Pro Thr Ile
50 55 60

Met Ala Ala Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile
65 70 75 80

Thr Asn Leu Gln Tyr Glu Glu Asn Met Gly His Pro Gly Ser Arg Lys
85 90 95

Phe Asn Ile Met Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe
100 105 110

Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu
115 120 125

Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys
130 135 140

Ser His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu
145 150 155 160

Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro
165 170 175

Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg
180 185 190

Ser Ser Val Ala Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu
195 200 205

Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Val
210 215 220

Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys
225 230 235 240

Tyr Glu Glu Asp Met His Cys Pro Gly Ser Arg Lys Phe Asn Thr Thr
245 250 255

Glu Arg Val Leu Gln Ser Leu Phe Gly Pro Met Phe Lys Asn Thr Ser
260 265 270

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu
275 280 285

Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu
290 295 300

Asp Pro Lys Ser Leu Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu
305 310 315 320

Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp
325 330 335

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr Ser Ala Pro
340 345 350

Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
355 360 365

Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly Pro Leu Leu Val
370 375 380

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
385 390 395 400

Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Ser Val Leu
405 410 415

Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
420 425 430

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala
435 440 445

Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser
450 455 460

Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu
465 470 475

<210> 81

<211> 5465

<212> DNA

<213> Homo sapiens

<400> 81
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acagaggtac cataagacca gtcaaaggcc ctcagacatc cacttcgcct gccagtccta 180

aaggactaca cacaggaggg acaaaaagaa tggagaccac caccacagct ttgaagacca 240

ccaccacagc tttgaagacc acttccagag ccaccttgac caccagtgtc tatactccca 300

ctttgggaac actgactccc ctcaatgcat caaggcaaat ggccagcaca atcctcacag 360

aaatgatgat cacaacccca tatgttttcc ctgatgttcc agaaacgaca tcctcattgg 420

ctaccagcct gggagcagaa accagcacag ctcttcccag gacaacccca tctgttctca 480

atagagaatc agagaccaca gcctcactgg tctctcgttc tggggcagag agaagtccgg 540

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atcctgcaga gaccatccca actgtttcca agacaacccc caatttttc cacagtgaat 660

tagacactgt atcttccaca gccaccagtc atggggcaga cgtcagctca gccattccaa 720

caaatatctc acctagtgaa ctagatgcac tgaccccact ggtcactatt tcggggacag 780

atactagtac aacattccca acactgacta agtccccaca tgaaacagag acaagaacca 840

catggctcac tcatcctgca gagaccagct caactattcc cagaacaatc cccaattttt 900

ctcatcatga atcagatgcc acaccttcaa tagccaccag tcctggggca gaaaccagtt 960

cagctattcc aattatgact gtctcacctg gtgcagaaga tctggtgacc tcacaggtca 1020

ctagttctgg gacagacaga aatatgacta ttccaacttt gactctttct cctggtgaac 1080

caaagacgat agcctcatta gtcacccatc ctgaagcaca gacaagttcg gccattccaa 1140

cttcaactat ctcgcctgct gtatcacggt tggtgacctc aatggtcacc agtttggcgg 1200

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ccacg 5465

<210> 82

<211> 1821

<212> PRT

<213> Homo sapiens

<400> 82

Glu Ser Val Leu Glu Gly Thr Val Thr Ser Ala Tyr Gln Val Pro Ser
1 5 10 15

Leu Ser Thr Arg Leu Thr Arg Thr Asp Gly Ile Met Glu His Ile Thr
20 25 30

Lys Ile Pro Asn Glu Ala Ala His Arg Gly Thr Ile Arg Pro Val Lys
35 40 45

Gly Pro Gln Thr Ser Thr Ser Pro Ala Ser Pro Lys Gly Leu His Thr
50 55 60

Gly Gly Thr Lys Arg Met Glu Thr Thr Thr Thr Ala Leu Lys Thr Thr
65 70 75 80

Thr Thr Ala Leu Lys Thr Thr Ser Arg Ala Thr Leu Thr Thr Ser Val
85 90 95

Tyr Thr Pro Thr Leu Gly Thr Leu Thr Pro Leu Asn Ala Ser Arg Gln
100 105 110

Met Ala Ser Thr Ile Leu Thr Glu Met Met Ile Thr Thr Pro Tyr Val
115 120 125

Phe Pro Asp Val Pro Glu Thr Thr Ser Ser Leu Ala Thr Ser Leu Gly
130 135 140

Ala Glu Thr Ser Thr Ala Leu Pro Arg Thr Thr Pro Ser Val Leu Asn
145 150 155 160

Arg Glu Ser Glu Thr Thr Ala Ser Leu Val Ser Arg Ser Gly Ala Glu
165 170 175

Arg Ser Pro Val Ile Gln Thr Leu Asp Val Ser Ser Ser Glu Pro Asp
180 185 190

Thr Thr Ala Ser Trp Val Ile His Pro Ala Glu Thr Ile Pro Thr Val
195 200 205

Ser Lys Thr Thr Pro Asn Phe Phe His Ser Glu Leu Asp Thr Val Ser
210 215 220

Ser Thr Ala Thr Ser His Gly Ala Asp Val Ser Ser Ala Ile Pro Thr
225 230 235 240

Asn Ile Ser Pro Ser Glu Leu Asp Ala Leu Thr Pro Leu Val Thr Ile
245 250 255

Ser Gly Thr Asp Thr Ser Thr Thr Phe Pro Thr Leu Thr Lys Ser Pro
260 265 270

His Glu Thr Glu Thr Arg Thr Thr Trp Leu Thr His Pro Ala Glu Thr
275 280 285

Ser Ser Thr Ile Pro Arg Thr Ile Pro Asn Phe Ser His His Glu Ser
290 295 300

Asp Ala Thr Pro Ser Ile Ala Thr Ser Pro Gly Ala Glu Thr Ser Ser
305 310 315 320

Ala Ile Pro Ile Met Thr Val Ser Pro Gly Ala Glu Asp Leu Val Thr
325 330 335

Ser Gln Val Thr Ser Ser Gly Thr Asp Arg Asn Met Thr Ile Pro Thr
340 345 350

Leu Thr Leu Ser Pro Gly Glu Pro Lys Thr Ile Ala Ser Leu Val Thr
355 360 365

His Pro Glu Ala Gln Thr Ser Ser Ala Ile Pro Thr Ser Thr Ile Ser
370 375 380

Pro Ala Val Ser Arg Leu Val Thr Ser Met Val Thr Ser Leu Ala Ala
385 390 395 400

Lys Thr Ser Thr Thr Asn Arg Ala Leu Thr Asn Ser Pro Gly Glu Pro
405 410 415

Ala Thr Thr Val Ser Leu Val Thr His Pro Ala Gln Thr Ser Pro Thr
420 425 430

Val Pro Trp Thr Thr Ser Ile Phe Phe His Ser Lys Ser Asp Thr Thr
435 440 445

Pro Ser Met Thr Thr Ser His Gly Ala Glu Ser Ser Ser Ala Val Pro
450 455 460

Thr Pro Thr Val Ser Thr Glu Val Pro Gly Val Val Thr Pro Leu Val
465 470 475 480

Thr Ser Ser Arg Ala Val Ile Ser Thr Thr Ile Pro Ile Leu Thr Leu
485 490 495

Ser Pro Gly Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His Gly
500 505 510

Glu Glu Ala Ser Ser Ala Ile Pro Thr Pro Thr Val Ser Pro Gly Val
515 520 525

Pro Gly Val Val Thr Ser Leu Val Thr Ser Ser Arg Ala Val Thr Ser
530 535 540

Thr Thr Ile Pro Ile Leu Thr Phe Ser Leu Gly Glu Pro Glu Thr Thr
545 550 555 560

Pro Ser Met Ala Thr Ser His Gly Thr Glu Ala Gly Ser Ala Val Pro
565 570 575

Thr Val Leu Pro Glu Val Pro Gly Met Val Thr Ser Leu Val Ala Ser
580 585 590

Ser Arg Ala Val Thr Ser Thr Thr Leu Pro Thr Leu Thr Leu Ser Pro
595 600 605

Gly Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His Gly Ala Glu
610 615 620

Ala Ser Ser Thr Val Pro Thr Val Ser Pro Glu Val Pro Gly Val Val
625 630 635 640

Thr Ser Leu Val Thr Ser Ser Ser Gly Val Asn Ser Thr Ser Ile Pro
645 650 655

Thr Leu Ile Leu Ser Pro Gly Glu Leu Glu Thr Thr Pro Ser Met Ala
660 665 670

Thr Ser His Gly Ala Glu Ala Ser Ser Ala Val Pro Thr Pro Thr Val
675 680 685

Ser Pro Gly Val Ser Gly Val Val Thr Pro Leu Val Thr Ser Ser Arg
690 695 700

Ala Val Thr Ser Thr Thr Ile Pro Ile Leu Thr Leu Ser Ser Ser Glu
705 710 715 720

Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His Gly Val Glu Ala Ser
725 730 735

Ser Ala Val Leu Thr Val Ser Pro Glu Val Pro Gly Met Val Thr Ser
740 745 750

Leu Val Thr Ser Ser Arg Ala Val Thr Ser Thr Thr Ile Pro Thr Leu
755 760 765

Thr Ile Ser Ser Asp Glu Pro Glu Thr Thr Thr Ser Leu Val Thr His
770 775 780

Ser Glu Ala Lys Met Ile Ser Ala Ile Pro Thr Leu Ala Val Ser Pro
785 790 795 800

```
Thr Val Gln Gly Leu Val Thr Ser Leu Val Thr Ser Ser Gly Ser Glu
                805                 810                 815

Thr Ser Ala Phe Ser Asn Leu Thr Val Ala Ser Ser Gln Pro Glu Thr
            820                 825                 830

Ile Asp Ser Trp Val Ala His Pro Gly Thr Glu Ala Ser Ser Val Val
        835                 840                 845

Pro Thr Leu Thr Val Ser Thr Gly Glu Pro Phe Thr Asn Ile Ser Leu
    850                 855                 860

Val Thr His Pro Ala Glu Ser Ser Ser Thr Leu Pro Arg Thr Thr Ser
865                 870                 875                 880

Arg Phe Ser His Ser Glu Leu Asp Thr Met Pro Ser Thr Val Thr Ser
                885                 890                 895

Pro Glu Ala Glu Ser Ser Ser Ala Ile Ser Thr Thr Ile Ser Pro Gly
            900                 905                 910

Ile Pro Gly Val Leu Thr Ser Leu Val Thr Ser Ser Gly Arg Asp Ile
        915                 920                 925

Ser Ala Thr Phe Pro Thr Val Pro Glu Ser Pro His Glu Ser Glu Ala
    930                 935                 940

Thr Ala Ser Trp Val Thr His Pro Ala Val Thr Ser Thr Thr Val Pro
945                 950                 955                 960

Arg Thr Thr Pro Asn Tyr Ser His Ser Glu Pro Asp Thr Thr Pro Ser
                965                 970                 975

Ile Ala Thr Ser Pro Gly Ala Glu Ala Thr Ser Asp Phe Pro Thr Ile
            980                 985                 990

Thr Val Ser Pro Asp Val Pro Asp  Met Val Thr Ser Gln  Val Thr Ser
        995                 1000                1005

Ser Gly  Thr Asp Thr Ser Ile  Thr Ile Pro Thr Leu  Thr Leu Ser
    1010                1015                1020
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Ser Gly Glu Pro Glu Thr Thr Thr Ser Phe Ile Thr Tyr Ser Glu
1025 1030 1035

Thr His Thr Ser Ser Ala Ile Pro Thr Leu Pro Val Ser Pro Gly
1040 1045 1050

Ala Ser Lys Met Leu Thr Ser Leu Val Ile Ser Ser Gly Thr Asp
1055 1060 1065

Ser Thr Thr Thr Phe Pro Thr Leu Thr Glu Thr Pro Tyr Glu Pro
1070 1075 1080

Glu Thr Thr Ala Ile Gln Leu Ile His Pro Ala Glu Thr Asn Thr
1085 1090 1095

Met Val Pro Arg Thr Thr Pro Lys Phe Ser His Ser Lys Ser Asp
1100 1105 1110

Thr Thr Leu Pro Val Ala Ile Thr Ser Pro Gly Pro Glu Ala Ser
1115 1120 1125

Ser Ala Val Ser Thr Thr Thr Ile Ser Pro Asp Met Ser Asp Leu
1130 1135 1140

Val Thr Ser Leu Val Pro Ser Ser Gly Thr Asp Thr Ser Thr Thr
1145 1150 1155

Phe Pro Thr Leu Ser Glu Thr Pro Tyr Glu Pro Glu Thr Thr Ala
1160 1165 1170

Thr Trp Leu Thr His Pro Ala Glu Thr Ser Thr Thr Val Ser Gly
1175 1180 1185

Thr Ile Pro Asn Phe Ser His Arg Gly Ser Asp Thr Ala Pro Ser
1190 1195 1200

Met Val Thr Ser Pro Gly Val Asp Thr Arg Ser Gly Val Pro Thr
1205 1210 1215

Thr Thr Ile Pro Pro Ser Ile Pro Gly Val Val Thr Ser Gln Val
1220 1225 1230

Thr Ser Ser Ala Thr Asp Thr Ser Thr Ala Ile Pro Thr Leu Thr
1235 1240 1245

Pro Ser Pro Gly Glu Pro Glu Thr Thr Ala Ser Ser Ala Thr His
1250 1255 1260

Pro Gly Thr Gln Thr Gly Phe Thr Val Pro Ile Arg Thr Val Pro
1265 1270 1275

Ser Ser Glu Pro Asp Thr Met Ala Ser Trp Val Thr His Pro Pro
1280 1285 1290

Gln Thr Ser Thr Pro Val Ser Arg Thr Thr Ser Ser Phe Ser His
1295 1300 1305

Ser Ser Pro Asp Ala Thr Pro Val Met Ala Thr Ser Pro Arg Thr
1310 1315 1320

Glu Ala Ser Ser Ala Val Leu Thr Thr Ile Ser Pro Gly Ala Pro
1325 1330 1335

Glu Met Val Thr Ser Gln Ile Thr Ser Ser Gly Ala Ala Thr Ser
1340 1345 1350

Thr Thr Val Pro Thr Leu Thr His Ser Pro Gly Met Pro Glu Thr
1355 1360 1365

Thr Ala Leu Leu Ser Thr His Pro Arg Thr Glu Thr Ser Lys Thr
1370 1375 1380

Phe Pro Ala Ser Thr Val Phe Pro Gln Val Ser Glu Thr Thr Ala
1385 1390 1395

Ser Leu Thr Ile Arg Pro Gly Ala Glu Thr Ser Thr Ala Leu Pro
1400 1405 1410

Thr Gln Thr Thr Ser Ser Leu Phe Thr Leu Leu Val Thr Gly Thr
1415 1420 1425

Ser Arg Val Asp Leu Ser Pro Thr Ala Ser Pro Gly Val Ser Ala
1430 1435 1440

Lys Thr Ala Pro Leu Ser Thr His Pro Gly Thr Glu Thr Ser Thr
1445 1450 1455

Met Ile Pro Thr Ser Thr Leu Ser Leu Gly Leu Leu Glu Thr Thr
1460 1465 1470

Gly Leu Leu Ala Thr Ser Ser Ser Ala Glu Thr Ser Thr Ser Thr
1475 1480 1485

Leu Thr Leu Thr Val Ser Pro Ala Val Ser Gly Leu Ser Ser Ala
1490 1495 1500

Ser Ile Thr Thr Asp Lys Pro Gln Thr Val Thr Ser Trp Asn Thr
1505 1510 1515

Glu Thr Ser Pro Ser Val Thr Ser Val Gly Pro Pro Glu Phe Ser
1520 1525 1530

Arg Thr Val Thr Gly Thr Thr Met Thr Leu Ile Pro Ser Glu Met
1535 1540 1545

Pro Thr Pro Pro Lys Thr Ser His Gly Glu Gly Val Ser Pro Thr
1550 1555 1560

Thr Ile Leu Arg Thr Thr Met Val Glu Ala Thr Asn Leu Ala Thr
1565 1570 1575

Thr Gly Ser Ser Pro Thr Val Ala Lys Thr Thr Thr Thr Phe Asn
1580 1585 1590

Thr Leu Ala Gly Ser Leu Phe Thr Pro Leu Thr Thr Pro Gly Met
1595 1600 1605

Ser Thr Leu Ala Ser Glu Ser Val Thr Ser Arg Thr Ser Tyr Asn
1610 1615 1620

His Arg Ser Trp Ile Ser Thr Thr Ser Ser Tyr Asn Arg Arg Tyr
1625 1630 1635

Trp Thr Pro Ala Thr Ser Thr Pro Val Thr Ser Thr Phe Ser Pro
1640 1645 1650

Gly Ile Ser Thr Ser Ser Ile Pro Ser Ser Thr Ala Ala Thr Val
1655 1660 1665

Pro Phe Met Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
1670 1675 1680

Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn
1685 1690 1695

Ala Thr Glu Arg Glu Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg
1700 1705 1710

Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser
1715 1720 1725

Leu Arg Pro Glu Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile
1730 1735 1740

Cys Thr His Arg Pro Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu
1745 1750 1755

Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn Gly Ile Gln Glu
1760 1765 1770

Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
1775 1780 1785

Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr Pro Gly Thr
1790 1795 1800

Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser Ser Pro
1805 1810 1815

Ser Pro Thr
1820

<210> 83

<211> 468

<212> DNA

<213> Homo sapiens

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ggtctgctca aacccttgtt caggaatagc agtctggaat acctctattc aggctgcaga 180

ctagcctcac tcaggccaga gaaggatagc tcagccatgg cagtggatgc catctgcata 240

catcgccctg accctgaaga cctcggactg gacagagagc gactgtactg ggagctgagc 300

aatctgacaa atggcatcca ggagctgggc ccctacaccc tggaccggaa cagtctctat 360

gtcaatggtt tcacccatcg aagctctatg cccaccacca gcactcctgg gacctccaca 420

gtggatgtgg gaacctcagg gactccatcc tccagcccca gccccacg 468

<210> 84

<211> 474

<212> DNA

<213> Homo sapiens

<400> 84
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ggtctgctca agcccttgtt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ttgaccttgc tcaggcccaa gaaagatggg gcagccactg gagtggatgc catctgcacc 240

caccgccttg accccaaaag ccctggactc aacagggagc agctgtactg ggagctaagc 300

aaactgacca atgacattga agagctgggc ccctacaccc tggacaggaa cagtctctat 360

gtcaatggtt tcacccatca gagctctgtg tccaccacca gcactcctgg gacctccaca 420

gtggatctca gaacctcagg gactccatcc tccctctcca gccccacaat tatg 474

<210> 85

<211> 468

<212> DNA

<213> Homo sapiens

<400> 85
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ggtctgcttg gtcccatatt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgacctctc tcaggtctga gaaggatgga gcagccactg gagtggatgc catctgcatc 240

catcatcttg accccaaaag ccctggactc aacagagagc ggctgtactg ggagctgagc 300

caactgacca atggcatcaa agagctgggc ccctacaccc tggacaggaa cagtctctat 360

gtcaatggtt tcacccatcg gacctctgtg cccaccacca gcactcctgg gacctccaca 420

gtggaccttg gaacctcagg gactccattc tccctcccaa gccccgca 468

<210> 86

<211> 465

<212> DNA

<213> Homo sapiens

<400> 86
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gaggaggaca tgcatcgccc tggctccagg aagttcaaca ccactgagag ggtcctgcag 120

actctgcttg gtcctatgtt caagaacacc agtgttggcc ttctgtactc tggctgcaga 180

ctgaccttgc tcaggtccga gaaggatgga gcagccactg gagtggatgc catctgcacc 240

caccgtcttg accccaaaag ccctggactg gacagagagc agctatactg ggagctgagc 300

cagctgacca atggcatcaa agagctgggc ccctacaccc tggacaggaa cagtctctat 360

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gtggaccttg ggtcagggac tccatcctcc ctccccagcc ccaca 465

<210> 87

<211> 468

<212> DNA

<213> Homo sapiens

<400> 87
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ggtctgcttg gtcccatgtt caagaacacc agtgtcggcc ttctgtactc tggctgcaga 180

ctgaccttgc tcaggtccga gaaggatgga gcagccactg gagtggatgc catctgcacc 240

caccgtcttg accccaaaag ccctggagtg gacagggagc agctatactg ggagctgagc 300

cagctgacca atggcatcaa agagctgggt ccctacaccc tggacagaaa cagtctctat 360

gtcaatggtt tcacccatca gacctctgcg cccaacacca gcactcctgg gacctccaca 420

gtggaccttg ggacctcagg gactccatcc tccctcccca gccctaca 468

<210> 88

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 88
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ggtctgctnn nnccccntntt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcaggtccga gaaggatgga gcagccactg gagtggatgc catctgcacc 240

caccgtcttg accccaaaag ccctggagtg gacagggagc agctatactg ggagctgagc 300

cagctgacca atggcatcaa agagctgggt ccctacaccc tggacagaaa cagtctctat 360

gtcaatggtt tcacccatca gacctctgcg cccaacacca gcactcctgg gacctccaca 420

gtggaccttg ggacctcagg gactccatcc tccctcccca gccctaca 468

<210> 89

<211> 468

<212> DNA

<213> Homo sapiens

<400> 89
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ggtctgcttg gtcccatgtt caagaacacc agtgtcggcc ttctgtactc tggctgcaga 180

ctgaccttgc tcaggcctga gaagaatggg gcagccactg gaatggatgc catctgcagc 240

caccgtcttg accccaaaag ccctggactc aacagagagc agctgtactg ggagctgagc 300

cagctgaccc atggcatcaa agagctgggc ccctacaccc tggacaggaa cagtctctat 360

gtcaatggtt tcacccatcg gagctctgtg gcccccacca gcactcctgg gacctccaca 420

gtggaccttg ggacctcagg gactccatcc tccctcccca gccccaca 468

<210> 90

<211> 468

<212> DNA

<213> Homo sapiens

<400> 90
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ggggaggaca tgcgtcaccc tggctccagg aagttcaaca ccacagagag ggtcctgcag 120

ggtctgcttg gtcccttgtt caagaactcc agtgtcggcc ctctgtactc tggctgcaga 180

ctgatctctc tcaggtctga gaaggatggg gcagccactg gagtggatgc catctgcacc 240

caccacctta accctcaaag ccctggactg gacagggagc agctgtactg gcagctgagc 300

cagatgacca atggcatcaa agagctgggc ccctacaccc tggaccggaa cagtctctac 360

gtcaatggtt tcacccatcg gagctctggg ctcaccacca gcactccttg gacttccaca 420

gttgaccttg gaacctcagg gactccatcc cccgtcccca gccccaca 468

<210> 91

<211> 468

<212> DNA

<213> Homo sapiens

<400> 91
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gaggaggaca tgcatcgccc tggatctagg aagttcaaca ccacagagag ggtcctgcag 120

ggtctgctta gtcccatttt caagaactcc agtgttggcc ctctgtactc tggctgcaga 180

ctgacctctc tcaggcccga gaaggatggg gcagcaactg gaatggatgc tgtctgcctc 240

taccacccta atcccaaaag acctggactg gacagagagc agctgtactg ggagctaagc 300

cagctgaccc acaacatcac tgagctgggc ccctacagcc tggacaggga cagtctctat 360

gtcaatggtt tcacccatca gaactctgtg cccaccacca gtactcctgg gacctccaca 420

gtgtactggg caaccactgg gactccatcc tccttccccg gccacaca 468

<210> 92

<211> 468

<212> DNA

<213> Homo sapiens

<400> 92
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ggtctgctca agcccttgtt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgacctctc tcaggcccga gaaggatggg gcagcaactg gaatggatgc tgtctgcctc 240

taccacccta atcccaaaag acctgggctg gacagagagc agctgtactg ggagctaagc 300

cagctgaccc acaacatcac tgagctgggc ccctacagcc tggacaggga cagtctctat 360

gtcaatggtt tcacccatca gaactctgtg cccaccacca gtactcctgg gacctccaca 420

gtgtactggg caaccactgg gactccatcc tccttccccg gccacaca 468

<210> 93

<211> 468

<212> DNA

<213> Homo sapiens

<400> 93
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gaggaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagag ggttctgcag 120

ggtctgctca agcccttgtt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcagacctga gaagcatgag gcagccactg gagtggacac catctgtacc 240

caccgcgttg atcccatcgg acctggactg gacagggagc ggctatactg ggagctgagc 300

cagctgacca acagcattac cgaactggga ccctacaccc tggacaggga cagtctctat 360

gtcaatggct tcaaccctcg gagctctgtg ccaaccacca gcactcctgg gacctccaca 420

gtgcacctgg caacctctgg gactccatcc tccctgcctg gccacaca 468

<210> 94

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 94
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ggtctgctca agcccttgtt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcagacctga gaagcatgag gcagccactg gagtggacac catctgtacc 240

caccgcgttg atcccatcgg acctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntccccn gccncaca 468

<210> 95

<211> 468

<212> DNA

<213> Homo sapiens

<400> 95
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ggtctgcttg gtcccatgtt caagaacacc agtgtcggcc ttctgtactc tggctgcaga 180

ctgaccttgc tcaggcctga gaagaatggg gcagccactg gaatggatgc catctgcagc 240

caccgtcttg accccaaaag ccctggactc gacagagagc agctgtactg ggagctgagc 300

cagctgaccc atggcatcaa agagctgggc ccctacaccc tggacaggaa cagtctctat 360

gtcaatggtt tcacccatcg gagctctgtg gcccccacca gcactcctgg gacctccaca 420

gtggaccttg ggacctcagg gactccatcc tccctcccca gccccaca 468

<210> 96

<211> 468

<212> DNA

<213> Homo sapiens

<400> 96

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ggggaggaca tgcgtcaccc tggctccagg aagttcaaca ccacagagag ggtcctgcag 120

ggtctgcttg gtcccttgtt caagaactcc agtgtcggcc ctctgtactc tggctgcaga 180

ctgatctctc tcaggtctga gaaggatggg gcagccactg gagtggatgc catctgcacc 240

caccacctta accctcaaag ccctggactg gacagggagc agctgtactg gcagctgagc 300

cagatgacca atggcatcaa agagctgggc ccctacaccc tggaccggaa cagtctctac 360

gtcaatggtt tcacccatcg gagctctggg ctcaccacca gcactccttg gacttccaca 420

gttgaccttg gaacctcagg gactccatcc cccgtcccca gccccaca 468

<210> 97

<211> 468

<212> DNA

<213> Homo sapiens

<400> 97

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gaggaggaca tgcatcgccc tggatctagg aagttcaacg ccacagagag ggtcctgcag 120

ggtctgctta gtcccatatt caagaactcc agtgttggcc ctctgtactc tggctgcaga 180

ctgacctctc tcaggcccga gaaggatggg gcagcaactg gaatggatgc tgtctgcctc 240

taccacccta atcccaaaag acctggactg gacagagagc agctgtactg ggagctaagc 300

cagctgaccc acaacatcac tgagctgggc ccctacagcc tggacaggga cagtctctat 360

gtcaatggtt tcacccatca gagctctatg acgaccacca gaactcctga tacctccaca 420

atgcacctgg caacctcgag aactccagcc tccctgtctg gacctacg 468

<210> 98

<211> 474

<212> DNA

<213> Homo sapiens

<400> 98

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gaggaggaca tgcgtcgcac tggctccagg aagttcaaca ccatggagag tgtcctgcag 120

ggtctgctca agcccttgtt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ttgaccttgc tcaggcccaa gaaagatggg gcagccactg gagtggatgc catctgcacc 240

caccgccttg accccaaaag ccctggactc aacagggagc agctgtactg ggagctaagc 300

aaactgacca atgacattga agagctgggc ccctacaccc tggacaggaa cagtctctat 360

gtcaatggtt tcacccatca gagctctgtg tccaccacca gcactcctgg gacctccaca 420

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<210> 99

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 99
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ggtctgctca ggcccttgtt caagaacacc agtgtcagct ctctgtactc tggttgcaga 180
ctgaccttgc tcaggcctga gaaggatggg gcagccacca gagtggatgc tgcctgcacc 240
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cagctaaccc acagcatcac tgagctggga ccctacaccc tggacagggt cagtctctat 360
gtcaatggct tcaaccctcg gagctctgtg ccaaccacca gcactcctgg gacctccaca 420
gtgcacctgg caacctctgg gactccatcc tccctgcctg gccacaca 468

<210> 100
<211> 468
<212> DNA
<213> Homo sapiens

<400> 100
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ggtctgctca agcccttgtt caagagcacc agcgttggcc ctctgtactc tggctgcaga 180
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cagctgacca acagcgttac agagctgggc ccctacaccc tggacaggga cagtctctat 360
gtcaatggct tcacccagcg gagctctgtg ccaaccacca gtattcctgg gacctctgca 420
gtgcacctgg aaacctctgg gactccagcc tccctccctg gccacaca 468

<210> 101
<211> 468

<212> DNA

<213> Homo sapiens

<400> 101
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ggtctgctca agcccttgtt caagagcacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcaggcctga aaaacgtggg gcagccaccg gcgtggacac catctgcact 240

caccgccttg accctctaaa ccctggactg gacagagagc agctatactg ggagctgagc 300

aaactgaccc gtggcatcat cgagctgggc ccctacctcc tggacagagg cagtctctat 360

gtcaatggtt tcacccatcg gaactttgtg cccatcacca gcactcctgg gacctccaca 420

gtacacctag gaacctctga aactccatcc tccctaccta gacccata 468

<210> 102

<211> 468

<212> DNA

<213> Homo sapiens

<400> 102
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ggtctgctca ggcccttgtt caagaatacc agtatcggcc ctctgtactc cagctgcaga 180

ctgaccttgc tcaggccaga gaaggacaag gcagccacca gagtggatgc catctgtacc 240

caccaccctg accctcaaag ccctggactg aacagagagc agctgtactg ggagctgagc 300

cagctgaccc acggcatcac tgagctgggc ccctacaccc tggacaggga cagtctctat 360

gtcgatggtt tcactcattg gagccccata ccgaccacca gcactcctgg gacctccata 420

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<210> 103

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

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ggtctgctca aacccttgtt caggaatagc agtctggaat acctctattc aggctgcaga 180

ctagcctcac tcaggccaga gaaggatagc tcagccatgg cagtggatgc catctgcaca 240

catcgccctg accctgaaga cctcggactg gacagagagc gactgtactg ggagctgagc 300

aatctgacaa atggcatcca ggagctgggc ccctacaccc tggaccggaa cagtctctac 360

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gttgaccttg gaacctcagg gactccatcc cccgtcccca gccccaca 468

<210> 104

<211> 468

<212> DNA

<213> Homo sapiens

<400> 104
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caccgcgttg atcccatcgg acctggactg gacagagagc ggctatactg ggagctgagc 300

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gtgcacctgg caacctctgg gactccatcc tccctgcctg gccacaca 468

<210> 105

<211> 468

<212> DNA

<213> Homo sapiens

<400> 105
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ggtctgctca agcccttgtt caagagcacc agcgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcagacctga gaaacatggg gcagccactg gagtggacgc catctgcacc 240

ctccgccttg atcccactgg tcctggactg gacagagagc ggctatactg ggagctgagc 300

cagctgacca acagcgttac agagctgggc ccctacaccc tggacaggga cagtctctat 360

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gtgcacctgg aaacctctgg gactccagcc tccctccctg gccacaca 468

<210> 106

<211> 468

<212> DNA

<213> Homo sapiens

<400> 106
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gaggaggaca tgcgtcaccc tggttccagg aagttcagca ccacggagag agtcctgcag 120

ggtctgctca agcccttgtt caagaacacc agtgtcagct ctctgtactc tggttgcaga 180

ctgaccttgc tcaggcctga gaaggatggg gcagccacca gagtggatgc tgtctgcacc 240

catcgtcctg accccaaaag ccctggactg gacagagagc ggctgtactg gaagctgagc 300

cagctgaccc acggcatcac tgagctgggc ccctacaccc tggacaggca cagtctctat 360

gtcaatggtt tcacccatca gagctctatg acgaccacca gaactcctga tacctccaca 420

atgcacctgg caacctcgag aactccagcc tccctgtctg gacctacg 468

<210> 107

<211> 468

<212> DNA

<213> Homo sapiens

<400> 107

accgccagcc ctctcctggt gctattcaca attaacttca ccatcactaa cctgcggtat 60

gaggagaaca tgcatcaccc tggctctaga aagtttaaca ccacggagag agtccttcag 120

ggtctgctca ggcctgtgtt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccacgc tcaggcccaa gaaggatggg gcagccacca aagtggatgc catctgcacc 240

taccgccctg atcccaaaag ccctggactg gacagagagc agctatactg ggagctgagc 300

cagctaaccc acagcatcac tgagctgggc ccctacaccc aggacaggga cagtctctat 360

gtcaatggct tcacccatcg gagctctgtg ccaaccacca gtattcctgg gacctctgca 420

gtgcacctgg aaacctctgg gactccagcc tccctccctg gccacaca 468

<210> 108

<211> 468

<212> DNA

<213> Homo sapiens

<400> 108

gcccctggcc ctctcctggt gccattcacc ctcaacttca ctatcaccaa cctgcagtat 60

gaggaggaca tgcgtcaccc tggttccagg aagttcaaca ccacggagag agtcctgcag 120

ggtctgctca agcccttgtt caagagcacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcaggcctga aaaacgtggg gcagccaccg gcgtggacac catctgcact 240

caccgccttg accctctaaa cccaggactg gacagagagc agctatactg ggagctgagc 300

aaactgaccc gtggcatcat cgagctgggc ccctacctcc tggacagagg cagtctctat 360

gtcaatggtt tcacccatcg gacctctgtg cccaccacca gcactcctgg gacctccaca 420

gtggaccttg gaacctcagg gactccattc tccctcccaa gccccgca 468

<210> 109

<211> 465

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(465)

<223> All N's = any nucleotide

<400> 109

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gnggannaca tgcnncnccc nggntccagg aagttcaaca ccacngagag ggtcctgcag 120

actctgcttg gtcctatgtt caagaacacc agtgttggcc ttctgtactc tggctgcaga 180

ctgaccttgc tcaggtccga gaaggatgga gcagccactg gagtggatgc catctgcacc 240

caccgtcttg accccaaaag ccctggagtg gacagggagc aactatactg ggagctgagc 300

cagctgacca atggcattaa agaactgggc ccctacaccc tggacaggaa cagtctctat 360

gtcaatgggt tcacccattg gatccctgtg cccaccagca gcactcctgg gacctccaca 420

gtggaccttg ggtcagggac tccatcctcc ctccccagcc ccaca 465

<210> 110

<211> 468

<212> DNA

<213> Homo sapiens

<400> 110
actgctggcc ctctcctggt gccgttcacc ctcaacttca ccatcaccaa cctgaagtac 60

gaggaggaca tgcattgccc tggctccagg aagttcaaca ccacagagag agtcctgcag 120

agtctgcttg gtcccatgtt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcaggtccga gaaggatgga gcagccactg gagtggatgc catctgcacc 240

caccgtcttg accccaaaag ccctggagtg gacagggagc agctatactg ggagctgagc 300

cagctgacca atggcatcaa agagctgggt ccctacaccc tggacagaaa cagtctctat 360

gtcaatggtt tcacccatca gacctctgcg cccaacacca gcactcctgg gacctccaca 420

gtggaccttg ggacctcagg gactccatcc tccctcccca gccctaca 468

<210> 111

<211> 465

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(465)

<223> All N's = any nucleotide

<400> 111
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gnggannaca tgcnncnccc nggntccagg aagttcaaca ccacngagng ngtnctgcag 120

ggtctgctnn nncccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga 180

ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc 240

caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccattg gatccctgtg cccaccagca gcactcctgg gacctccaca 420

gtggaccttg ggtcagggac tccatcctcc ctccccagcc ccaca 465

<210> 112

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 112

actgctggcc ctctcctggt gccgttcacc ctcaacttca ccatcaccaa cctgaagtac 60

gaggaggaca tgcattgccc tggctccagg aagttcaaca ccacagagag agtcctgcag 120

agtctgcttg gtcccatgtt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgacctcgc tcaggtccga gaaggatgga gcagccactg gagtggatgc catctgcacc 240

caccgtgttg accccaaaag ccctggagtg gacagggagc agctatactg ggagctgagc 300

cagctgacca atggcatcaa agagctgggt ccctacaccc tggacagaaa cagtctctat 360

gtcaatggtt tcacccatca gacctctgcg cccaacacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntccccn gccncaca 468

<210> 113

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 113
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gaggaggaca tgcatcaccc aggctccagg aagttcaaca ccacggagcg ggtcctgcag 120

ggtctgcttg gtcccatgtt caagaacacc agtgtcggcc ttctgtactc tggctgcaga 180

ctgaccttgc tcaggcctga gaagaatggg gcaaccactg gaatggatgc catctgcacc 240

caccgtcttg accccaaaag ccctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntccccn gccncaca 468

<210> 114

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 114
ncnnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan 60

gnggannaca tgcnncnccc nggntccagg aagttcaaca ccacngagag ggttctgcag 120

ggtctgctca aacccttgtt caggaatagc agtctggaat acctctattc aggctgcaga 180

ctagcctcac tcaggccaga gaaggatagc tcagccatgg cagtggatgc catctgcaca 240

catcgccctg accctgaaga cctcggactg gacagagagc gactgtactg ggagctgagc 300

aatctgacaa atggcatcca ggagctgggc ccctacaccc tggaccggaa cagtctctat 360

gtcaatggtt tcacccatcg aagctctatg cccaccacca gcactcctgg gacctccaca 420

gtggatgtgg gaacctcagg gactccatcc tccagcccca gccccacg 468

<210> 115

<211> 468

<212> DNA

<213> Homo sapiens

<400> 115

actgctggcc ctctcctgat accattcacc ctcaacttca ccatcaccaa cctgcagtat 60

ggggaggaca tgggtcaccc tggctccagg aagttcaaca ccacagagag ggtcctgcag 120

ggtctgcttg gtcccatatt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgacctctc tcaggtctga gaaggatgga gcagccactg gagtggatgc catctgcatc 240

catcatcttg accccaaaag ccctggactc aacagagagc ggctgtactg ggagctgagc 300

caactgacca atggcatcaa agagctgggc ccctacaccc tggacaggaa cagtctctat 360

gtcaatggtt tcacccatcg gacctctgtg cccaccacca gcactcctgg gacctccaca 420

gtggaccttg gaacctcagg gactccattc tccctcccaa gccccgca 468

<210> 116

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 116
actgctggcc ctctcctggt gctgttcacc ctcaacttca ccatcaccaa cctgaagtat 60

gaggaggaca tgcatcgccc tggctccagg aagttcaaca ccactgagag ggtcctgcag 120

actctgcttg gtcctatgtt caagaacacc agtgttggcc ttctgtactc tggctgcaga 180

ctgaccttgc tcaggtccga gaaggatgga gcagccactg gagtggatgc catctgcacc 240

caccgtcttg accccaaaag ccctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntccccn gccncaca 468

<210> 117

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 117
ncnnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan 60

gnggannaca tgcnncnccc nggntccagg aagttcaaca ccacngagag agtccttcag 120

ggtctgctca ggcctgtgtt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcaggcccaa gaaggatggg gcagccacca aagtggatgc catctgcacc 240

taccgccctg atcccaaaag ccctggactg gacagagagc agctatactg ggagctgagc 300

cagctaaccc acagcatcac tgagctgggc ccctacaccc aggacaggga cagtctctat 360

gtcaatggct tcacccatcg gagctctgtg ccaaccacca gtattcctgg gacctctgca 420

gtgcacctgg aaaccactgg gactccatcc tccttccccg gccacaca 468

<210> 118

<211> 468

<212> DNA

<213> Homo sapiens

<400> 118

gagcctggcc ctctcctgat accattcact ttcaacttta ccatcaccaa cctgcgttat 60

gaggaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagag ggttctgcag 120

ggtctgctca cgcccttgtt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcagacctga gaagcaggag gcagccactg gagtggacac catctgtacc 240

caccgcgttg atcccatcgg acctggactg gacagagagc ggctatactg ggagctgagc 300

cagctgacca acagcatcac agagctggga ccctacaccc tggataggga cagtctctat 360

gtcgatggct tcaacccttg gagctctgtg ccaaccacca gcactcctgg gacctccaca 420

gtgcacctgg caacctctgg gactccatcc cccctgcctg gccacaca 468

<210> 119

<211> 468

<212> DNA

<213> Homo sapiens

<400> 119

gcccctgtcc ctctcttgat accattcacc ctcaacttta ccatcaccga cctgcattat 60

gaagaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagag ggttctgcag 120

ggtctgctca agcccttgtt caagagcacc agcgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcagacctga gaaacatggg gcagccactg gagtggacgc catctgcacc 240

ctccgccttg atcccactgg tcctggactg gacagagagc ggctatactg ggagctgagc 300

cagctgacca acagcatcac agagctggga ccctacaccc tggataggga cagtctctat 360

gtcaatggct tcaacccttg gagctctgtg ccaaccacca gcactcctgg gacctccaca 420

gtgcacctgg caacctctgg gactccatcc tccctgcctg gccacaca 468

<210> 120

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 120

actgctggcc ctctcctggt gccgttcacc ctcaacttca ccatcaccaa cctgaagtac 60

gaggaggaca tgcattgccc tggctccagg aagttcaaca ccacagagag agtcctgcag 120

agtctgcatg gtcccatgtt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcaggtccga gaaggatgga gcagccactg gagtggatgc catctgcacc 240

caccgtcttg accccaaaag ccctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntccccn gccncaca 468

<210> 121

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 121
ncnnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan 60

gnggannaca tgcnncnccc nggntccagg aagttcaaca ccacngagng ngtnctgcag 120

ggtctgctnn nncccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga 180

ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc 240

caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca acagcatcac agagctggga ccctacaccc tggataggga cagtctctat 360

gtcaatggtt tcacccatcg aagctctatg cccaccacca gtattcctgg gacctctgca 420

gtgcacctgg aaacctctgg gactccagcc tccctccctg gccacaca 468

<210> 122

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 122
gcccctggcc ctctcctggt gccattcacc ctcaacttca ctatcaccaa cctgcagtat 60

gaggaggaca tgcgtcaccc tggttccagg aagttcaaca ccacggagag agtcctgcag 120

ggtctgctca agcccttgtt caagagcacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcaggcctga aaaacgtggg gcagccaccg gcgtggacac catctgcact 240

caccgccttg accctctaaa ccctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntccccn gccncaca 468

<210> 123

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 123
ncnnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan 60

gnggannaca tgcnncnccc nggntccagg aagttcaaca ccacngagng ngtnctgcag 120

ggtctgctnn nncccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga 180

ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc 240

caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt ttcaccctcg gagctctgtg ccaaccacca gcactcctgg gacctccaca 420

gtgcacctgg caacctctgg gactccatcc tccctgcctg gccacaca 468

<210> 124

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 124
gcccctgtcc ctctcttgat accattcacc ctcaacttta ccatcaccaa cctgcattat 60

gaagaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagcg ggtcctgcag 120

ggtctgcttg gtcccatgtt caagaacaca agtgtcggcc ttctgtactc tggctgcaga 180

ctgaccttgc tcaggcctga gaagaatggg gcagccactg gaatggatgc catctgcagc 240

caccgtcttg accccaaaag ccctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntccccn gccncaca 468

<210> 125

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 125
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gnggannaca tgcnncnccc nggntccagg aagttcaaca ccacngagng ngtnctgcag 120

ggtctgctnn nncccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga 180

ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc 240

caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatca gaactctgtg cccaccacca gtactcctgg gacctccaca 420

gtgtactggg caaccactgg gactccatcc tccttccccg gccacaca 468

<210> 126

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 126
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gaggaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagag ggttctgcag 120

ggtctgctca cgcccttgtt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcagacctga gaagcaggag gcagccactg gagtggacac catctgtacc 240

caccgcgttg atcccatcgg acctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntccccn gccncaca 468

<210> 127

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 127
ncnnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan 60

gnggannaca tgcnncnccc nggntccagg aagttcaaca ccacngagng ngtnctgcag 120

ggtctgctnn nncccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga 180

ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc 240

caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcg gagctctgtg ccaaccacca gcagtcctgg gacctccaca 420

gtgcacctgg caacctctgg gactccatcc tccctgcctg gccacaca 468

<210> 128

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 128
gcccctgtcc ctctcttgat accattcacc ctcaacttta ccatcaccaa cctgcattat 60

gaagaaaaca tgcaacaccc tggttccagg aagttcaaca ccacggagag ggttctgcag 120

ggtctgctca agcccttgtt caagagcacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcagacctga gaaacatggg gcagccactg gagtggacgc catctgcacc 240

ctccgccttg atcccactgg tcctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntccccn gccncaca 468

<210> 129

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 129
ncnnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan 60

gnggannaca tgcnncnccc nggntccagg aagttcaaca ccacngagng ngtnctgcag 120

ggtctgctnn nncccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga 180

ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc 240

caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcg gacctctgtg cccaccacca gcactcctgg gacctccaca 420

gtgcacctgg caacctctgg gactccatcc tccctgcctg gccacaca 468

<210> 130

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 130
gcccctgtcc ctctcttgat accattcacc ctcaacttta ccatcaccaa cctgcagtat 60

gaggaggaca tgcatcgccc tggatctagg aagttcaaca ccacagagag ggtcctgcag 120

ggtctgctta gtcccatttt caagaactcc agtgttggcc ctctgtactc tggctgcaga 180

ctgacctctc tcaggcccga gaaggatggg gcagcaactg gaatggatgc tgtctgcctc 240

taccacccta atcccaaaag acctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntccccn gccncaca 468

<210> 131

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 131

ncnnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan 60

gnggannaca tgcnncnccc nggntccagg aagttcaaca ccacngagng ngtnctgcag 120

ggtctgctnn nncccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga 180

ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc 240

caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccattg gagctctggg ctcaccacca gcactccttg gacttccaca 420

gttgaccttg gaacctcagg gactccatcc cccgtcccca gccccaca 468

<210> 132

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 132
actgctggcc ctctcctggt gccattcacc ctaaacttca ccatcaccaa cctgcagtat 60

gaggaggaca tgcatcgccc tggatctagg aagttcaacg ccacagagag ggtcctgcag 120

ggtctgctta gtcccatatt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcagacctga gaagcaggag gcagccactg gagtggacac catctgtacc 240

caccgcgttg atcccatcgg acctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntccccn gccncaca 468

<210> 133

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 133
ncnnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan 60

gnggannaca tgcnncnccc nggntccagg aagttcaaca ccacngagng ngtnctgcag 120

ggtctgctnn nncccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga 180

ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc 240

caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcg gagctttggg ctcaccacca gcactccttg gacttccaca 420

gttgaccttg gaacctcagg gactccatcc cccgtcccca gccccaca 468

<210> 134

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 134

actgctggcc ctctcctggt gccattcacc ctaaacttca ccatcaccaa cctgcagtat 60

gaggaggaca tgcatcgccc tggctccagg aagttcaaca ccacggagag ggtccttcag 120

ggtctgctta cgcccttgtt caggaacacc agtgtcagct ctctgtactc tggttgcaga 180

ctgaccttgc tcaggcctga gaaggatggg gcagccacca gagtggatgc tgtctgcacc 240

catcgtcctg accccaaaag ccctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntccccn gccncaca 468

<210> 135

<211> 465

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(465)

<223> All N's = any nucleotide

<400> 135
ncnnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan 60

gnggannaca tgcnncnccc nggntccagg aagttcaaca ccacngagng ngtnctgcag 120

ggtctgctnn nncccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga 180

ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc 240

caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccattg gatccctgtg cccaccagca gcactcctgg gacctccaca 420

gtggaccttg ggtcagggac tccatcctcc ctccccagcc ccaca 465

<210> 136

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 136
actgctggcc ctctcctggt accattcacc ctcaacttca ccatcaccaa cctgcagtat 60

ggggaggaca tgggtcaccc tggctccagg aagttcaaca ccacagagag ggtcctgcag 120

ggtctgcttg gtcccatatt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgacctctc tcaggtccga gaaggatgga gcagccactg gagtggatgc catctgcatc 240

catcatcttg accccaaaag ccctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntccccn gccncaca 468

<210> 137

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 137

ncnnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan 60

gnggannaca tgcnncnccc nggntccagg aagttcaaca ccacngagng ngtnctgcag 120

ggtctgctnn nncccntntt caagaacncc agtgtnggcc ntctgtactc tggctgcaga 180

ctgacctnnc tcaggncnga gaagnatggn gcagccactg gantggatgc catctgcanc 240

caccnncntn ancccaaaag ncctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatca gacctttgcg cccaacacca gcactcctgg gacctccaca 420

gtggaccttg ggacctcagg gactccatcc tccctcccca gccctaca 468

<210> 138

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 138
tctgctggcc ctctcctggt gccattcacc ctcaacttca ccatcaccaa cctgcagtac 60

gaggaggaca tgcatcaccc aggctccagg aagttcaaca ccacggagcg ggtcctgcag 120

ggtctgcttg gtcccatgtt caagaacacc agtgtcggcc ttctgtactc tggctgcaga 180

ctgaccttgc tcaggcctga gaagaatggg gcagccacca gagtggatgc tgtctgcacc 240

catcgtcctg accccaaaag ccctggactg nacagngagc ngctntactg ggagctnagc 300

canctgacca annncatcnn ngagctgggn ccctacaccc tggacaggna cagtctctat 360

gtcaatggtt tcacccatcn ganctctgng cccaccacca gcactcctgg gacctccaca 420

gtgnacntng gnacctcngg gactccatcc tccntccccn gccncaca 468

<210> 139

<211> 468

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)..(468)

<223> All N's = any nucleotide

<400> 139
ncnnctgncc ctctcctgnt nccnttcacc ntcaacttna ccatcaccaa cctgcantan 60

gnggannaca tgcnncnccc nggntccagg aagttcaaca ccacngagag ggttctgcag 120

ggtctgctca agcccttgtt caagagcacc agtgttggcc ctctgtattc tggctgcaga 180

ctgaccttgc tcaggcctga gaaggacgga gtagccacca gagtggacgc catctgcacc 240

caccgccctg accccaaaat ccctgggcta gacagacagc agctatactg ggagctgagc 300

cagctgaccc acagcatcac tgagctggga ccctacaccc tggataggga cagtctctat 360

gtcaatggtt tcacccagcg gagctctgtg cccaccacca gcactcctgg gactttcaca 420

gtacagccgg aaacctctga gactccatca tccctccctg gccccaca 468

<210> 140

<211> 468

<212> DNA

<213> Homo sapiens

<400> 140
gccactggcc ctgtcctgct gccattcacc ctcaatttta ccatcactaa cctgcagtat 60

gaggaggaca tgcatcgccc tggctccagg aagttcaaca ccacggagag ggtccttcag 120

ggtctgctta tgcccttgtt caagaacacc agtgtcagct ctctgtactc tggttgcaga 180

ctgaccttgc tcaggcctga gaaggatggg gcagccacca gagtggatgc tgtctgcacc 240

catcgtcctg accccaaaag ccctggactg gacagagagc ggctgtactg gaagctgagc 300

cagctgaccc acggcatcac tgagctgggc ccctacaccc tggacaggca cagtctctat 360

gtcaatggtt tcacccatca gagctctatg acgaccacca gaactcctga tacctccaca 420

atgcacctgg caacctcgag aactccagcc tccctgtctg gacctacg 468

<210> 141

<211> 468

<212> DNA

<213> Homo sapiens

<400> 141
accgccagcc ctctcctggt gctattcaca attaacttca ccatcactaa cctgcggtat 60

gaggagaaca tgcatcaccc tggctctaga aagtttaaca ccacggagag agtccttcag 120

ggtctgctca ggcctgtgtt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgaccttgc tcaggcccaa gaaggatggg gcagccacca aagtggatgc catctgcacc 240

taccgccctg atcccaaaag ccctggactg gacagagagc agctatactg ggagctgagc 300

cagctaaccc acagcatcac tgagctgggc ccctacaccc tggacaggga cagtctctat 360

gtcaatggtt tcacacagcg gagctctgtg cccaccacta gcattcctgg gacccccaca 420

gtggacctgg gaacatctgg gactccagtt tctaaacctg gtccctcg 468

<210> 142

<211> 468

<212> DNA

<213> Homo sapiens

<400> 142
gctgccagcc ctctcctggt gctattcact ctcaacttca ccatcaccaa cctgcggtat 60

gaggagaaca tgcagcaccc tggctccagg aagttcaaca ccacggagag ggtccttcag 120

ggcctgctca ggtccctgtt caagagcacc agtgttggcc ctctgtactc tggctgcaga 180

ctgactttgc tcaggcctga aaaggatggg acagccactg gagtggatgc catctgcacc 240

caccaccctg accccaaaag ccctaggctg gacagagagc agctgtattg ggagctgagc 300

cagctgaccc acaatatcac tgagctgggc cactatgccc tggacaacga cagcctcttt 360

gtcaatggtt tcactcatcg gagctctgtg tccaccacca gcactcctgg gacccccaca 420

gtgtatctgg gagcatctaa gactccagcc tcgatatttg gcccttca 468

<210> 143

<211> 399

<212> DNA

<213> Homo sapiens

<400> 143
gctgccagcc atctcctgat actattcacc ctcaacttca ccatcactaa cctgcggtat 60

gaggagaaca tgtggcctgg ctccaggaag ttcaacacta cagagagggt ccttcagggc 120

ctgctaaggc ccttgttcaa gaacaccagt gttggccctc tgtactctgg ctccaggctg 180

accttgctca ggccagagaa agatggggaa gccaccggag tggatgccat ctgcacccac 240

cgccctgacc ccacaggccc tgggctggac agagagcagc tgtatttgga gctgagccag 300

ctgacccaca gcatcactga gctgggcccc tacacactgg acagggacag tctctatgtc 360

aatggtttca cccatcggag ctctgtaccc accaccagc 399

<210> 144

<211> 453

<212> DNA

<213> Homo sapiens

<400> 144
accggggtgg tcagcgagga gccattcaca ctgaacttca ccatcaacaa cctgcgctac 60

atggcggaca tgggccaacc cggctccctc aagttcaaca tcacagacaa cgtcatgaag 120

cacctgctca gtcctttgtt ccagaggagc agcctgggtg cacggtacac aggctgcagg 180

gtcatcgcac taaggtctgt gaagaacggt gctgagacac gggtggacct cctctgcacc 240

tacctgcagc ccctcagcgg cccaggtctg cctatcaagc aggtgttcca tgagctgagc 300

cagcagaccc atggcatcac ccggctgggc ccctactctc tggacaaaga cagcctctac 360

cttaacggtt acaatgaacc tggtctagat gagcctccta caactcccaa gccagccacc 420

acattcctgc ctcctctgtc agaagccaca aca 453

<210> 145

<211> 465

<212> DNA

<213> Homo sapiens

<400> 145
gccatggggt accacctgaa gaccctcaca ctcaacttca ccatctccaa tctccagtat 60

tcaccagata tgggcaaggg ctcagctaca ttcaactcca ccgagggggt ccttcagcac 120

ctgctcagac ccttgttcca gaagagcagc atgggcccct tctacttggg ttgccaactg 180

atctccctca ggcctgagaa ggatggggca gccactggtg tggacaccac ctgcacctac 240

caccctgacc ctgtgggccc cgggctggac atacagcagc tttactggga gctgagtcag 300

ctgacccatg gtgtcaccca actgggcttc tatgtcctgg acagggatag cctcttcatc 360

aatggctatg caccccagaa tttatcaatc cggggcgagt accagataaa tttccacatt 420

gtcaactgga acctcagtaa tccagacccc acatcctcag agtac 465

<210> 146

<211> 9799

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(9799)

<223> Any "X" = any amino acid

<400> 146

Ala Thr Val Pro Phe Met Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Ala Thr Glu Arg Glu Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg
35 40 45

```
Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu
    50                  55                  60

Arg Pro Glu Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr
65                  70                  75                  80

His Arg Pro Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr
                85                  90                  95

Trp Glu Leu Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr
            100                 105                 110

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
        115                 120                 125

Ser Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly
    130                 135                 140

Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Ala Ala Gly Pro
145                 150                 155                 160

Leu Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
                165                 170                 175

Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu
            180                 185                 190

Ser Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val
        195                 200                 205

Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
    210                 215                 220

Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp
225                 230                 235                 240

Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser
                245                 250                 255
```

Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg
260 265 270

Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr
275 280 285

Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr
290 295 300

Pro Ser Ser Leu Ser Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu
305 310 315 320

Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu
325 330 335

Asp Met Gly His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
340 345 350

Leu Gln Gly Leu Leu Gly Pro Ile Phe Lys Asn Thr Ser Val Gly Pro
355 360 365

Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Ser Glu Lys Asp Gly
370 375 380

Ala Ala Thr Gly Val Asp Ala Ile Cys Ile His His Leu Asp Pro Lys
385 390 395 400

Ser Pro Gly Leu Asn Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu
405 410 415

Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser
420 425 430

Leu Tyr Val Asn Gly Phe Thr His Arg Thr Ser Val Pro Thr Ser Ser
435 440 445

Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Phe
450 455 460

Ser Leu Pro Ser Pro Ala Thr Ala Gly Pro Leu Leu Val Leu Phe Thr
465 470 475 480

Leu Asn Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Arg
485 490 495

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Thr Leu
500 505 510

Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly
515 520 525

Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly
530 535 540

Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu
545 550 555 560

Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile
565 570 575

Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
580 585 590

Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr
595 600 605

Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro
610 615 620

Thr Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile
625 630 635 640

Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys
645 650 655

Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe
660 665 670

Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu
675 680 685

Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys
690 695 700

Thr His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu
705 710 715 720

Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro
725 730 735

Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln
740 745 750

Thr Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu
755 760 765

Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly
770 775 780

Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln
785 790 795 800

Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr
805 810 815

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
820 825 830

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu
835 840 845

Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu
850 855 860

Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu
865 870 875 880

Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp
885 890 895

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr Ser Ala Pro
900 905 910

Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly
915 920 925

Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly Pro Leu Leu Val
930 935 940

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
945 950 955 960

Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
965 970 975

Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu
980 985 990

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asn Gly Ala
995 1000 1005

Ala Thr Gly Met Asp Ala Ile Cys Ser His Arg Leu Asp Pro Lys
1010 1015 1020

Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln
1025 1030 1035

Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg
1040 1045 1050

Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Ala
1055 1060 1065

Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser
1070 1075 1080

Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Val Pro Leu
1085 1090 1095

Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
1100 1105 1110

Gly Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr
1115 1120 1125

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys Asn Ser
1130 1135 1140

Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu Arg
1145 1150 1155

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr
1160 1165 1170

His His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu
1175 1180 1185

Tyr Trp Gln Leu Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly
1190 1195 1200

Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr
1205 1210 1215

His Arg Ser Ser Gly Leu Thr Thr Ser Thr Pro Trp Thr Ser Thr
1220 1225 1230

Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val Pro Ser Pro
1235 1240 1245

Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
1250 1255 1260

Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser
1265 1270 1275

Arg Lys Phe Asn Ala Thr Glu Arg Val Leu Gln Gly Leu Leu Ser
1280 1285 1290

Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys
1295 1300 1305

Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly
1310 1315 1320

Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly
1325 1330 1335

Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His
1340 1345 1350

Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
1355 1360 1365

Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser
1370 1375 1380

Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro
1385 1390 1395

Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro
1400 1405 1410

Phe Thr Phe Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
1415 1420 1425

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
1430 1435 1440

Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly
1445 1450 1455

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys
1460 1465 1470

Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
1475 1480 1485

Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Cys Glu
1490 1495 1500

Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser
1505 1510 1515

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn
1520 1525 1530

Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp
1535 1540 1545

Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro
1550 1555 1560

Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr Asn
1565 1570 1575

Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
1580 1585 1590

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe
1595 1600 1605

Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
1610 1615 1620

Leu Leu Arg Pro Glu Lys His Glu Ala Ala Thr Gly Val Asp Thr
1625 1630 1635

Ile Cys Thr His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg
1640 1645 1650

Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr
1655 1660 1665

Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn
1670 1675 1680

Gly Phe Asn Pro Arg Ser Ser Val Pro Thr Thr Ser Thr Pro Gly
1685 1690 1695

Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu
1700 1705 1710

Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu
1715 1720 1725

Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His
1730 1735 1740

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
1745 1750 1755

Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr
1760 1765 1770

Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Glu Ala
1775 1780 1785

Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val Asp Pro Ile
1790 1795 1800

Gly Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa
1805 1810 1815

Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg
1820 1825 1830

Xaa Ser Leu Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1835 1840 1845

Xaa Thr Ser Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser
1850 1855 1860

Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa Thr Ser Ala Gly Pro Leu
1865 1870 1875

Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
1880 1885 1890

Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr
1895 1900 1905

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr
1910 1915 1920

Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
1925 1930 1935

Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser
1940 1945 1950

His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu
1955 1960 1965

Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly
1970 1975 1980

Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr
1985 1990 1995

His Arg Ser Ser Val Ala Pro Thr Ser Thr Pro Gly Thr Ser Thr
2000 2005 2010

Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro
2015 2020 2025

Thr Thr Ala Val Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
2030 2035 2040

Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Arg His Pro Gly Ser
2045 2050 2055

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly
2060 2065 2070

Pro Leu Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys
2075 2080 2085

Arg Leu Ile Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly
2090 2095 2100

Val Asp Ala Ile Cys Thr His His Leu Asn Pro Gln Ser Pro Gly
2105 2110 2115

Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser Gln Met Thr Asn
2120 2125 2130

Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
2135 2140 2145

Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu Thr Thr Ser
2150 2155 2160

Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro
2165 2170 2175

Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro
2180 2185 2190

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
2195 2200 2205

Met His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Val
2210 2215 2220

Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly
2225 2230 2235

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys
2240 2245 2250

Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro
2255 2260 2265

Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu
2270 2275 2280

Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser
2285 2290 2295

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser
2300 2305 2310

Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu
2315 2320 2325

Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala
2330 2335 2340

Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Cys Thr Ile Thr Asn
2345 2350 2355

Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe
2360 2365 2370

Asn Thr Met Glu Ser Val Leu Gln Gly Leu Leu Lys Pro Leu Phe
2375 2380 2385

Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
2390 2395 2400

Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Gly Val Asp Ala
2405 2410 2415

Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg
2420 2425 2430

Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu
2435 2440 2445

Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
2450 2455 2460

Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr Pro Gly
2465 2470 2475

Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser Leu
2480 2485 2490

Ser Ser Pro Thr Ile Met Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe
2495 2500 2505

Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met
2510 2515 2520

Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
2525 2530 2535

Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Ser Ser
2540 2545 2550

Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp
2555 2560 2565

Gly Ala Ala Thr Arg Val Asp Ala Ala Cys Thr Tyr Arg Pro Asp
2570 2575 2580

Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
2585 2590 2595

Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu
2600 2605 2610

Asp Arg Val Ser Leu Tyr Val Asn Gly Phe Asn Pro Arg Ser Ser
2615 2620 2625

Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala
2630 2635 2640

Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val
2645 2650 2655

Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
2660 2665 2670

His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn
2675 2680 2685

Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys
2690 2695 2700

Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
2705 2710 2715

Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile
2720 2725 2730

Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu
2735 2740 2745

Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu
2750 2755 2760

Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
2765 2770 2775

Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr
2780 2785 2790

Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro
2795 2800 2805

Gly His Thr Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn
2810 2815 2820

Phe Thr Ile Thr Asn Leu Gln Tyr Glu Val Asp Met Arg His Pro
2825 2830 2835

Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
2840 2845 2850

Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser
2855 2860 2865

Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala Ala
2870 2875 2880

Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn
2885 2890 2895

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu
2900 2905 2910

Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly
2915 2920 2925

Ser Leu Tyr Val Asn Gly Phe Thr His Arg Asn Phe Val Pro Ile
2930 2935 2940

Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu
2945 2950 2955

Thr Pro Ser Ser Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu
2960 2965 2970

Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu
2975 2980 2985

Glu Ala Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
2990 2995 3000

Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser
3005 3010 3015

Ile Gly Pro Leu Tyr Ser Ser Cys Arg Leu Thr Leu Leu Arg Pro
3020 3025 3030

Glu Lys Asp Lys Ala Ala Thr Arg Val Asp Ala Ile Cys Thr His
3035 3040 3045

His Pro Asp Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr
3050 3055 3060

Trp Glu Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro
3065 3070 3075

Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asp Gly Phe Thr His
3080 3085 3090

Trp Ser Pro Ile Pro Thr Thr Ser Thr Pro Gly Thr Ser Ile Val
3095 3100 3105

Asn Leu Gly Thr Ser Gly Ile Pro Pro Ser Leu Pro Glu Thr Thr
3110 3115 3120

Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile
3125 3130 3135

Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg
3140 3145 3150

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro
3155 3160 3165

Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg
3170 3175 3180

Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala Met Ala Val
3185 3190 3195

Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp Leu Gly Leu
3200 3205 3210

Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn Gly
3215 3220 3225

Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr
3230 3235 3240

Val Asn Gly Phe Thr His Arg Ser Ser Phe Leu Thr Thr Ser Thr
3245 3250 3255

Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser
3260 3265 3270

Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe
3275 3280 3285

Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met
3290 3295 3300

His Arg Pro Gly Ser Arg Arg Phe Asn Thr Thr Glu Arg Val Leu
3305 3310 3315

Gln Gly Leu Leu Thr Pro Leu Phe Lys Asn Thr Ser Val Gly Pro
3320 3325 3330

Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Gln
3335 3340 3345

Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val Asp
3350 3355 3360

Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
3365 3370 3375

Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu
3380 3385 3390

Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Trp Ser Ser
3395 3400 3405

Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala
3410 3415 3420

Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val
3425 3430 3435

Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asp Leu
3440 3445 3450

His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn
3455 3460 3465

Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys
3470 3475 3480

Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
3485 3490 3495

Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile
3500 3505 3510

Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu
3515 3520 3525

Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu
3530 3535 3540

Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
3545 3550 3555

Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr
3560 3565 3570

Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro
3575 3580 3585

Gly His Thr Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn
3590 3595 3600

Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro
3605 3610 3615

Gly Ser Arg Lys Phe Ser Thr Thr Glu Arg Val Leu Gln Gly Leu
3620 3625 3630

Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser
3635 3640 3645

Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala
3650 3655 3660

Thr Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser
3665 3670 3675

Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu
3680 3685 3690

Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg His
3695 3700 3705

Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr Thr
3710 3715 3720

Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg
3725 3730 3735

Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu
3740 3745 3750

Val Leu Phe Thr Ile Asn Phe Thr Ile Thr Asn Gln Arg Tyr Glu
3755 3760 3765

Glu Asn Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
3770 3775 3780

Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser
3785 3790 3795

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro
3800 3805 3810

Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr
3815 3820 3825

Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr
3830 3835 3840

Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro
3845 3850 3855

Tyr Thr Gln Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His
3860 3865 3870

Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala Val
3875 3880 3885

His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr
3890 3895 3900

Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile
3905 3910 3915

Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg
3920 3925 3930

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro
3935 3940 3945

Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
3950 3955 3960

Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val
3965 3970 3975

Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu
3980 3985 3990

Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Arg Gly
3995 4000 4005

Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu Tyr
4010 4015 4020

Val Asn Gly Phe Thr His Arg Thr Ser Val Pro Thr Thr Ser Thr
4025 4030 4035

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Phe
4040 4045 4050

Ser Leu Pro Ser Pro Ala Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe
4055 4060 4065

Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met
4070 4075 4080

Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
4085 4090 4095

Gln Thr Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu
4100 4105 4110

Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp
4115 4120 4125

Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp
4130 4135 4140

Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu
4145 4150 4155

Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu
4160 4165 4170

Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Trp Ile Pro
4175 4180 4185

Val Pro Thr Ser Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly
4190 4195 4200

Ser Gly Thr Pro Ser Leu Pro Ser Ser Pro Thr Thr Ala Gly Pro
4205 4210 4215

Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys
4220 4225 4230

Tyr Glu Glu Asp Met His Cys Pro Gly Ser Arg Lys Phe Asn Thr
4235 4240 4245

Thr Glu Arg Val Leu Gln Ser Leu Leu Gly Pro Met Phe Lys Asn
4250 4255 4260

Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
4265 4270 4275

Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys
4280 4285 4290

Thr His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln
4295 4300 4305

Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu
4310 4315 4320

Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe
4325 4330 4335

Thr His Gln Thr Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser
4340 4345 4350

Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser
4355 4360 4365

Pro Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe
4370 4375 4380

Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly
4385 4390 4395

Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu
4400 4405 4410

Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr Ser Gly
4415 4420 4425

Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala Ala Thr
4430 4435 4440

Xaa Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa Xaa Pro
4445 4450 4455

Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr
4460 4465 4470

Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser
4475 4480 4485

Leu Tyr Val Asn Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser
4490 4495 4500

Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro
4505 4510 4515

Ser Ser Leu Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro
4520 4525 4530

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp
4535 4540 4545

Met His Cys Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
4550 4555 4560

Leu Gln Ser Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly
4565 4570 4575

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Ser Glu Lys
4580 4585 4590

Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Val
4595 4600 4605

Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu
4610 4615 4620

Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
4625 4630 4635

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr
4640 4645 4650

Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu
4655 4660 4665

Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala
4670 4675 4680

Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
4685 4690 4695

Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe
4700 4705 4710

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe
4715 4720 4725

Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr
4730 4735 4740

Leu Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala
4745 4750 4755

Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg
4760 4765 4770

Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa
4775 4780 4785

Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn
4790 4795 4800

Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly
4805 4810 4815

Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa
4820 4825 4830

Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu
4835 4840 4845

Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa
4850 4855 4860

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
4865 4870 4875

Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu Tyr
4880 4885 4890

Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser
4895 4900 4905

Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu
4910 4915 4920

Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn
4925 4930 4935

Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg
4940 4945 4950

Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro
4955 4960 4965

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser
4970 4975 4980

Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu
4985 4990 4995

Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
5000 5005 5010

Gly Glu Asp Met Gly His Pro Gly Ser Arg Lys Phe Asn Thr Thr
5015 5020 5025

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Ile Phe Lys Asn Thr
5030 5035 5040

Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg
5045 5050 5055

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Ile
5060 5065 5070

His His Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Arg Leu
5075 5080 5085

Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly
5090 5095 5100

Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr
5105 5110 5115

His Arg Thr Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr
5120 5125 5130

Val Asp Leu Gly Thr Ser Gly Thr Pro Phe Ser Leu Pro Ser Pro
5135 5140 5145

Ala Thr Ala Gly Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr
5150 5155 5160

Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Arg Pro Gly Ser
5165 5170 5175

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Thr Leu Leu Gly
5180 5185 5190

Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys
5195 5200 5205

Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly
5210 5215 5220

Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly
5225 5230 5235

Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa
5240 5245 5250

Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu
5255 5260 5265

Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser
5270 5275 5280

Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly Thr Pro
5285 5290 5295

Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro
5300 5305 5310

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa
5315 5320 5325

Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
5330 5335 5340

Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly
5345 5350 5355

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys
5360 5365 5370

Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro
5375 5380 5385

Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu
5390 5395 5400

Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr
5405 5410 5415

Gln Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
5420 5425 5430

Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu
5435 5440 5445

Glu Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro
5450 5455 5460

Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr Asn
5465 5470 5475

Leu Arg Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
5480 5485 5490

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Thr Pro Leu Phe
5495 5500 5505

Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
5510 5515 5520

Leu Leu Arg Pro Glu Lys Gln Glu Ala Ala Thr Gly Val Asp Thr
5525 5530 5535

Ile Cys Thr His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg
5540 5545 5550

Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr
5555 5560 5565

Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asp
5570 5575 5580

Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly
5585 5590 5595

Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Pro Leu
5600 5605 5610

Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu
5615 5620 5625

Asn Phe Thr Ile Thr Asp Leu His Tyr Glu Glu Asn Met Gln His
5630 5635 5640

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
5645 5650 5655

Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr
5660 5665 5670

Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala
5675 5680 5685

Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr
5690 5695 5700

Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln
5705 5710 5715

Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg
5720 5725 5730

Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Trp Ser Ser Val Pro
5735 5740 5745

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser
5750 5755 5760

Gly Thr Pro Ser Ser Leu Pro Gly His Thr Thr Ala Gly Pro Leu
5765 5770 5775

Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys Tyr
5780 5785 5790

Glu Glu Asp Met His Cys Pro Gly Ser Arg Lys Phe Asn Thr Thr
5795 5800 5805

Glu Arg Val Leu Gln Ser Leu His Gly Pro Met Phe Lys Asn Thr
5810 5815 5820

Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
5825 5830 5835

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr
5840 5845 5850

His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Xaa Leu
5855 5860 5865

Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly
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ctgctcagac ccttgttcca gaagagcagc atgggcccct tctacttggg ttgccaactg 180

atctccctca ggcctgagaa ggatggggca gccactggtg tggacaccac ctgcacctac 240

caccctgacc ctgtgggccc cgggctggac atacagcagc tttactggga gctgagtcag 300

ctgacccatg gtgtcaccca actgggcttc tatgtcctgg acagggatag cctcttcatc 360

aatggctatg caccccagaa tttatcaatc cggggcgagt accagataaa tttccacatt 420

gtcaactgga acctcagtaa tccagacccc acatcctcag agtacatcac cctgctgagg 480

gacatccagg acaaggtcac cacactctac aaaggcagtc aactacatga cacattccgc 540

ttctgcctgg tcaccaactt gacgatggac tccgtgttgg tcactgtcaa ggcattgttc 600

tcctccaatt tggaccccag cctggtggag caagtctttc tagataagac cctgaatgcc 660

tcattccatt ggctgggctc cacctaccag ttggtggaca tccatgtgac agaaatggag 720

tcatcagttt atcaaccaac aagcagctcc agcacccagc acttctacct gaatttcacc 780

atcaccaacc taccatattc ccaggacaaa gcccagccag gcaccaccaa ttaccagagg 840

aacaaaagga atattgagga tgcgctcaac caactcttcc gaaacagcag catcaagagt 900

tatttttctg actgtcaagt ttcaacattc aggtctgtcc ccaacaggca ccacaccggg 960

gtggactccc tgtgtaactt ctcgccactg gctcggagag tagacagagt tgccatctat 1020

gaggaatttc tgcggatgac ccggaatggt acccagctgc agaacttcac cctggacagg 1080

agcagtgtcc ttgtggatgg gtattctccc aacagaaatg agcccttaac tgggaattct 1140

gaccttccct tctgggctgt catcctcatc ggcttggcag gactcctggg actcatcaca 1200

tgcctgatct gcggtgtcct ggtgaccacc cgccggcgga agaaggaagg agaatacaac 1260

gtccagcaac agtgcccagg ctactaccag tcacacctag acctggagga tctgcaatga 1320

ctggaacttg ccggtgcctg gggtgccttt cccccagcca gggtccaaag aagcttggct 1380

ggggcagaaa taaaccatat tggtcggaaa aaaaaaaaaa aa 1422

<210> 148

<211> 439

<212> PRT

<213> Homo sapiens

<400> 148

Ala Met Gly Tyr His Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser
1 5 10 15

Asn Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn
20 25 30

Ser Thr Glu Gly Val Leu Gln His Leu Leu Arg Pro Leu Phe Gln Lys
35 40 45

Ser Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln Leu Ile Ser Leu Arg
50 55 60

Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr
65 70 75 80

His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp
85 90 95

Glu Leu Ser Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val
100 105 110

Leu Asp Arg Asp Ser Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu
115 120 125

Ser Ile Arg Gly Glu Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn
130 135 140

Leu Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg
145 150 155 160

```
Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu His
                165                 170                 175

Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val
            180                 185                 190

Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu
        195                 200                 205

Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp
    210                 215                 220

Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu Met Glu
225                 230                 235                 240

Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr
                245                 250                 255

Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala Gln
            260                 265                 270

Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu Asp Ala
        275                 280                 285

Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr Phe Ser Asp
    290                 295                 300

Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg His His Thr Gly
305                 310                 315                 320

Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala Arg Arg Val Asp Arg
                325                 330                 335

Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr Arg Asn Gly Thr Gln
            340                 345                 350

Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val Leu Val Asp Gly Tyr
        355                 360                 365
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Ser Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn Ser Asp Leu Pro Phe
370 375 380

Trp Ala Val Ile Leu Ile Gly Leu Ala Gly Leu Leu Gly Leu Ile Thr
385 390 395 400

Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg Arg Arg Lys Lys Glu
405 410 415

Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His
420 425 430

Leu Asp Leu Glu Asp Leu Gln
435

<210> 149

<211> 1799

<212> PRT

<213> Homo sapiens

<400> 149

Arg Thr Asp Gly Ile Met Glu His Ile Thr Lys Ile Pro Asn Glu Ala
1 5 10 15

Ala His Arg Gly Thr Ile Arg Pro Val Lys Gly Pro Gln Thr Ser Thr
20 25 30

Ser Pro Ala Ser Pro Lys Gly Leu His Thr Gly Gly Thr Lys Arg Met
35 40 45

Glu Thr Thr Thr Thr Ala Leu Lys Thr Thr Thr Thr Ala Leu Lys Thr
50 55 60

Thr Ser Arg Ala Thr Leu Thr Thr Ser Val Tyr Thr Pro Thr Leu Gly
65 70 75 80

Thr Leu Thr Pro Leu Asn Ala Ser Arg Gln Met Ala Ser Thr Ile Leu
85 90 95

Thr Glu Met Met Ile Thr Thr Pro Tyr Val Phe Pro Asp Val Pro Glu
100 105 110

Thr Thr Ser Ser Leu Ala Thr Ser Leu Gly Ala Glu Thr Ser Thr Ala
115 120 125

Leu Pro Arg Thr Thr Pro Ser Val Leu Asn Arg Glu Ser Glu Thr Thr
130 135 140

Ala Ser Leu Val Ser Arg Ser Gly Ala Glu Arg Ser Pro Val Ile Gln
145 150 155 160

Thr Leu Asp Val Ser Ser Ser Glu Pro Asp Thr Thr Ala Ser Trp Val
165 170 175

Ile His Pro Ala Glu Thr Ile Pro Thr Val Ser Lys Thr Thr Pro Asn
180 185 190

Phe Phe His Ser Glu Leu Asp Thr Val Ser Ser Thr Ala Thr Ser His
195 200 205

Gly Ala Asp Val Ser Ser Ala Ile Pro Thr Asn Ile Ser Pro Ser Glu
210 215 220

Leu Asp Ala Leu Thr Pro Leu Val Thr Ile Ser Gly Thr Asp Thr Ser
225 230 235 240

Thr Thr Phe Pro Thr Leu Thr Lys Ser Pro His Glu Thr Glu Thr Arg
245 250 255

Thr Thr Trp Leu Thr His Pro Ala Glu Thr Ser Ser Thr Ile Pro Arg
260 265 270

Thr Ile Pro Asn Phe Ser His His Glu Ser Asp Ala Thr Pro Ser Ile
275 280 285

Ala Thr Ser Pro Gly Ala Glu Thr Ser Ser Ala Ile Pro Ile Met Thr
290 295 300

Val Ser Pro Gly Ala Glu Asp Leu Val Thr Ser Gln Val Thr Ser Ser
305 310 315 320

Gly Thr Asp Arg Asn Met Thr Ile Pro Thr Leu Thr Leu Ser Pro Gly
325 330 335

Glu Pro Lys Thr Ile Ala Ser Leu Val Thr His Pro Glu Ala Gln Thr
340 345 350

Ser Ser Ala Ile Pro Thr Ser Thr Ile Ser Pro Ala Val Ser Arg Leu
355 360 365

Val Thr Ser Met Val Thr Ser Leu Ala Ala Lys Thr Ser Thr Thr Asn
370 375 380

Arg Ala Leu Thr Asn Ser Pro Gly Glu Pro Ala Thr Thr Val Ser Leu
385 390 395 400

Val Thr His Pro Ala Gln Thr Ser Pro Thr Val Pro Trp Thr Thr Ser
405 410 415

Ile Phe Phe His Ser Lys Ser Asp Thr Thr Pro Ser Met Thr Thr Ser
420 425 430

His Gly Ala Glu Ser Ser Ser Ala Val Pro Thr Pro Thr Val Ser Thr
435 440 445

Glu Val Pro Gly Val Val Thr Pro Leu Val Thr Ser Ser Arg Ala Val
450 455 460

Ile Ser Thr Thr Ile Pro Ile Leu Thr Leu Ser Pro Gly Glu Pro Glu
465 470 475 480

Thr Thr Pro Ser Met Ala Thr Ser His Gly Glu Glu Ala Ser Ser Ala
485 490 495

Ile Pro Thr Pro Thr Val Ser Pro Gly Val Pro Gly Val Val Thr Ser
500 505 510

Leu Val Thr Ser Ser Arg Ala Val Thr Ser Thr Thr Ile Pro Ile Leu
515 520 525

Thr Phe Ser Leu Gly Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser
530 535 540

His Gly Thr Glu Ala Gly Ser Ala Val Pro Thr Val Leu Pro Glu Val
545 550 555 560

Pro Gly Met Val Thr Ser Leu Val Ala Ser Ser Arg Ala Val Thr Ser
565 570 575

Thr Thr Leu Pro Thr Leu Thr Leu Ser Pro Gly Glu Pro Glu Thr Thr
580 585 590

Pro Ser Met Ala Thr Ser His Gly Ala Glu Ala Ser Ser Thr Val Pro
595 600 605

Thr Val Ser Pro Glu Val Pro Gly Val Val Thr Ser Leu Val Thr Ser
610 615 620

Ser Ser Gly Val Asn Ser Thr Ser Ile Pro Thr Leu Ile Leu Ser Pro
625 630 635 640

Gly Glu Leu Glu Thr Thr Pro Ser Met Ala Thr Ser His Gly Ala Glu
645 650 655

Ala Ser Ser Ala Val Pro Thr Pro Thr Val Ser Pro Gly Val Ser Gly
660 665 670

Val Val Thr Pro Leu Val Thr Ser Ser Arg Ala Val Thr Ser Thr Thr
675 680 685

Ile Pro Ile Leu Thr Leu Ser Ser Ser Glu Pro Glu Thr Thr Pro Ser
690 695 700

Met Ala Thr Ser His Gly Val Glu Ala Ser Ser Ala Val Leu Thr Val
705 710 715 720

Ser Pro Glu Val Pro Gly Met Val Thr Ser Leu Val Thr Ser Ser Arg
725 730 735

Ala Val Thr Ser Thr Thr Ile Pro Thr Leu Thr Ile Ser Ser Asp Glu
740 745 750

Pro Glu Thr Thr Thr Ser Leu Val Thr His Ser Glu Ala Lys Met Ile
755 760 765

Ser Ala Ile Pro Thr Leu Ala Val Ser Pro Thr Val Gln Gly Leu Val
770 775 780

Thr Ser Leu Val Thr Ser Ser Gly Ser Glu Thr Ser Ala Phe Ser Asn
785 790 795 800

Leu Thr Val Ala Ser Ser Gln Pro Glu Thr Ile Asp Ser Trp Val Ala
805 810 815

His Pro Gly Thr Glu Ala Ser Ser Val Val Pro Thr Leu Thr Val Ser
820 825 830

Thr Gly Glu Pro Phe Thr Asn Ile Ser Leu Val Thr His Pro Ala Glu
835 840 845

Ser Ser Ser Thr Leu Pro Arg Thr Thr Ser Arg Phe Ser His Ser Glu
850 855 860

Leu Asp Thr Met Pro Ser Thr Val Thr Ser Pro Glu Ala Glu Ser Ser
865 870 875 880

Ser Ala Ile Ser Thr Thr Ile Ser Pro Gly Ile Pro Gly Val Leu Thr
885 890 895

Ser Leu Val Thr Ser Ser Gly Arg Asp Ile Ser Ala Thr Phe Pro Thr
900 905 910

Val Pro Glu Ser Pro His Glu Ser Glu Ala Thr Ala Ser Trp Val Thr
915 920 925

His Pro Ala Val Thr Ser Thr Thr Val Pro Arg Thr Thr Pro Asn Tyr
930 935 940

Ser His Ser Glu Pro Asp Thr Thr Pro Ser Ile Ala Thr Ser Pro Gly
945 950 955 960

Ala Glu Ala Thr Ser Asp Phe Pro Thr Ile Thr Val Ser Pro Asp Val
965 970 975

Pro Asp Met Val Thr Ser Gln Val Thr Ser Ser Gly Thr Asp Thr Ser
980 985 990

Ile Thr Ile Pro Thr Leu Thr Leu Ser Ser Gly Glu Pro Glu Thr Thr
995 1000 1005

Thr Ser Phe Ile Thr Tyr Ser Glu Thr His Thr Ser Ser Ala Ile
1010 1015 1020

Pro Thr Leu Pro Val Ser Pro Gly Ala Ser Lys Met Leu Thr Ser
1025 1030 1035

Leu Val Ile Ser Ser Gly Thr Asp Ser Thr Thr Thr Phe Pro Thr
1040 1045 1050

Leu Thr Glu Thr Pro Tyr Glu Pro Glu Thr Thr Ala Ile Gln Leu
1055 1060 1065

Ile His Pro Ala Glu Thr Asn Thr Met Val Pro Arg Thr Thr Pro
1070 1075 1080

Lys Phe Ser His Ser Lys Ser Asp Thr Thr Leu Pro Val Ala Ile
1085 1090 1095

Thr Ser Pro Gly Pro Glu Ala Ser Ser Ala Val Ser Thr Thr Thr
1100 1105 1110

Ile Ser Pro Asp Met Ser Asp Leu Val Thr Ser Leu Val Pro Ser
1115 1120 1125

Ser Gly Thr Asp Thr Ser Thr Thr Phe Pro Thr Leu Ser Glu Thr
1130 1135 1140

Pro Tyr Glu Pro Glu Thr Thr Ala Thr Trp Leu Thr His Pro Ala
1145 1150 1155

Glu Thr Ser Thr Thr Val Ser Gly Thr Ile Pro Asn Phe Ser His
1160 1165 1170

Arg Gly Ser Asp Thr Ala Pro Ser Met Val Thr Ser Pro Gly Val
1175 1180 1185

Asp Thr Arg Ser Gly Val Pro Thr Thr Thr Ile Pro Pro Ser Ile
1190 1195 1200

Pro Gly Val Val Thr Ser Gln Val Thr Ser Ser Ala Thr Asp Thr
1205 1210 1215

Ser Thr Ala Ile Pro Thr Leu Thr Pro Ser Pro Gly Glu Pro Glu
1220 1225 1230

Thr Thr Ala Ser Ser Ala Thr His Pro Gly Thr Gln Thr Gly Phe
1235 1240 1245

Thr Val Pro Ile Arg Thr Val Pro Ser Ser Glu Pro Asp Thr Met
1250 1255 1260

Ala Ser Trp Val Thr His Pro Pro Gln Thr Ser Thr Pro Val Ser
1265 1270 1275

Arg Thr Thr Ser Ser Phe Ser His Ser Ser Pro Asp Ala Thr Pro
1280 1285 1290

Val Met Ala Thr Ser Pro Arg Thr Glu Ala Ser Ser Ala Val Leu
1295 1300 1305

Thr Thr Ile Ser Pro Gly Ala Pro Glu Met Val Thr Ser Gln Ile
1310 1315 1320

Thr Ser Ser Gly Ala Ala Thr Ser Thr Thr Val Pro Thr Leu Thr
1325 1330 1335

His Ser Pro Gly Met Pro Glu Thr Thr Ala Leu Leu Ser Thr His
1340 1345 1350

Pro Arg Thr Glu Thr Ser Lys Thr Phe Pro Ala Ser Thr Val Phe
1355 1360 1365

Pro Gln Val Ser Glu Thr Thr Ala Ser Leu Thr Ile Arg Pro Gly
1370 1375 1380

Ala Glu Thr Ser Thr Ala Leu Pro Thr Gln Thr Thr Ser Ser Leu
1385 1390 1395

Phe Thr Leu Leu Val Thr Gly Thr Ser Arg Val Asp Leu Ser Pro
1400 1405 1410

Thr Ala Ser Pro Gly Val Ser Ala Lys Thr Ala Pro Leu Ser Thr
1415 1420 1425

His Pro Gly Thr Glu Thr Ser Thr Met Ile Pro Thr Ser Thr Leu
1430 1435 1440

Ser Leu Gly Leu Leu Glu Thr Thr Gly Leu Leu Ala Thr Ser Ser
1445 1450 1455

Ser Ala Glu Thr Ser Thr Ser Thr Leu Thr Leu Thr Val Ser Pro
1460 1465 1470

Ala Val Ser Gly Leu Ser Ser Ala Ser Ile Thr Thr Asp Lys Pro
1475 1480 1485

Gln Thr Val Thr Ser Trp Asn Thr Glu Thr Ser Pro Ser Val Thr
1490 1495 1500

Ser Val Gly Pro Pro Glu Phe Ser Arg Thr Val Thr Gly Thr Thr
1505 1510 1515

Met Thr Leu Ile Pro Ser Glu Met Pro Thr Pro Pro Lys Thr Ser
1520 1525 1530

His Gly Glu Gly Val Ser Pro Thr Thr Ile Leu Arg Thr Thr Met
1535 1540 1545

Val Glu Ala Thr Asn Leu Ala Thr Thr Gly Ser Ser Pro Thr Val
1550 1555 1560

Ala Lys Thr Thr Thr Thr Phe Asn Thr Leu Ala Gly Ser Leu Phe
1565 1570 1575

Thr Pro Leu Thr Thr Pro Gly Met Ser Thr Leu Ala Ser Glu Ser
1580 1585 1590

Val Thr Ser Arg Thr Ser Tyr Asn His Arg Ser Trp Ile Ser Thr
1595 1600 1605

Thr Ser Ser Tyr Asn Arg Arg Tyr Trp Thr Pro Ala Thr Ser Thr
1610 1615 1620

Pro Val Thr Ser Thr Phe Ser Pro Gly Ile Ser Thr Ser Ser Ile
1625 1630 1635

Pro Ser Ser Thr Ala Ala Thr Val Pro Phe Met Val Pro Phe Thr
1640 1645 1650

Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg
1655 1660 1665

His Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Glu Leu Gln
1670 1675 1680

Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu
1685 1690 1695

Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser
1700 1705 1710

Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro
1715 1720 1725

Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser
1730 1735 1740

Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp
1745 1750 1755

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met
1760 1765 1770

Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr
1775 1780 1785

Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr
1790 1795

<210> 150

<211> 156

<212> PRT

<213> Homo sapiens

<400> 150

Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys
35 40 45

Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
50 55 60

Arg Pro Glu Lys His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr
65 70 75 80

His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr
85 90 95

Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr
100 105 110

Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Arg Ser
115 120 125

Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala
130 135 140

Thr Ser Gly Thr Pro Ser Ser Leu Pro Lys Leu Thr
145 150 155

<210> 151

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(507)

<223>

<400> 151

atg aga gga tcg cat cac cat cac cat cac gga tcc atg ggc cac aca 48
Met Arg Gly Ser His His His His His His Gly Ser Met Gly His Thr
1 5 10 15

gag cct ggc cct ctc ctg ata cca ttc act ttc aac ttt acc atc acc 96
Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr
20 25 30

aac ctg cat tat gag gaa aac atg caa cac cct ggt tcc agg aag ttc 144
Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
35 40 45

aac acc acg gag agg gtt ctg cag ggt ctg ctc aag ccc ttg ttc aag 192
Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys
50 55 60

aac acc agt gtt ggc cct ctg tac tct ggc tgc aga ctg acc ttg ctc 240
Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
65 70 75 80

aga cct gag aag cat gag gca gcc act gga gtg gac acc atc tgt acc 288
Arg Pro Glu Lys His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr
85 90 95

cac cgc gtt gat ccc atc gga cct gga ctg gac aga gag cgg cta tac 336

```
His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr
            100                 105                 110

tgg gag ctg agc cag ctg acc aac agc atc aca gag ctg gga ccc tac      384
Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr
        115                 120                 125

acc ctg gac agg gac agt ctc tat gtc aat ggc ttc aac cct cgg agc      432
Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Arg Ser
    130                 135                 140

tct gtg cca acc acc agc act cct ggg acc tcc aca gtg cac ctg gca      480
Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala
145                 150                 155                 160

acc tct ggg act cca tcc tcc ctg cct                                  507
Thr Ser Gly Thr Pro Ser Ser Leu Pro
                165
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<210> 152

<211> 169

<212> PRT

<213> Homo sapiens

<400> 152

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Met Arg Gly Ser His His His His His His Gly Ser Met Gly His Thr
1               5                   10                  15

Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr
            20                  25                  30

Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
        35                  40                  45

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys
    50                  55                  60

Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
65                  70                  75                  80

Arg Pro Glu Lys His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr
                85                  90                  95
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His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr
100 105 110

Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr
115 120 125

Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Arg Ser
130 135 140

Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala
145 150 155 160

Thr Ser Gly Thr Pro Ser Ser Leu Pro
165

<210> 153

<211> 507

<212> DNA

<213> Homo sapiens

<400> 153
aggcagggag gatggagtcc cagaggttgc caggtgcact gtggaggtcc caggagtgct 60

ggtggttggc acagagctcc gagggttgaa gccattgaca tagagactgt ccctgtccag 120

ggtgtagggt cccagctctg tgatgctgtt ggtcagctgg ctcagctccc agtatagccg 180

ctctctgtcc agtccaggtc cgatgggatc aacgcggtgg gtacagatgg tgtccactcc 240

agtggctgcc tcatgcttct caggtctgag caaggtcagt ctgcagccag agtacagagg 300

gccaacactg gtgttcttga acaagggctt gagcagaccc tgcagaaccc tctccgtggt 360

gttgaacttc ctggaaccag ggtgttgcat gttttcctca taatgcaggt tggtgatggt 420

aaagttgaaa gtgaatggta tcaggagagg gccaggctct gtgtggccca tggatccgtg 480

atggtgatgg tgatgcgatc ctctcat 507

<210> 154

<211> 9

<212> PRT

<213> Homo sapiens

<400> 154

Arg Leu Tyr Trp Glu Leu Ser Gln Leu
1 5

<210> 155

<211> 9

<212> PRT

<213> Homo sapiens

<400> 155

Thr Leu Asp Arg Asp Ser Leu Tyr Val
1 5

<210> 156

<211> 9

<212> PRT

<213> Homo sapiens

<400> 156

Val Leu Gln Gly Leu Leu Lys Pro Leu
1 5

<210> 157

<211> 9

<212> PRT

<213> Homo sapiens

<400> 157

Gln Leu Thr Asn Ser Ile Thr Glu Leu
1 5

<210> 158

<211> 780

<212> PRT

<213> Homo sapiens

<400> 158

Ala Thr Val Pro Phe Met Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Ala Thr Glu Arg Glu Leu Gln Gly Leu Leu Lys Pro Leu Phe Arg
35 40 45

Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu
50 55 60

Arg Pro Glu Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr
65 70 75 80

His Arg Pro Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr
85 90 95

Trp Glu Leu Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr
100 105 110

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
115 120 125

Ser Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly
130 135 140

Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Ala Ala Gly Pro
145 150 155 160

Leu Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
165 170 175

Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu
180 185 190

Ser Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val
195 200 205

Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
210 215 220

Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp
225 230 235 240

Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser
245 250 255

Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg
260 265 270

Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr
275 280 285

Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr
290 295 300

Pro Ser Ser Leu Ser Ser Pro Thr Ile Met Ala Gly Pro Leu Leu Val
305 310 315 320

Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp
325 330 335

Met Gly His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
340 345 350

Gln Gly Leu Leu Gly Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu
355 360 365

Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Ser Glu Lys Asp Gly Ala
370 375 380

Ala Thr Gly Val Asp Ala Ile Cys Ile His His Leu Asp Pro Lys Ser
385 390 395 400

Pro Gly Leu Asn Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr
405 410 415

Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
420 425 430

Tyr Val Asn Gly Phe Thr His Arg Thr Ser Val Pro Thr Ser Ser Thr
435 440 445

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Phe Ser
450 455 460

Leu Pro Ser Pro Ala Thr Ala Gly Pro Leu Leu Val Leu Phe Thr Leu
465 470 475 480

Asn Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Arg Pro
485 490 495

Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Thr Leu Leu
500 505 510

Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys
515 520 525

Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val
530 535 540

Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp
545 550 555 560

Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys
565 570 575

Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
580 585 590

Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr Ser
595 600 605

Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr
610 615 620

Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
625 630 635 640

Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe
645 650 655

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys
660 665 670

Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
675 680 685

Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr
690 695 700

His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr
705 710 715 720

Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr
725 730 735

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr
740 745 750

Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly
755 760 765

Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr
770 775 780

<210> 159

<211> 780

<212> PRT

<213> Homo sapiens

<400> 159

Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys
35 40 45

Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
50 55 60

Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser
65 70 75 80

His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr
85 90 95

Trp Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr
100 105 110

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
115 120 125

Ser Val Ala Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly
130 135 140

Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Val Pro
145 150 155 160

Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
165 170 175

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Gly Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
            180                 185                 190

Arg Val Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys Asn Ser Ser Val
        195                 200                 205

Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu Lys
    210                 215                 220

Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His His Leu Asn
225                 230                 235                 240

Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser
                245                 250                 255

Gln Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg
            260                 265                 270

Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu Thr
        275                 280                 285

Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr
    290                 295                 300

Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro
305                 310                 315                 320

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met
                325                 330                 335

His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Val Leu Gln
            340                 345                 350

Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr
        355                 360                 365

Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala
    370                 375                 380
```

Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro
385 390 395 400

Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His
405 410 415

Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr
420 425 430

Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro
435 440 445

Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe
450 455 460

Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn
465 470 475 480

Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly
485 490 495

Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys
500 505 510

Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
515 520 525

Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp
530 535 540

Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg
545 550 555 560

Glu Gln Leu Tyr Cys Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu
565 570 575

Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe
580 585 590

Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr
595 600 605

Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His Thr
610 615 620

Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr
625 630 635 640

Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
645 650 655

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys
660 665 670

Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
675 680 685

Arg Pro Glu Lys His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr
690 695 700

His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr
705 710 715 720

Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr
725 730 735

Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Arg Ser
740 745 750

Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala
755 760 765

Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His Thr
770 775 780

<210> 160

<211> 624

<212> PRT

<213> Homo sapiens

<400> 160

Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Arg Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Thr Pro Leu Phe Lys
35 40 45

Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
50 55 60

Arg Pro Glu Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr
65 70 75 80

His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr
85 90 95

Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr
100 105 110

Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Trp Ser
115 120 125

Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala
130 135 140

Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val Pro
145 150 155 160

Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asp Leu His Tyr
165 170 175

Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
180 185 190

Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val
195 200 205

Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
210 215 220

His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp
225 230 235 240

Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser
245 250 255

Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg
260 265 270

Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr
275 280 285

Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly Thr
290 295 300

Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Val Pro
305 310 315 320

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met
325 330 335

Arg His Pro Gly Ser Arg Lys Phe Ser Thr Thr Glu Arg Val Leu Gln
340 345 350

Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr
355 360 365

Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala
370 375 380

Thr Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser Pro
385 390 395 400

Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu Thr His
405 410 415

Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr
420 425 430

Val Asn Gly Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro
435 440 445

Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu
450 455 460

Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn
465 470 475 480

Phe Thr Ile Thr Asn Gln Arg Tyr Glu Glu Asn Met His His Pro Gly
485 490 495

Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg
500 505 510

Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
515 520 525

Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp
530 535 540

Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg
545 550 555 560

Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu
565 570 575

Leu Gly Pro Tyr Thr Gln Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe
580 585 590

Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala
595 600 605

Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr
610 615 620

<210> 161

<211> 468

<212> PRT

<213> Homo sapiens

<400> 161

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Ala Thr Gly Pro Val Leu Leu Pro Phe Thr Leu Asn Phe Thr Ile Thr
1               5                  10                  15

Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
            20                  25                  30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Met Pro Leu Phe Lys
        35                  40                  45

Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
    50                  55                  60

Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val Cys Thr
65                  70                  75                  80

His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg Leu Tyr
                85                  90                  95

Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr
            100                 105                 110

Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser
        115                 120                 125

Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala
    130                 135                 140

Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro
145                 150                 155                 160

Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr
                165                 170                 175
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Glu Glu Asn Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
180 185 190

Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val
195 200 205

Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys
210 215 220

Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro Asp
225 230 235 240

Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser
245 250 255

Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Gln Asp Arg
260 265 270

Asp Ser Leu Tyr Asn Val Gly Phe Thr Gln Arg Ser Ser Val Pro Thr
275 280 285

Thr Ser Val Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly Thr
290 295 300

Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser Pro Leu Leu Val Leu
305 310 315 320

Phe Thr Leu Asn Gly Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met
325 330 335

Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln
340 345 350

Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr
355 360 365

Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala
370 375 380

Thr Gly Val Asp Ala Ile Cys Thr His His Pro Asp Pro Lys Ser Pro
385 390 395 400

Arg Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His
405 410 415

Asn Ile Thr Glu Leu Gly His Tyr Ala Leu Asp Asn Asp Ser Leu Phe
420 425 430

Val Asn Gly Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser Thr Pro
435 440 445

Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile
450 455 460

Phe Gly Pro Ser
465

<210> 162

<211> 11721

<212> PRT

<213> Homo sapiens

<220>

<221> MISC_FEATURE

<222> (1)..(11721)

<223> Any "X" = any amino acid

<400> 162

Met Glu His Ile Thr Lys Ile Pro Asn Glu Ala Ala His Arg Gly Thr
1 5 10 15

Ile Arg Pro Val Lys Gly Pro Gln Thr Ser Thr Ser Pro Ala Ser Pro
20 25 30

Lys Gly Leu His Thr Gly Gly Thr Lys Arg Met Glu Thr Thr Thr Thr
35 40 45

Ala Leu Lys Thr Thr Thr Thr Ala Leu Lys Thr Thr Ser Arg Ala Thr
50 55 60

Leu Thr Thr Ser Val Tyr Thr Pro Thr Leu Gly Thr Leu Thr Pro Leu
65 70 75 80

Asn Ala Ser Arg Gln Met Ala Ser Thr Ile Leu Thr Glu Met Met Ile
85 90 95

Thr Thr Pro Tyr Val Phe Pro Asp Val Pro Glu Thr Thr Ser Ser Leu
100 105 110

Ala Thr Ser Leu Gly Ala Glu Thr Ser Thr Ala Leu Pro Arg Thr Thr
115 120 125

Pro Ser Val Leu Asn Arg Glu Ser Glu Thr Thr Ala Ser Leu Val Ser
130 135 140

Arg Ser Gly Ala Glu Arg Ser Pro Val Ile Gln Thr Leu Asp Val Ser
145 150 155 160

Ser Ser Glu Pro Asp Thr Thr Ala Ser Trp Val Ile His Pro Ala Glu
165 170 175

Thr Ile Pro Thr Val Ser Lys Thr Thr Pro Asn Phe Phe His Ser Glu
180 185 190

Leu Asp Thr Val Ser Ser Thr Ala Thr Ser His Gly Ala Asp Val Ser
195 200 205

Ser Ala Ile Pro Thr Asn Ile Ser Pro Ser Glu Leu Asp Ala Leu Thr
210 215 220

Pro Leu Val Thr Ile Ser Gly Thr Asp Thr Ser Thr Thr Phe Pro Thr
225 230 235 240

Leu Thr Lys Ser Pro His Glu Thr Glu Thr Arg Thr Thr Trp Leu Thr
245 250 255

His Pro Ala Glu Thr Ser Ser Thr Ile Pro Arg Thr Ile Pro Asn Phe
260 265 270

Ser His His Glu Ser Asp Ala Thr Pro Ser Ile Ala Thr Ser Pro Gly
275 280 285

Ala Glu Thr Ser Ser Ala Ile Pro Ile Met Thr Val Ser Pro Gly Ala
290 295 300

Glu Asp Leu Val Thr Ser Gln Val Thr Ser Ser Gly Thr Asp Arg Asn
305 310 315 320

Met Thr Ile Pro Thr Leu Thr Leu Ser Pro Gly Glu Pro Lys Thr Ile
325 330 335

Ala Ser Leu Val Thr His Pro Glu Ala Gln Thr Ser Ser Ala Ile Pro
340 345 350

Thr Ser Thr Ile Ser Pro Ala Val Ser Arg Leu Val Thr Ser Met Val
355 360 365

Thr Ser Leu Ala Ala Lys Thr Ser Thr Thr Asn Arg Ala Leu Thr Asn
370 375 380

Ser Pro Gly Glu Pro Ala Thr Thr Val Ser Leu Val Thr His Pro Ala
385 390 395 400

Gln Thr Ser Pro Thr Val Pro Trp Thr Thr Ser Ile Phe Phe His Ser
405 410 415

Lys Ser Asp Thr Thr Pro Ser Met Thr Thr Ser His Gly Ala Glu Ser
420 425 430

Ser Ser Ala Val Pro Thr Pro Thr Val Ser Thr Glu Val Pro Gly Val
435 440 445

Val Thr Pro Leu Val Thr Ser Ser Arg Ala Val Ile Ser Thr Thr Ile
450 455 460

Pro Ile Leu Thr Leu Ser Pro Gly Glu Pro Glu Thr Thr Pro Ser Met
465 470 475 480

Ala Thr Ser His Gly Glu Glu Ala Ser Ser Ala Ile Pro Thr Pro Thr
485 490 495

Val Ser Pro Gly Val Pro Gly Val Val Thr Ser Leu Val Thr Ser Ser
500 505 510

Arg Ala Val Thr Ser Thr Thr Ile Pro Ile Leu Thr Phe Ser Leu Gly
515 520 525

Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His Gly Thr Glu Ala
530 535 540

Gly Ser Ala Val Pro Thr Val Leu Pro Glu Val Pro Gly Met Val Thr
545 550 555 560

Ser Leu Val Ala Ser Ser Arg Ala Val Thr Ser Thr Thr Leu Pro Thr
565 570 575

Leu Thr Leu Ser Pro Gly Glu Pro Glu Thr Thr Pro Ser Met Ala Thr
580 585 590

Ser His Gly Ala Glu Ala Ser Ser Thr Val Pro Thr Val Ser Pro Glu
595 600 605

Val Pro Gly Val Val Thr Ser Leu Val Thr Ser Ser Ser Gly Val Asn
610 615 620

Ser Thr Ser Ile Pro Thr Leu Ile Leu Ser Pro Gly Glu Leu Glu Thr
625 630 635 640

Thr Pro Ser Met Ala Thr Ser His Gly Ala Glu Ala Ser Ser Ala Val
645 650 655

Pro Thr Pro Thr Val Ser Pro Gly Val Ser Gly Val Val Thr Pro Leu
660 665 670

Val Thr Ser Ser Arg Ala Val Thr Ser Thr Thr Ile Pro Ile Leu Thr
675 680 685

Leu Ser Ser Ser Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His
690 695 700

Gly Val Glu Ala Ser Ser Ala Val Leu Thr Val Ser Pro Glu Val Pro
705 710 715 720

Gly Met Val Thr Ser Leu Val Thr Ser Ser Arg Ala Val Thr Ser Thr
725 730 735

Thr Ile Pro Thr Leu Thr Ile Ser Ser Asp Glu Pro Glu Thr Thr Thr
740 745 750

Ser Leu Val Thr His Ser Glu Ala Lys Met Ile Ser Ala Ile Pro Thr
755 760 765

Leu Ala Val Ser Pro Thr Val Gln Gly Leu Val Thr Ser Leu Val Thr
770 775 780

Ser Ser Gly Ser Glu Thr Ser Ala Phe Ser Asn Leu Thr Val Ala Ser
785 790 795 800

Ser Gln Pro Glu Thr Ile Asp Ser Trp Val Ala His Pro Gly Thr Glu
805 810 815

Ala Ser Ser Val Val Pro Thr Leu Thr Val Ser Thr Gly Glu Pro Phe
820 825 830

Thr Asn Ile Ser Leu Val Thr His Pro Ala Glu Ser Ser Ser Thr Leu
835 840 845

Pro Arg Thr Thr Ser Arg Phe Ser His Ser Glu Leu Asp Thr Met Pro
850 855 860

Ser Thr Val Thr Ser Pro Glu Ala Glu Ser Ser Ser Ala Ile Ser Thr
865 870 875 880

Thr Ile Ser Pro Gly Ile Pro Gly Val Leu Thr Ser Leu Val Thr Ser
885 890 895

Ser Gly Arg Asp Ile Ser Ala Thr Phe Pro Thr Val Pro Glu Ser Pro
900 905 910

His Glu Ser Glu Ala Thr Ala Ser Trp Val Thr His Pro Ala Val Thr
915 920 925

Ser Thr Thr Val Pro Arg Thr Thr Pro Asn Tyr Ser His Ser Glu Pro
930 935 940

Asp Thr Thr Pro Ser Ile Ala Thr Ser Pro Gly Ala Glu Ala Thr Ser
945 950 955 960

Asp Phe Pro Thr Ile Thr Val Ser Pro Asp Val Pro Asp Met Val Thr
965 970 975

Ser Gln Val Thr Ser Ser Gly Thr Asp Thr Ser Ile Thr Ile Pro Thr
980 985 990

Leu Thr Leu Ser Ser Gly Glu Pro Glu Thr Thr Thr Ser Phe Ile Thr
995 1000 1005

Tyr Ser Glu Thr His Thr Ser Ser Ala Ile Pro Thr Leu Pro Val
1010 1015 1020

Ser Pro Gly Ala Ser Lys Met Leu Thr Ser Leu Val Ile Ser Ser
1025 1030 1035

Gly Thr Asp Ser Thr Thr Thr Phe Pro Thr Leu Thr Glu Thr Pro
1040 1045 1050

Tyr Glu Pro Glu Thr Thr Ala Ile Gln Leu Ile His Pro Ala Glu
1055 1060 1065

Thr Asn Thr Met Val Pro Arg Thr Thr Pro Lys Phe Ser His Ser
1070 1075 1080

Lys Ser Asp Thr Thr Leu Pro Val Ala Ile Thr Ser Pro Gly Pro
1085 1090 1095

Glu Ala Ser Ser Ala Val Ser Thr Thr Thr Ile Ser Pro Asp Met
1100 1105 1110

Ser Asp Leu Val Thr Ser Leu Val Pro Ser Ser Gly Thr Asp Thr
1115 1120 1125

Ser Thr Thr Phe Pro Thr Leu Ser Glu Thr Pro Tyr Glu Pro Glu
1130 1135 1140

Thr Thr Ala Thr Trp Leu Thr His Pro Ala Glu Thr Ser Thr Thr
1145 1150 1155

Val Ser Gly Thr Ile Pro Asn Phe Ser His Arg Gly Ser Asp Thr
1160 1165 1170

Ala Pro Ser Met Val Thr Ser Pro Gly Val Asp Thr Arg Ser Gly
1175 1180 1185

Val Pro Thr Thr Thr Ile Pro Pro Ser Ile Pro Gly Val Val Thr
1190 1195 1200

Ser Gln Val Thr Ser Ser Ala Thr Asp Thr Ser Thr Ala Ile Pro
1205 1210 1215

Thr Leu Thr Pro Ser Pro Gly Glu Pro Glu Thr Thr Ala Ser Ser
1220 1225 1230

Ala Thr His Pro Gly Thr Gln Thr Gly Phe Thr Val Pro Ile Arg
1235 1240 1245

Thr Val Pro Ser Ser Glu Pro Asp Thr Met Ala Ser Trp Val Thr
1250 1255 1260

His Pro Pro Gln Thr Ser Thr Pro Val Ser Arg Thr Thr Ser Ser
1265 1270 1275

Phe Ser His Ser Ser Pro Asp Ala Thr Pro Val Met Ala Thr Ser
1280 1285 1290

Pro Arg Thr Glu Ala Ser Ser Ala Val Leu Thr Thr Ile Ser Pro
1295 1300 1305

Gly Ala Pro Glu Met Val Thr Ser Gln Ile Thr Ser Ser Gly Ala
1310 1315 1320

Ala Thr Ser Thr Thr Val Pro Thr Leu Thr His Ser Pro Gly Met
1325 1330 1335

Pro Glu Thr Thr Ala Leu Leu Ser Thr His Pro Arg Thr Glu Thr
1340 1345 1350

Ser Lys Thr Phe Pro Ala Ser Thr Val Phe Pro Gln Val Ser Glu
1355 1360 1365

Thr Thr Ala Ser Leu Thr Ile Arg Pro Gly Ala Glu Thr Ser Thr
1370 1375 1380

Ala Leu Pro Thr Gln Thr Thr Ser Ser Leu Phe Thr Leu Leu Val
1385 1390 1395

Thr Gly Thr Ser Arg Val Asp Leu Ser Pro Thr Ala Ser Pro Gly
1400 1405 1410

Val Ser Ala Lys Thr Ala Pro Leu Ser Thr His Pro Gly Thr Glu
1415 1420 1425

Thr Ser Thr Met Ile Pro Thr Ser Thr Leu Ser Leu Gly Leu Leu
1430 1435 1440

Glu Thr Thr Gly Leu Leu Ala Thr Ser Ser Ser Ala Glu Thr Ser
1445 1450 1455

Thr Ser Thr Leu Thr Leu Thr Val Ser Pro Ala Val Ser Gly Leu
1460 1465 1470

Ser Ser Ala Ser Ile Thr Thr Asp Lys Pro Gln Thr Val Thr Ser
1475 1480 1485

Trp Asn Thr Glu Thr Ser Pro Ser Val Thr Ser Val Gly Pro Pro
1490 1495 1500

Glu Phe Ser Arg Thr Val Thr Gly Thr Thr Met Thr Leu Ile Pro
1505 1510 1515

Ser Glu Met Pro Thr Pro Pro Lys Thr Ser His Gly Glu Gly Val
1520 1525 1530

Ser Pro Thr Thr Ile Leu Arg Thr Thr Met Val Glu Ala Thr Asn
1535 1540 1545

Leu Ala Thr Thr Gly Ser Ser Pro Thr Val Ala Lys Thr Thr Thr
1550 1555 1560

Thr Phe Asn Thr Leu Ala Gly Ser Leu Phe Thr Pro Leu Thr Thr
1565 1570 1575

Pro Gly Met Ser Thr Leu Ala Ser Glu Ser Val Thr Ser Arg Thr
1580 1585 1590

Ser Tyr Asn His Arg Ser Trp Ile Ser Thr Thr Ser Ser Tyr Asn
1595 1600 1605

Arg Arg Tyr Trp Thr Pro Ala Thr Ser Thr Pro Val Thr Ser Thr
1610 1615 1620

Phe Ser Pro Gly Ile Ser Thr Ser Ser Ile Pro Ser Ser Thr Ala
1625 1630 1635

Ala Thr Val Pro Phe Met Val Pro Phe Thr Leu Asn Phe Thr Ile
1640 1645 1650

Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg
1655 1660 1665

Lys Phe Asn Ala Thr Glu Arg Glu Leu Gln Gly Leu Leu Lys Pro
1670 1675 1680

Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg
1685 1690 1695

Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala Met Ala Val
1700 1705 1710

Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp Leu Gly Leu
1715 1720 1725

Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn Gly
1730 1735 1740

Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr
1745 1750 1755

Val Asn Gly Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr
1760 1765 1770

Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser
1775 1780 1785

Ser Ser Pro Ser Pro Thr Ala Ala Gly Pro Leu Leu Met Pro Phe
1790 1795 1800

Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met
1805 1810 1815

Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Ser Val Leu
1820 1825 1830

Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro
1835 1840 1845

Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp
1850 1855 1860

Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp
1865 1870 1875

Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu
1880 1885 1890

Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu
1895 1900 1905

Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser
1910 1915 1920

Val Ser Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Arg
1925 1930 1935

Thr Ser Gly Thr Pro Ser Ser Leu Ser Ser Pro Thr Ile Met Ala
1940 1945 1950

Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1955 1960 1965

Asn Leu Gln Tyr Gly Glu Asp Met Gly His Pro Gly Ser Arg Lys
1970 1975 1980

Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Ile
1985 1990 1995

Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu
2000 2005 2010

Thr Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp
2015 2020 2025

Ala Ile Cys Ile His His Leu Asp Pro Lys Ser Pro Gly Leu Asn
2030 2035 2040

Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile
2045 2050 2055

Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val
2060 2065 2070

Asn Gly Phe Thr His Arg Thr Ser Val Pro Thr Ser Ser Thr Pro
2075 2080 2085

Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Phe Ser
2090 2095 2100

Leu Pro Ser Pro Ala Thr Ala Gly Pro Leu Leu Val Leu Phe Thr
2105 2110 2115

Leu Asn Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His
2120 2125 2130

Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln
2135 2140 2145

Thr Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu
2150 2155 2160

Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly
2165 2170 2175

Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro
2180 2185 2190

Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser
2195 2200 2205

Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp
2210 2215 2220

Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Trp Ile Pro Val
2225 2230 2235

Pro Thr Ser Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Ser
2240 2245 2250

Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Ala Ala Gly Pro Leu
2255 2260 2265

Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
2270 2275 2280

Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr
2285 2290 2295

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr
2300 2305 2310

Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
2315 2320 2325

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr
2330 2335 2340

His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu
2345 2350 2355

Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly
2360 2365 2370

Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr
2375 2380 2385

His Gln Thr Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr
2390 2395 2400

Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro
2405 2410 2415

Thr Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
2420 2425 2430

Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser
2435 2440 2445

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys
2450 2455 2460

Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
2465 2470 2475

Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly
2480 2485 2490

Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly
2495 2500 2505

Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn
2510 2515 2520

Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
2525 2530 2535

Tyr Val Asn Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr Ser
2540 2545 2550

Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro
2555 2560 2565

Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly Pro Leu Leu Val Pro
2570 2575 2580

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
2585 2590 2595

Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
2600 2605 2610

Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly
2615 2620 2625

Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
2630 2635 2640

Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser His Arg Leu
2645 2650 2655

Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu
2660 2665 2670

Leu Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr
2675 2680 2685

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
2690 2695 2700

Ser Val Ala Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu
2705 2710 2715

Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala
2720 2725 2730

Val Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
2735 2740 2745

Leu Gln Tyr Gly Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
2750 2755 2760

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu Phe
2765 2770 2775

Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile
2780 2785 2790

Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala
2795 2800 2805

Ile Cys Thr His His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg
2810 2815 2820

Glu Gln Leu Tyr Trp Gln Leu Ser Gln Met Thr Asn Gly Ile Lys
2825 2830 2835

Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
2840 2845 2850

Gly Phe Thr His Arg Ser Ser Gly Leu Thr Thr Ser Thr Pro Trp
2855 2860 2865

Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val
2870 2875 2880

Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu
2885 2890 2895

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His Arg
2900 2905 2910

Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Val Leu Gln Gly
2915 2920 2925

Leu Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr
2930 2935 2940

Ser Gly Cys Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala
2945 2950 2955

Ala Thr Gly Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys
2960 2965 2970

Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln
2975 2980 2985

Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg
2990 2995 3000

Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro
3005 3010 3015

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr
3020 3025 3030

Gly Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu
3035 3040 3045

Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr Asn Leu His Tyr
3050 3055 3060

Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr
3065 3070 3075

Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr
3080 3085 3090

Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg
3095 3100 3105

Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu
3110 3115 3120

Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu
3125 3130 3135

Tyr Cys Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly
3140 3145 3150

Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr
3155 3160 3165

His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr
3170 3175 3180

Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His
3185 3190 3195

Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr
3200 3205 3210

Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser
3215 3220 3225

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys
3230 3235 3240

Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
3245 3250 3255

Arg Leu Thr Leu Leu Arg Pro Glu Lys His Glu Ala Ala Thr Gly
3260 3265 3270

Val Asp Thr Ile Cys Thr His Arg Val Asp Pro Ile Gly Pro Gly
3275 3280 3285

Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn
3290 3295 3300

Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
3305 3310 3315

Tyr Val Asn Gly Phe Asn Pro Arg Ser Ser Val Pro Thr Thr Ser
3320 3325 3330

Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro
3335 3340 3345

Ser Ser Leu Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro
3350 3355 3360

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
3365 3370 3375

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
3380 3385 3390

Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly
3395 3400 3405

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
3410 3415 3420

His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val
3425 3430 3435

Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu
3440 3445 3450

Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa
3455 3460 3465

Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa
3470 3475 3480

Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly Thr Ser Xaa Val Xaa Leu
3485 3490 3495

Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa Thr Ser Ala
3500 3505 3510

Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
3515 3520 3525

Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe
3530 3535 3540

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe
3545 3550 3555

Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr
3560 3565 3570

Leu Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala
3575 3580 3585

Ile Cys Ser His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg
3590 3595 3600

Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Lys
3605 3610 3615

Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
3620 3625 3630

Gly Phe Thr His Arg Ser Ser Val Ala Pro Thr Ser Thr Pro Gly
3635 3640 3645

Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu
3650 3655 3660

Pro Ser Pro Thr Thr Ala Val Pro Leu Leu Val Pro Phe Thr Leu
3665 3670 3675

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Arg His
3680 3685 3690

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
3695 3700 3705

Leu Leu Gly Pro Leu Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr
3710 3715 3720

Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu Lys Asp Gly Ala
3725 3730 3735

Ala Thr Gly Val Asp Ala Ile Cys Thr His His Leu Asn Pro Gln
3740 3745 3750

Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser Gln
3755 3760 3765

Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg
3770 3775 3780

Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu
3785 3790 3795

Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser
3800 3805 3810

Gly Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu
3815 3820 3825

Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
3830 3835 3840

Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr
3845 3850 3855

Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser
3860 3865 3870

Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg
3875 3880 3885

Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu
3890 3895 3900

Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu
3905 3910 3915

Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly
3920 3925 3930

Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr
3935 3940 3945

His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser Thr
3950 3955 3960

Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro
3965 3970 3975

Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Cys Thr
3980 3985 3990

Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser
3995 4000 4005

Arg Lys Phe Asn Thr Met Glu Ser Val Leu Gln Gly Leu Leu Lys
4010 4015 4020

Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
4025 4030 4035

Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Gly
4040 4045 4050

Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly
4055 4060 4065

Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn
4070 4075 4080

Asp Ile Glu Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
4085 4090 4095

Tyr Val Asn Gly Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser
4100 4105 4110

Thr Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro
4115 4120 4125

Ser Ser Leu Ser Ser Pro Thr Ile Met Xaa Xaa Xaa Pro Leu Leu
4130 4135 4140

Xaa Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu
4145 4150 4155

Glu Xaa Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
4160 4165 4170

Arg Val Leu Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser
4175 4180 4185

Val Ser Ser Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro
4190 4195 4200

Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Ala Cys Thr Tyr
4205 4210 4215

Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr
4220 4225 4230

Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro
4235 4240 4245

Tyr Thr Leu Asp Arg Val Ser Leu Tyr Val Asn Gly Phe Asn Pro
4250 4255 4260

Arg Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val
4265 4270 4275

His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His Thr
4280 4285 4290

Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile
4295 4300 4305

Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg
4310 4315 4320

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro
4325 4330 4335

Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly Cys Arg
4340 4345 4350

Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala Met Ala Val
4355 4360 4365

Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp Leu Gly Leu
4370 4375 4380

Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn Gly
4385 4390 4395

Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr
4400 4405 4410

Val Asn Gly Phe Thr His Arg Ser Ser Phe Leu Thr Thr Ser Thr
4415 4420 4425

Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser
4430 4435 4440

Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe
4445 4450 4455

Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met
4460 4465 4470

His Arg Pro Gly Ser Arg Arg Phe Asn Thr Thr Glu Arg Val Leu
4475 4480 4485

Gln Gly Leu Leu Thr Pro Leu Phe Lys Asn Thr Ser Val Gly Pro
4490 4495 4500

Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Gln
4505 4510 4515

Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val Asp
4520 4525 4530

Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
4535 4540 4545

Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu
4550 4555 4560

Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Trp Ser Ser
4565 4570 4575

Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala
4580 4585 4590

Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val
4595 4600 4605

Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asp Leu
4610 4615 4620

His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn
4625 4630 4635

Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys
4640 4645 4650

Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
4655 4660 4665

Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile
4670 4675 4680

Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu
4685 4690 4695

Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu
4700 4705 4710

Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
4715 4720 4725

Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr
4730 4735 4740

Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro
4745 4750 4755

Gly His Thr Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn
4760 4765 4770

Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro
4775 4780 4785

Gly Ser Arg Lys Phe Ser Thr Thr Glu Arg Val Leu Gln Gly Leu
4790 4795 4800

Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser
4805 4810 4815

Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala
4820 4825 4830

Thr Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser
4835 4840 4845

Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu
4850 4855 4860

Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg His
4865 4870 4875

Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr Thr
4880 4885 4890

Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg
4895 4900 4905

Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu
4910 4915 4920

Val Leu Phe Thr Ile Asn Phe Thr Ile Thr Asn Gln Arg Tyr Glu
4925 4930 4935

Glu Asn Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
4940 4945 4950

Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser
4955 4960 4965

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro
4970 4975 4980

Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr
4985 4990 4995

Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr
5000 5005 5010

Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro
5015 5020 5025

Tyr Thr Gln Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His
5030 5035 5040

Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala Val
5045 5050 5055

His Leu Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr
5060 5065 5070

Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile
5075 5080 5085

Thr Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg
5090 5095 5100

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro
5105 5110 5115

Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
5120 5125 5130

Leu Thr Leu Leu Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val
5135 5140 5145

Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu
5150 5155 5160

Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Arg Gly
5165 5170 5175

Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu Tyr
5180 5185 5190

Val Asn Gly Phe Thr His Arg Thr Ser Val Pro Thr Thr Ser Thr
5195 5200 5205

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Phe
5210 5215 5220

Ser Leu Pro Ser Pro Ala Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe
5225 5230 5235

Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met
5240 5245 5250

Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
5255 5260 5265

Gln Thr Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu
5270 5275 5280

Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp
5285 5290 5295

Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp
5300 5305 5310

Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu
5315 5320 5325

Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu
5330 5335 5340

Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Trp Ile Pro
5345 5350 5355

Val Pro Thr Ser Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly
5360 5365 5370

Ser Gly Thr Pro Ser Leu Pro Ser Ser Pro Thr Thr Ala Gly Pro
5375 5380 5385

Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys
5390 5395 5400

Tyr Glu Glu Asp Met His Cys Pro Gly Ser Arg Lys Phe Asn Thr
5405 5410 5415

Thr Glu Arg Val Leu Gln Ser Leu Leu Gly Pro Met Phe Lys Asn
5420 5425 5430

Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
5435 5440 5445

Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys
5450 5455 5460

Thr His Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln
5465 5470 5475

Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu
5480 5485 5490

Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe
5495 5500 5505

Thr His Gln Thr Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser
5510 5515 5520

Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser
5525 5530 5535

Pro Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe
5540 5545 5550

Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly
5555 5560 5565

Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu
5570 5575 5580

Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr Ser Gly
5585 5590 5595

Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala Ala Thr
5600 5605 5610

Xaa Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa Xaa Pro
5615 5620 5625

Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr
5630 5635 5640

Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser
5645 5650 5655

Leu Tyr Val Asn Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser
5660 5665 5670

Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro
5675 5680 5685

Ser Ser Leu Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro
5690 5695 5700

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp
5705 5710 5715

Met His Cys Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
5720 5725 5730

Leu Gln Ser Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly
5735 5740 5745

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Ser Glu Lys
5750 5755 5760

Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Val
5765 5770 5775

Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu
5780 5785 5790

Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
5795 5800 5805

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr
5810 5815 5820

Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu
5825 5830 5835

Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala
5840 5845 5850

Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
5855 5860 5865

Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe
5870 5875 5880

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe
5885 5890 5895

Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr
5900 5905 5910

Leu Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala
5915 5920 5925

Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg
5930 5935 5940

Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa
5945 5950 5955

Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn
5960 5965 5970

Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly
5975 5980 5985

Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa
5990 5995 6000

Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu
6005 6010 6015

Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa
6020 6025 6030

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
6035 6040 6045

Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu Tyr
6050 6055 6060

Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser
6065 6070 6075

Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu
6080 6085 6090

Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn
6095 6100 6105

Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg
6110 6115 6120

Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro
6125 6130 6135

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser
6140 6145 6150

Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Thr Ala Gly Pro Leu
6155 6160 6165

Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
6170 6175 6180

Gly Glu Asp Met Gly His Pro Gly Ser Arg Lys Phe Asn Thr Thr
6185 6190 6195

Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Ile Phe Lys Asn Thr
6200 6205 6210

Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg
6215 6220 6225

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Ile
6230 6235 6240

His His Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Arg Leu
6245 6250 6255

Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly
6260 6265 6270

Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr
6275 6280 6285

His Arg Thr Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr
6290 6295 6300

Val Asp Leu Gly Thr Ser Gly Thr Pro Phe Ser Leu Pro Ser Pro
6305 6310 6315

Ala Thr Ala Gly Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr
6320 6325 6330

Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Arg Pro Gly Ser
6335 6340 6345

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Thr Leu Leu Gly
6350 6355 6360

Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys
6365 6370 6375

Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly
6380 6385 6390

Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly
6395 6400 6405

Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa
6410 6415 6420

Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu
6425 6430 6435

Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser
6440 6445 6450

Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly Thr Pro
6455 6460 6465

Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro
6470 6475 6480

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa
6485 6490 6495

Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
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Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly
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Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys
6530 6535 6540

Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro
6545 6550 6555

Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu
6560 6565 6570

Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr
6575 6580 6585

Gln Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
6590 6595 6600

Ser Val Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu
6605 6610 6615

Glu Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His Thr Glu Pro
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Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr Asn
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Leu Arg Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
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Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Thr Pro Leu Phe
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Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
6680 6685 6690

Leu Leu Arg Pro Glu Lys Gln Glu Ala Ala Thr Gly Val Asp Thr
6695 6700 6705

Ile Cys Thr His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg
6710 6715 6720

Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr
6725 6730 6735

Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asp
6740 6745 6750

Gly Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly
6755 6760 6765

Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Pro Leu
6770 6775 6780

Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu
6785 6790 6795

Asn Phe Thr Ile Thr Asp Leu His Tyr Glu Glu Asn Met Gln His
6800 6805 6810

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
6815 6820 6825

Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr
6830 6835 6840

Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala
6845 6850 6855

Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr
6860 6865 6870

Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln
6875 6880 6885

Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg
6890 6895 6900

Asp Ser Leu Tyr Val Asn Gly Phe Asn Pro Trp Ser Ser Val Pro
6905 6910 6915

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser
6920 6925 6930

Gly Thr Pro Ser Ser Leu Pro Gly His Thr Thr Ala Gly Pro Leu
6935 6940 6945

Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys Tyr
6950 6955 6960

Glu Glu Asp Met His Cys Pro Gly Ser Arg Lys Phe Asn Thr Thr
6965 6970 6975

Glu Arg Val Leu Gln Ser Leu His Gly Pro Met Phe Lys Asn Thr
6980 6985 6990

Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
6995 7000 7005

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr
7010 7015 7020

His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Xaa Leu
7025 7030 7035

Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly
7040 7045 7050

Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Xaa
7055 7060 7065

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly Thr Ser Xaa
7070 7075 7080

Val Xaa Leu Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa
7085 7090 7095

Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr
7100 7105 7110

Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser
7115 7120 7125

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Xaa
7130 7135 7140

Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr Ser Gly Cys
7145 7150 7155

Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa
7160 7165 7170

Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly
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Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Asn
7190 7195 7200

Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu
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Tyr Val Asn Gly Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser
7220 7225 7230

Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro
7235 7240 7245

Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Val Pro
7250 7255 7260

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
7265 7270 7275

Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
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Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly
7295 7300 7305

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
7310 7315 7320

Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu
7325 7330 7335

Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu
7340 7345 7350

Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa
7355 7360 7365

Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa
7370 7375 7380

Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly Thr Ser Xaa Val Xaa Leu
7385 7390 7395

Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa
7400 7405 7410

Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
7415 7420 7425

Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg Lys Phe
7430 7435 7440

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Xaa Pro Xaa Phe
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Lys Xaa Thr Ser Val Gly Xaa Leu Tyr Ser Gly Cys Arg Leu Thr
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Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa
7475 7480 7485

Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly Leu Asp Arg
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Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa
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Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn
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Gly Phe His Pro Arg Ser Ser Val Pro Thr Thr Ser Thr Pro Gly
7535 7540 7545

Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu
7550 7555 7560

Pro Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu
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Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His
7580 7585 7590

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
7595 7600 7605

Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr
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Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asn Gly Ala
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Ala Thr Gly Met Asp Ala Ile Cys Ser His Arg Leu Asp Pro Lys
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Ser Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa
7655 7660 7665

Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg
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Xaa Ser Leu Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa Thr Ser Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser
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Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu
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Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr
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Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr
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Glu Arg Val Leu Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr
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Ser Val Gly Xaa Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
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Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa
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Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Thr
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His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr
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Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His
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Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr
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Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
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Val Asp Thr Ile Cys Thr His Arg Val Asp Pro Ile Gly Pro Gly
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7970 7975 7980

Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu
7985 7990 7995

Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser
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Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly Thr Pro
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Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro
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Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa
8045 8050 8055

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8060 8065 8070

Leu Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly
8075 8080 8085

Xaa Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys
8090 8095 8100

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Asp Pro Xaa Xaa Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu
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Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa
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Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
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Ser Val Pro Thr Thr Ser Ser Pro Gly Thr Ser Thr Val His Leu
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Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro
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Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
8195 8200 8205

Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
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Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe
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Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
8240 8245 8250

Leu Leu Arg Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala
8255 8260 8265

Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg
8270 8275 8280

Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa
8285 8290 8295

Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn
8300 8305 8310

Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly
8315 8320 8325

Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa
8330 8335 8340

Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu
8345 8350 8355

Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa
8360 8365 8370

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
8375 8380 8385

Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr
8390 8395 8400

Ser Gly Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala
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Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa
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Xaa Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa
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Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg
8450 8455 8460

Xaa Ser Leu Tyr Val Asn Gly Phe Thr His Arg Thr Ser Val Pro
8465 8470 8475

Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser
8480 8485 8490

Gly Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val Pro Leu
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Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
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Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser
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Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg
8555 8560 8565

Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu
8570 8575 8580

Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu
8585 8590 8595

Tyr Cys Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly
8600 8605 8610

Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr
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His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr
8630 8635 8640

Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His
8645 8650 8655

Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr
8660 8665 8670

Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser
8675 8680 8685

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Xaa
8690 8695 8700

Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr Ser Gly Cys
8705 8710 8715

Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa
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Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly
8735 8740 8745

Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa
8750 8755 8760

Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu
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Tyr Val Asn Gly Phe Thr His Trp Ser Ser Gly Leu Thr Thr Ser
8780 8785 8790

Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro
8795 8800 8805

Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro
8810 8815 8820

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
8825 8830 8835

Met His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Val
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Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Thr Ser Val Gly
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Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
8870 8875 8880

Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val
8885 8890 8895

Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu
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Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa
8915 8920 8925

Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa
8930 8935 8940

Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly Thr Ser Xaa Val Xaa Leu
8945 8950 8955

Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa
8960 8965 8970

Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
8975 8980 8985

Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg Lys Phe
8990 8995 9000

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Xaa Pro Xaa Phe
9005 9010 9015

Lys Xaa Thr Ser Val Gly Xaa Leu Tyr Ser Gly Cys Arg Leu Thr
9020 9025 9030

Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa
9035 9040 9045

Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly Leu Asp Arg
9050 9055 9060

Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa
9065 9070 9075

Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn
9080 9085 9090

Gly Phe Thr His Arg Ser Phe Gly Leu Thr Thr Ser Thr Pro Trp
9095 9100 9105

Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val
9110 9115 9120

Pro Ser Pro Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu
9125 9130 9135

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His Arg
9140 9145 9150

Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
9155 9160 9165

Leu Leu Thr Pro Leu Phe Arg Asn Thr Ser Val Ser Ser Leu Tyr
9170 9175 9180

Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala
9185 9190 9195

Ala Thr Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys
9200 9205 9210

Ser Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa
9215 9220 9225

Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg
9230 9235 9240

Xaa Ser Leu Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
9245 9250 9255

Xaa Thr Ser Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser
9260 9265 9270

Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu
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Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr
9290 9295 9300

Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr
9305 9310 9315

Glu Arg Val Leu Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr
9320 9325 9330

Ser Val Gly Xaa Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
9335 9340 9345

Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa
9350 9355 9360

Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly Leu Asp Arg Glu Xaa Leu
9365 9370 9375

Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly
9380 9385 9390

Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Thr
9395 9400 9405

His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr Ser Thr
9410 9415 9420

Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr
9425 9430 9435

Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile
9440 9445 9450

Thr Asn Leu Gln Tyr Gly Glu Asp Met Gly His Pro Gly Ser Arg
9455 9460 9465

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro
9470 9475 9480

Ile Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
9485 9490 9495

Leu Thr Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val
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Asp Ala Ile Cys Ile His His Leu Asp Pro Lys Ser Pro Gly Leu
9515 9520 9525

Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa
9530 9535 9540

Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr
9545 9550 9555

Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Thr
9560 9565 9570

Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly Thr Pro Xaa
9575 9580 9585

Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe
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Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met
9605 9610 9615

Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
9620 9625 9630

Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa
9635 9640 9645

Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa
9650 9655 9660

Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Asp
9665 9670 9675

Pro Xaa Xaa Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu
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Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu
9695 9700 9705

Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr Phe
9710 9715 9720

Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly
9725 9730 9735

Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly
9740 9745 9750

Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
9755 9760 9765

Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe Asn
9770 9775 9780

Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys
9785 9790 9795

Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu
9800 9805 9810

Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Arg Val Asp Ala Val
9815 9820 9825

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Cys Thr  His Arg Pro Asp Pro  Lys Ser Pro Gly Leu  Asp Arg Glu
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Xaa Leu  Tyr Trp Glu Leu Ser  Xaa Leu Thr Xaa Xaa  Ile Xaa Glu
    9845                 9850                 9855

Leu Gly  Pro Tyr Xaa Leu Asp  Arg Xaa Ser Leu Tyr  Val Asn Gly
    9860                 9865                 9870

Phe Xaa  Xaa Xaa Xaa Xaa Xaa  Xaa Xaa Thr Ser Thr  Pro Gly Thr
    9875                 9880                 9885

Ser Xaa  Val Xaa Leu Xaa Thr  Ser Gly Thr Pro Xaa  Xaa Xaa Pro
    9890                 9895                 9900

Xaa Xaa  Thr Ala Pro Val Pro  Leu Leu Ile Pro Phe  Thr Leu Asn
    9905                 9910                 9915

Phe Thr  Ile Thr Asn Leu His  Tyr Glu Glu Asn Met  Gln His Pro
    9920                 9925                 9930

Gly Ser  Arg Lys Phe Asn Thr  Thr Glu Arg Val Leu  Gln Gly Leu
    9935                 9940                 9945

Leu Arg  Pro Leu Phe Lys Ser  Thr Ser Val Gly Pro  Leu Tyr Ser
    9950                 9955                 9960

Gly Cys  Arg Leu Thr Leu Leu  Arg Pro Glu Lys His  Gly Ala Ala
    9965                 9970                 9975

Thr Gly  Val Asp Ala Ile Cys  Thr Leu Arg Leu Asp  Pro Thr Gly
    9980                 9985                 9990

Pro Gly  Leu Asp Arg Glu Arg   Leu Tyr Trp Glu Leu   Ser Gln Leu
    9995                 10000                10005

Thr Asn   Ser Val Thr Glu Leu   Gly Pro Tyr Thr Leu   Asp Arg Asp
    10010                10015                10020
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Ser Leu Tyr Val Asn Gly Phe Thr Gln Arg Ser Ser Val Pro Thr
10025 10030 10035

Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly
10040 10045 10050

Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu
10055 10060 10065

Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu
10070 10075 10080

Val Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
10085 10090 10095

Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser
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Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro
10115 10120 10125

Glu Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His
10130 10135 10140

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Trp Glu Leu Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro
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Tyr Leu Leu Asp Arg Gly Ser Leu Tyr Val Asn Gly Phe Thr His
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His Leu Gly Thr Ser Glu Thr Pro Ser Ser Leu Pro Arg Pro Ile
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Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro
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Leu Thr Leu Leu Arg Pro Glu Lys Asp Lys Ala Ala Thr Arg Val
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10310 10315 10320

Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr
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Val Asp Gly Phe Thr His Trp Ser Pro Ile Pro Thr Thr Ser Thr
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Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro
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Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu
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Cys Thr His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu
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Leu Gly Pro Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly
10640 10645 10650

Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr
10655 10660 10665

Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser
10670 10675 10680

Gly Pro Thr Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn
10685 10690 10695

Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met His His Pro
10700 10705 10710

Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
10715 10720 10725

Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser
10730 10735 10740

Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala
10745 10750 10755

Thr Lys Val Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser
10760 10765 10770

Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu
10775 10780 10785

Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr Gln Asp Arg Asp
10790 10795 10800

Ser Leu Tyr Asn Val Gly Phe Thr Gln Arg Ser Ser Val Pro Thr
10805 10810 10815

Thr Ser Val Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly
10820 10825 10830

Thr Pro Val Ser Lys Pro Gly Pro Ser Ala Ala Ser Pro Leu Leu
10835 10840 10845

Val Leu Phe Thr Leu Asn Gly Thr Ile Thr Asn Leu Arg Tyr Glu
10850 10855 10860

Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
10865 10870 10875

Arg Val Leu Gln Gly Leu Leu Arg Ser Leu Phe Lys Ser Thr Ser
10880 10885 10890

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro
10895 10900 10905

Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile Cys Thr His
10910 10915 10920

His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln Leu Tyr
10925 10930 10935

Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly His
10940 10945 10950

Tyr Ala Leu Asp Asn Asp Ser Leu Phe Val Asn Gly Phe Thr His
10955 10960 10965

Arg Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Pro Thr Val
10970 10975 10980

Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser Ile Phe Gly Pro Ser
10985 10990 10995

Ala Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile
11000 11005 11010

Thr Asn Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys
11015 11020 11025

Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Leu
11030 11035 11040

Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Ser Arg Leu
11045 11050 11055

Thr Leu Leu Arg Pro Glu Lys Asp Gly Glu Ala Thr Gly Val Asp
11060 11065 11070

Ala Ile Cys Thr His Arg Pro Asp Pro Thr Gly Pro Gly Leu Asp
11075 11080 11085

Arg Glu Gln Leu Tyr Leu Glu Leu Ser Gln Leu Thr His Ser Ile
11090 11095 11100

Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val
11105 11110 11115

Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Thr Gly
11120 11125 11130

Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn Asn
11135 11140 11145

Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe
11150 11155 11160

Asn Ile Thr Asp Asn Val Met Lys His Leu Leu Ser Pro Leu Phe
11165 11170 11175

Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly Cys Arg Val Ile
11180 11185 11190

Ala Leu Arg Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu
11195 11200 11205

Leu Cys Thr Tyr Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile
11210 11215 11220

Lys Gln Val Phe His Glu Leu Ser Gln Gln Thr His Gly Ile Thr
11225 11230 11235

Arg Leu Gly Pro Tyr Ser Leu Asp Lys Asp Ser Leu Tyr Leu Asn
11240 11245 11250

Gly Tyr Asn Glu Pro Gly Leu Asp Glu Pro Pro Thr Thr Pro Lys
11255 11260 11265

Pro Ala Thr Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr Ala
11270 11275 11280

Met Gly Tyr His Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser
11285 11290 11295

Asn Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe
11300 11305 11310

Asn Ser Thr Glu Gly Val Leu Gln His Leu Leu Arg Pro Leu Phe
11315 11320 11325

Gln Lys Ser Ser Met Gly Pro Phe Tyr Leu Gly Cys Gln Leu Ile
11330 11335 11340

Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr
11345 11350 11355

Thr Cys Thr Tyr His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile
11360 11365 11370

Gln Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Val Thr
11375 11380 11385

Gln Leu Gly Phe Tyr Val Leu Asp Arg Asp Ser Leu Phe Ile Asn
11390 11395 11400

Gly Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr Gln Ile
11405 11410 11415

Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro Thr
11420 11425 11430

Ser Ser Glu Tyr Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val
11435 11440 11445

Thr Thr Leu Tyr Lys Gly Ser Gln Leu His Asp Thr Phe Arg Phe
11450 11455 11460

Cys Leu Val Thr Asn Leu Thr Met Asp Ser Val Leu Val Thr Val
11465 11470 11475

Lys Ala Leu Phe Ser Ser Asn Leu Asp Pro Ser Leu Val Glu Gln
11480 11485 11490

Val Phe Leu Asp Lys Thr Leu Asn Ala Ser Phe His Trp Leu Gly
11495 11500 11505

Ser Thr Tyr Gln Leu Val Asp Ile His Val Thr Glu Met Glu Ser
11510 11515 11520

Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser Thr Gln His Phe Tyr
11525 11530 11535

Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser Gln Asp Lys Ala
11540 11545 11550

Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg Asn Ile Glu
11555 11560 11565

Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys Ser Tyr
11570 11575 11580

Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn Arg
11585 11590 11595

His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala
11600 11605 11610

Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met
11615 11620 11625

Thr Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser
11630 11635 11640

Ser Val Leu Val Asp Gly Tyr Ser Pro Asn Arg Asn Glu Pro Leu
11645 11650 11655

Thr Gly Asn Ser Asp Leu Pro Phe Trp Ala Val Ile Leu Ile Gly
11660 11665 11670

Leu Ala Gly Leu Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val
11675 11680 11685

Leu Val Thr Thr Arg Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val
11690 11695 11700

Gln Gln Gln Cys Pro Gly Tyr Tyr Gln Ser His Leu Asp Leu Glu
11705 11710 11715

Asp Leu Gln
11720

<210> 163

<211> 156

<212> PRT

<213> Homo sapiens

<400> 163

Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
20 25 30

Asn Ala Thr Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys
35 40 45

Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu
50 55 60

Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu
65 70 75 80

Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr
85 90 95

Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr
100 105 110

Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Gln Asn
115 120 125

Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala
130 135 140

Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His Thr
145 150 155

<210> 164

<211> 42

<212> PRT

<213> Homo sapiens

<400> 164

Ala Thr Val Pro Phe Met Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Ala Thr Glu Arg Glu Leu Gln Gly Leu
35 40

<210> 165

<211> 42

<212> PRT

<213> Homo sapiens

<400> 165

Thr Ala Val Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Gly Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 166

<211> 42

<212> PRT

<213> Homo sapiens

<400> 166

Val Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Ala Met Arg His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 167

<211> 42

<212> PRT

<213> Homo sapiens

<400> 167

Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
20 25 30

Ser Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 168

<211> 42

<212> PRT

<213> Homo sapiens

<400> 168

Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 169

<211> 42

<212> PRT

<213> Homo sapiens

<400> 169

Ala Pro Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Val Asp Met Arg His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 170

<211> 42

<212> PRT

<213> Homo sapiens

<400> 170

Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 171

<211> 42

<212> PRT

<213> Homo sapiens

<400> 171

Ala Ala Gly Pro Leu Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe
20 25 30

Asn Thr Met Glu Ser Val Leu Gln Gly Leu
35 40

<210> 172

<211> 42

<212> PRT

<213> Homo sapiens

<400> 172

Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Cys Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe
20 25 30

Asn Thr Met Glu Ser Val Leu Gln Gly Leu
35 40

<210> 173

<211> 42

<212> PRT

<213> Homo sapiens

<400> 173

Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Gly Glu Asp Met Gly His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 174

<211> 42

<212> PRT

<213> Homo sapiens

<400> 174

Thr Ala Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Gly Glu Asp Met Gly His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 175

<211> 42

<212> PRT

<213> Homo sapiens

<400> 175

Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Gly Glu Asp Met Gly His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 176

<211> 42

<212> PRT

<213> Homo sapiens

<400> 176

Thr Ala Gly Pro Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Lys Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Thr Leu
35 40

<210> 177

<211> 42

<212> PRT

<213> Homo sapiens

<400> 177

Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
20 25 30

Asn Ala Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 178

<211> 42

<212> PRT

<213> Homo sapiens

<400> 178

Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Arg Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 179

<211> 42

<212> PRT

<213> Homo sapiens

<400> 179

Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 180

<211> 42

<212> PRT

<213> Homo sapiens

<400> 180

Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 181

<211> 42

<212> PRT

<213> Homo sapiens

<400> 181

Ala Thr Gly Pro Val Leu Leu Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 182

<211> 42

<212> PRT

<213> Homo sapiens

<400> 182

Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 183

<211> 42

<212> PRT

<213> Homo sapiens

<400> 183

Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 184

<211> 42

<212> PRT

<213> Homo sapiens

<400> 184

Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile Thr
1 5 10 15

Asn Gln Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 185

<211> 42

<212> PRT

<213> Homo sapiens

<400> 185

Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 186

<211> 42

<212> PRT

<213> Homo sapiens

<400> 186

Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 187

<211> 42

<212> PRT

<213> Homo sapiens

<400> 187

Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Arg Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 188

<211> 42

<212> PRT

<213> Homo sapiens

<400> 188

Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 189

<211> 42

<212> PRT

<213> Homo sapiens

<400> 189

Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asp Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 190

<211> 42

<212> PRT

<213> Homo sapiens

<400> 190

Ala Ala Ser Pro Leu Leu Val Leu Phe Thr Leu Asn Gly Thr Ile Thr
1 5 10 15

Asn Leu Arg Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 191

<211> 42

<212> PRT

<213> Homo sapiens

<400> 191

Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Lys Tyr Glu Glu Asp Met His Cys Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Ser Leu
35 40

<210> 192

<211> 41

<212> PRT

<213> Homo sapiens

<400> 192

Ala Ala Ser His Leu Leu Ile Leu Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Arg Tyr Glu Glu Asn Met Trp Pro Gly Ser Arg Lys Phe Asn
20 25 30

Thr Thr Glu Arg Val Leu Gln Gly Leu
35 40

<210> 193

<211> 42

<212> PRT

<213> Homo sapiens

<400> 193

Thr Gly Val Val Ser Glu Glu Pro Phe Thr Leu Asn Phe Thr Ile Asn
1 5 10 15

Asn Leu Arg Tyr Met Ala Asp Met Gly Gln Pro Gly Ser Leu Lys Phe
20 25 30

Asn Ile Thr Asp Asn Val Met Lys His Leu
35 40

<210> 194

<211> 42

<212> PRT

<213> Homo sapiens

<400> 194

Ala Met Gly Tyr His Leu Lys Thr Leu Thr Leu Asn Phe Thr Ile Ser
1 5 10 15

Asn Leu Gln Tyr Ser Pro Asp Met Gly Lys Gly Ser Ala Thr Phe Asn
20 25 30

Ser Thr Glu Gly Val Leu Gln His Leu Leu
35 40

<210> 195

<211> 23

<212> PRT

<213> Homo sapiens

<400> 195

Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Ala Ser Leu Arg
20

<210> 196

<211> 23

<212> PRT

<213> Homo sapiens

<400> 196

Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 197

<211> 23

<212> PRT

<213> Homo sapiens

<400> 197

Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 198

<211> 23

<212> PRT

<213> Homo sapiens

<400> 198

Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 199

<211> 23

<212> PRT

<213> Homo sapiens

<400> 199

Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Ser
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 200

<211> 23

<212> PRT

<213> Homo sapiens

<400> 200

Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Ser Leu Arg
20

<210> 201

<211> 23

<212> PRT

<213> Homo sapiens

<400> 201

Leu Gly Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Ser Leu Arg
20

<210> 202

<211> 23

<212> PRT

<213> Homo sapiens

<400> 202

Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 203

<211> 23

<212> PRT

<213> Homo sapiens

<400> 203

Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 204

<211> 23

<212> PRT

<213> Homo sapiens

<400> 204

Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Ser Leu Arg
20

<210> 205

<211> 23

<212> PRT

<213> Homo sapiens

<400> 205

Leu Gly Pro Leu Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Ile Ser Leu Arg
20

<210> 206

<211> 23

<212> PRT

<213> Homo sapiens

<400> 206

Leu Gly Pro Leu Phe Lys Asn Ser Ser Val Asp Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Ser Leu Arg
20

<210> 207

<211> 23

<212> PRT

<213> Homo sapiens

<400> 207

Leu Ser Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Ser Leu Arg
20

<210> 208

<211> 23

<212> PRT

<213> Homo sapiens

<400> 208

Leu Ser Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 209

<211> 23

<212> PRT

<213> Homo sapiens

<400> 209

Leu Ser Pro Leu Phe Gln Arg Ser Ser Leu Gly Ala Arg Tyr Thr Gly
1 5 10 15

Cys Arg Val Ile Ala Leu Arg
20

<210> 210

<211> 23

<212> PRT

<213> Homo sapiens

<400> 210

Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 211

<211> 23

<212> PRT

<213> Homo sapiens

<400> 211

Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Ser Arg Leu Thr Leu Leu Arg
20

<210> 212

<211> 23

<212> PRT

<213> Homo sapiens

<400> 212

Leu Arg Pro Leu Phe Lys Asn Thr Ser Ile Gly Pro Leu Tyr Ser Ser
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 213

<211> 23

<212> PRT

<213> Homo sapiens

<400> 213

Leu Arg Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 214

<211> 23

<212> PRT

<213> Homo sapiens

<400> 214

Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 215

<211> 23

<212> PRT

<213> Homo sapiens

<400> 215

Leu Arg Pro Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 216

<211> 23

<212> PRT

<213> Homo sapiens

<400> 216

Leu Arg Ser Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 217

<211> 23

<212> PRT

<213> Homo sapiens

<400> 217

Leu Arg Ser Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Ser Leu Arg
20

<210> 218

<211> 23

<212> PRT

<213> Homo sapiens

<400> 218

Leu Thr Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 219

<211> 23

<212> PRT

<213> Homo sapiens

<400> 219

Leu Thr Pro Leu Phe Arg Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 220

<211> 23

<212> PRT

<213> Homo sapiens

<400> 220

Leu Met Pro Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly
1 5 10 15

Cys Arg Leu Thr Leu Leu Arg
20

<210> 221

<211> 22

<212> PRT

<213> Homo sapiens

<400> 221

Arg Pro Leu Phe Gln Lys Ser Ser Met Gly Pro Phe Tyr Leu Gly Cys
1 5 10 15

Gln Leu Ile Ser Leu Arg
20

<210> 222

<211> 58

<212> PRT

<213> Homo sapiens

<400> 222

Pro Glu Lys Asp Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His
1 5 10 15

Arg Pro Asp Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp
20 25 30

Glu Leu Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 223

<211> 58

<212> PRT

<213> Homo sapiens

<400> 223

Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His
1 5 10 15

Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 224

<211> 58

<212> PRT

<213> Homo sapiens

<400> 224

Pro Lys Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His
1 5 10 15

Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 225

<211> 58

<212> PRT

<213> Homo sapiens

<400> 225

Pro Glu Lys Asp Gly Thr Ala Thr Gly Val Asp Ala Ile Cys Thr His
1 5 10 15

His Pro Asp Pro Lys Ser Pro Arg Leu Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly His Tyr Ala
35 40 45

Leu Asp Asn Asp Ser Leu Phe Val Asn Gly
50 55

<210> 226

<211> 58

<212> PRT

<213> Homo sapiens

<400> 226

Pro Glu Lys Asp Gly Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His
1 5 10 15

Arg Pro Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Gln Leu Tyr Leu
20 25 30

Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
50 55

<210> 227

<211> 58

<212> PRT

<213> Homo sapiens

<400> 227

Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr
1 5 10 15

His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser
35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
50 55

<210> 228

<211> 58

<212> PRT

<213> Homo sapiens

<400> 228

Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu Tyr
1 5 10 15

His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu Tyr Cys
20 25 30

Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly Pro Tyr Ser
35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
50 55

<210> 229

<211> 58

<212> PRT

<213> Homo sapiens

<400> 229

Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Ala Cys Thr Tyr
1 5 10 15

Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Val Ser Leu Tyr Val Asn Gly
50 55

<210> 230

<211> 58

<212> PRT

<213> Homo sapiens

<400> 230

Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr
1 5 10 15

Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Gln Asp Arg Asp Ser Leu Tyr Val Asn Gly
50 55

<210> 231

<211> 58

<212> PRT

<213> Homo sapiens

<400> 231

Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr
1 5 10 15

Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Gln Asp Arg Asp Ser Leu Tyr Asn Val Gly
50 55

<210> 232

<211> 58

<212> PRT

<213> Homo sapiens

<400> 232

Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val Cys Thr His
1 5 10 15

Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp
20 25 30

Lys Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg His Ser Leu Tyr Val Asn Gly
50 55

<210> 233

<211> 58

<212> PRT

<213> Homo sapiens

<400> 233

Pro Glu Lys Asp Gly Val Ala Thr Arg Val Asp Ala Ile Cys Thr His
1 5 10 15

Arg Pro Asp Pro Lys Ile Pro Gly Leu Asp Arg Gln Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
50 55

<210> 234

<211> 58

<212> PRT

<213> Homo sapiens

<400> 234

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Ile His
1 5 10 15

His Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Arg Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 235

<211> 58

<212> PRT

<213> Homo sapiens

<400> 235

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His
1 5 10 15

Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 236

<211> 58

<212> PRT

<213> Homo sapiens

<400> 236

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His
1 5 10 15

Arg Leu Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 237

<211> 58

<212> PRT

<213> Homo sapiens

<400> 237

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His
1 5 10 15

Arg Val Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 238

<211> 58

<212> PRT

<213> Homo sapiens

<400> 238

Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His
1 5 10 15

His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Gln Leu Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 239

<211> 58

<212> PRT

<213> Homo sapiens

<400> 239

Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His
1 5 10 15

Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Lys Leu Thr Arg Gly Ile Ile Glu Leu Gly Pro Tyr Leu
35 40 45

Leu Asp Arg Gly Ser Leu Tyr Val Asn Gly
50 55

<210> 240

<211> 58

<212> PRT

<213> Homo sapiens

<400> 240

Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser His
1 5 10 15

Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 241

<211> 58

<212> PRT

<213> Homo sapiens

<400> 241

Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser His
1 5 10 15

Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
50 55

<210> 242

<211> 58

<212> PRT

<213> Homo sapiens

<400> 242

Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr Leu
1 5 10 15

Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
50 55

<210> 243

<211> 58

<212> PRT

<213> Homo sapiens

<400> 243

Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr Leu
1 5 10 15

Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
50 55

<210> 244

<211> 58

<212> PRT

<213> Homo sapiens

<400> 244

Pro Glu Lys His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His
1 5 10 15

Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
50 55

<210> 245

<211> 58

<212> PRT

<213> Homo sapiens

<400> 245

Pro Glu Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His
1 5 10 15

Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
50 55

<210> 246

<211> 58

<212> PRT

<213> Homo sapiens

<400> 246

Pro Glu Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His
1 5 10 15

Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asp Gly
50 55

<210> 247

<211> 58

<212> PRT

<213> Homo sapiens

<400> 247

Pro Glu Lys Asp Lys Ala Ala Thr Arg Val Asp Ala Ile Cys Thr His
1 5 10 15

His Pro Asp Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr
35 40 45

Leu Asp Arg Asp Ser Leu Tyr Val Asp Gly
50 55

<210> 248

<211> 58

<212> PRT

<213> Homo sapiens

<400> 248

Ser Val Lys Asn Gly Ala Glu Thr Arg Val Asp Leu Leu Cys Thr Tyr
1 5 10 15

Leu Gln Pro Leu Ser Gly Pro Gly Leu Pro Ile Lys Gln Val Phe His
20 25 30

Glu Leu Ser Gln Gln Thr His Gly Ile Thr Arg Leu Gly Pro Tyr Ser
35 40 45

Leu Asp Lys Asp Ser Leu Tyr Leu Asn Gly
50 55

<210> 249

<211> 58

<212> PRT

<213> Homo sapiens

<400> 249

Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr
1 5 10 15

His Pro Asp Pro Val Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp
20 25 30

Glu Leu Ser Gln Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val
35 40 45

Leu Asp Arg Asp Ser Leu Phe Ile Asn Gly
50 55

<210> 250

<211> 12

<212> PRT

<213> Homo sapiens

<400> 250

Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr
1 5 10

<210> 251

<211> 12

<212> PRT

<213> Homo sapiens

<400> 251

Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Ile
1 5 10

<210> 252

<211> 12

<212> PRT

<213> Homo sapiens

<400> 252

Phe Thr His Arg Thr Ser Val Pro Thr Ser Ser Thr
1 5 10

<210> 253

<211> 12

<212> PRT

<213> Homo sapiens

<400> 253

Phe Thr His Arg Thr Ser Val Pro Thr Thr Ser Thr
1 5 10

<210> 254

<211> 12

<212> PRT

<213> Homo sapiens

<400> 254

Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ser
1 5 10

<210> 255

<211> 12

<212> PRT

<213> Homo sapiens

<400> 255

Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser Thr
1 5 10

<210> 256

<211> 12

<212> PRT

<213> Homo sapiens

<400> 256

Phe Thr His Arg Ser Ser Val Ala Pro Thr Ser Thr
1 5 10

<210> 257

<211> 12

<212> PRT

<213> Homo sapiens

<400> 257

Phe Thr His Arg Ser Ser Gly Leu Thr Thr Ser Thr
1 5 10

<210> 258

<211> 12

<212> PRT

<213> Homo sapiens

<400> 258

Phe Thr His Arg Ser Phe Gly Leu Thr Thr Ser Thr
1 5 10

<210> 259

<211> 12

<212> PRT

<213> Homo sapiens

<400> 259

Phe Thr His Arg Ser Ser Phe Leu Thr Thr Ser Thr
1 5 10

<210> 260

<211> 12

<212> PRT

<213> Homo sapiens

<400> 260

Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr
1 5 10

<210> 261

<211> 12

<212> PRT

<213> Homo sapiens

<400> 261

Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile
1 5 10

<210> 262

<211> 12

<212> PRT

<213> Homo sapiens

<400> 262

Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr
1 5 10

<210> 263

<211> 12

<212> PRT

<213> Homo sapiens

<400> 263

Phe Thr His Gln Thr Ser Ala Pro Asn Thr Ser Thr
1 5 10

<210> 264

<211> 12

<212> PRT

<213> Homo sapiens

<400> 264

Phe Thr His Gln Thr Phe Ala Pro Asn Thr Ser Thr
1 5 10

<210> 265

<211> 12

<212> PRT

<213> Homo sapiens

<400> 265

Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser Thr
1 5 10

<210> 266

<211> 12

<212> PRT

<213> Homo sapiens

<400> 266

Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg Thr
1 5 10

<210> 267

<211> 12

<212> PRT

<213> Homo sapiens

<400> 267

Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr
1 5 10

<210> 268

<211> 12

<212> PRT

<213> Homo sapiens

<400> 268

Phe Thr His Trp Ser Pro Ile Pro Thr Thr Ser Thr
1 5 10

<210> 269

<211> 12

<212> PRT

<213> Homo sapiens

<400> 269

Phe Thr His Trp Ser Ser Gly Leu Thr Thr Ser Thr
1 5 10

<210> 270

<211> 12

<212> PRT

<213> Homo sapiens

<400> 270

Phe His Pro Arg Ser Ser Val Pro Thr Thr Ser Thr
1 5 10

<210> 271

<211> 12

<212> PRT

<213> Homo sapiens

<400> 271

Phe Asn Pro Arg Ser Ser Val Pro Thr Thr Ser Thr
1 5 10

<210> 272

<211> 12

<212> PRT

<213> Homo sapiens

<400> 272

Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr
1 5 10

<210> 273

<211> 12

<212> PRT

<213> Homo sapiens

<400> 273

Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Ile
1 5 10

<210> 274

<211> 12

<212> PRT

<213> Homo sapiens

<400> 274

Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Thr
1 5 10

<210> 275

<211> 12

<212> PRT

<213> Homo sapiens

<400> 275

Phe Thr Gln Arg Ser Ser Val Pro Thr Thr Ser Val
1 5 10

<210> 276

<211> 12

<212> PRT

<213> Homo sapiens

<400> 276

Tyr Asn Glu Pro Gly Leu Asp Glu Pro Pro Thr Thr
1 5 10

<210> 277

<211> 12

<212> PRT

<213> Homo sapiens

<400> 277

Tyr Ala Pro Gln Asn Leu Ser Ile Arg Gly Glu Tyr
1 5 10

<210> 278

<211> 21

<212> PRT

<213> Homo sapiens

<400> 278

Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser
1 5 10 15

Ser Pro Ser Pro Thr
20

<210> 279

<211> 23

<212> PRT

<213> Homo sapiens

<400> 279

Pro Gly Thr Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser
1 5 10 15

Leu Ser Ser Pro Thr Ile Met
20

<210> 280

<211> 21

<212> PRT

<213> Homo sapiens

<400> 280

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Phe Ser
1 5 10 15

Leu Pro Ser Pro Ala
20

<210> 281

<211> 20

<212> PRT

<213> Homo sapiens

<400> 281

Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu
1 5 10 15

Pro Ser Pro Thr
20

<210> 282

<211> 20

<212> PRT

<213> Homo sapiens

<400> 282

Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Leu Pro
1 5 10 15

Ser Ser Pro Thr
20

<210> 283

<211> 21

<212> PRT

<213> Homo sapiens

<400> 283

Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser
1 5 10 15

Leu Pro Ser Pro Thr
20

<210> 284

<211> 21

<212> PRT

<213> Homo sapiens

<400> 284

Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Val Ser
1 5 10 15

Lys Pro Gly Pro Ser
20

<210> 285

<211> 21

<212> PRT

<213> Homo sapiens

<400> 285

Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro
1 5 10 15

Val Pro Ser Pro Thr
20

<210> 286

<211> 21

<212> PRT

<213> Homo sapiens

<400> 286

Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser
1 5 10 15

Phe Pro Gly His Thr
20

<210> 287

<211> 21

<212> PRT

<213> Homo sapiens

<400> 287

Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser
1 5 10 15

Leu Pro Gly His Thr
20

<210> 288

<211> 21

<212> PRT

<213> Homo sapiens

<400> 288

Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Pro
1 5 10 15

Leu Pro Gly His Thr
20

<210> 289

<211> 21

<212> PRT

<213> Homo sapiens

<400> 289

Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro Ala Ser
1 5 10 15

Leu Ser Gly Pro Thr
20

<210> 290

<211> 21

<212> PRT

<213> Homo sapiens

<400> 290

Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala Ser
1 5 10 15

Leu Pro Gly His Thr
20

<210> 291

<211> 21

<212> PRT

<213> Homo sapiens

<400> 291

Pro Gly Thr Ser Ala Val His Leu Glu Thr Thr Gly Thr Pro Ser Ser
1 5 10 15

Phe Pro Gly His Thr
20

<210> 292

<211> 21

<212> PRT

<213> Homo sapiens

<400> 292

Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser Ser
1 5 10 15

Leu Pro Arg Pro Ile
20

<210> 293

<211> 21

<212> PRT

<213> Homo sapiens

<400> 293

Pro Gly Thr Ser Ile Val Asn Leu Gly Thr Ser Gly Ile Pro Pro Ser
1 5 10 15

Leu Pro Glu Thr Thr
20

<210> 294

<211> 21

<212> PRT

<213> Homo sapiens

<400> 294

Pro Gly Thr Phe Thr Val Gln Pro Glu Thr Ser Glu Thr Pro Ser Ser
1 5 10 15

Leu Pro Gly Pro Thr
20

<210> 295

<211> 21

<212> PRT

<213> Homo sapiens

<400> 295

Pro Gly Thr Pro Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Val Ser
1 5 10 15

Lys Pro Gly Pro Ser
20

<210> 296

<211> 21

<212> PRT

<213> Homo sapiens

<400> 296

Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala Ser
1 5 10 15

Ile Phe Gly Pro Ser
20

<210> 297

<211> 16

<212> PRT

<213> Homo sapiens

<400> 297

Pro Lys Pro Ala Thr Thr Phe Leu Pro Pro Leu Ser Glu Ala Thr Thr
1 5 10 15

<210> 298

<211> 21

<212> PRT

<213> Homo sapiens

<400> 298

Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu Ser Asn Pro Asp Pro
1 5 10 15

Thr Ser Ser Glu Tyr
20

<210> 299

<211> 1794

<212> PRT

<213> Homo sapiens

<400> 299

Met Glu His Ile Thr Lys Ile Pro Asn Glu Ala Ala His Arg Gly Thr
1 5 10 15

Ile Arg Pro Val Lys Gly Pro Gln Thr Ser Thr Ser Pro Ala Ser Pro
20 25 30

Lys Gly Leu His Thr Gly Gly Thr Lys Arg Met Glu Thr Thr Thr Thr
35 40 45

Ala Leu Lys Thr Thr Thr Thr Ala Leu Lys Thr Thr Ser Arg Ala Thr
50 55 60

Leu Thr Thr Ser Val Tyr Thr Pro Thr Leu Gly Thr Leu Thr Pro Leu
65 70 75 80

Asn Ala Ser Arg Gln Met Ala Ser Thr Ile Leu Thr Glu Met Met Ile
85 90 95

Thr Thr Pro Tyr Val Phe Pro Asp Val Pro Glu Thr Thr Ser Ser Leu
100 105 110

Ala Thr Ser Leu Gly Ala Glu Thr Ser Thr Ala Leu Pro Arg Thr Thr
115 120 125

Pro Ser Val Leu Asn Arg Glu Ser Glu Thr Thr Ala Ser Leu Val Ser
130 135 140

Arg Ser Gly Ala Glu Arg Ser Pro Val Ile Gln Thr Leu Asp Val Ser
145 150 155 160

Ser Ser Glu Pro Asp Thr Thr Ala Ser Trp Val Ile His Pro Ala Glu
165 170 175

Thr Ile Pro Thr Val Ser Lys Thr Thr Pro Asn Phe Phe His Ser Glu
180 185 190

Leu Asp Thr Val Ser Ser Thr Ala Thr Ser His Gly Ala Asp Val Ser
195 200 205

Ser Ala Ile Pro Thr Asn Ile Ser Pro Ser Glu Leu Asp Ala Leu Thr
210 215 220

Pro Leu Val Thr Ile Ser Gly Thr Asp Thr Ser Thr Thr Phe Pro Thr
225 230 235 240

Leu Thr Lys Ser Pro His Glu Thr Glu Thr Arg Thr Thr Trp Leu Thr
245 250 255

His Pro Ala Glu Thr Ser Ser Thr Ile Pro Arg Thr Ile Pro Asn Phe
260 265 270

Ser His His Glu Ser Asp Ala Thr Pro Ser Ile Ala Thr Ser Pro Gly
275 280 285

Ala Glu Thr Ser Ser Ala Ile Pro Ile Met Thr Val Ser Pro Gly Ala
290 295 300

Glu Asp Leu Val Thr Ser Gln Val Thr Ser Ser Gly Thr Asp Arg Asn
305 310 315 320

Met Thr Ile Pro Thr Leu Thr Leu Ser Pro Gly Glu Pro Lys Thr Ile
325 330 335

Ala Ser Leu Val Thr His Pro Glu Ala Gln Thr Ser Ser Ala Ile Pro
340 345 350

Thr Ser Thr Ile Ser Pro Ala Val Ser Arg Leu Val Thr Ser Met Val
355 360 365

Thr Ser Leu Ala Ala Lys Thr Ser Thr Thr Asn Arg Ala Leu Thr Asn
370 375 380

Ser Pro Gly Glu Pro Ala Thr Thr Val Ser Leu Val Thr His Pro Ala
385 390 395 400

Gln Thr Ser Pro Thr Val Pro Trp Thr Thr Ser Ile Phe Phe His Ser
405 410 415

Lys Ser Asp Thr Thr Pro Ser Met Thr Thr Ser His Gly Ala Glu Ser
420 425 430

Ser Ser Ala Val Pro Thr Pro Thr Val Ser Thr Glu Val Pro Gly Val
435 440 445

Val Thr Pro Leu Val Thr Ser Ser Arg Ala Val Ile Ser Thr Thr Ile
450 455 460

Pro Ile Leu Thr Leu Ser Pro Gly Glu Pro Glu Thr Thr Pro Ser Met
465 470 475 480

Ala Thr Ser His Gly Glu Glu Ala Ser Ser Ala Ile Pro Thr Pro Thr
485 490 495

Val Ser Pro Gly Val Pro Gly Val Val Thr Ser Leu Val Thr Ser Ser
500 505 510

Arg Ala Val Thr Ser Thr Thr Ile Pro Ile Leu Thr Phe Ser Leu Gly
515 520 525

Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His Gly Thr Glu Ala
530 535 540

Gly Ser Ala Val Pro Thr Val Leu Pro Glu Val Pro Gly Met Val Thr
545 550 555 560

Ser Leu Val Ala Ser Ser Arg Ala Val Thr Ser Thr Thr Leu Pro Thr
565 570 575

Leu Thr Leu Ser Pro Gly Glu Pro Glu Thr Thr Pro Ser Met Ala Thr
580 585 590

Ser His Gly Ala Glu Ala Ser Ser Thr Val Pro Thr Val Ser Pro Glu
595 600 605

Val Pro Gly Val Val Thr Ser Leu Val Thr Ser Ser Ser Gly Val Asn
610 615 620

Ser Thr Ser Ile Pro Thr Leu Ile Leu Ser Pro Gly Glu Leu Glu Thr
625 630 635 640

Thr Pro Ser Met Ala Thr Ser His Gly Ala Glu Ala Ser Ser Ala Val
645 650 655

Pro Thr Pro Thr Val Ser Pro Gly Val Ser Gly Val Val Thr Pro Leu
660 665 670

Val Thr Ser Ser Arg Ala Val Thr Ser Thr Thr Ile Pro Ile Leu Thr
675 680 685

Leu Ser Ser Ser Glu Pro Glu Thr Thr Pro Ser Met Ala Thr Ser His
690 695 700

Gly Val Glu Ala Ser Ser Ala Val Leu Thr Val Ser Pro Glu Val Pro
705 710 715 720

Gly Met Val Thr Ser Leu Val Thr Ser Ser Arg Ala Val Thr Ser Thr
725 730 735

Thr Ile Pro Thr Leu Thr Ile Ser Ser Asp Glu Pro Glu Thr Thr Thr
740 745 750

Ser Leu Val Thr His Ser Glu Ala Lys Met Ile Ser Ala Ile Pro Thr
755 760 765

Leu Ala Val Ser Pro Thr Val Gln Gly Leu Val Thr Ser Leu Val Thr
770 775 780

Ser Ser Gly Ser Glu Thr Ser Ala Phe Ser Asn Leu Thr Val Ala Ser
785 790 795 800

Ser Gln Pro Glu Thr Ile Asp Ser Trp Val Ala His Pro Gly Thr Glu
805 810 815

Ala Ser Ser Val Val Pro Thr Leu Thr Val Ser Thr Gly Glu Pro Phe
820 825 830

Thr Asn Ile Ser Leu Val Thr His Pro Ala Glu Ser Ser Ser Thr Leu
835 840 845

Pro Arg Thr Thr Ser Arg Phe Ser His Ser Glu Leu Asp Thr Met Pro
850 855 860

Ser Thr Val Thr Ser Pro Glu Ala Glu Ser Ser Ser Ala Ile Ser Thr
865 870 875 880

Thr Ile Ser Pro Gly Ile Pro Gly Val Leu Thr Ser Leu Val Thr Ser
885 890 895

Ser Gly Arg Asp Ile Ser Ala Thr Phe Pro Thr Val Pro Glu Ser Pro
900 905 910

His Glu Ser Glu Ala Thr Ala Ser Trp Val Thr His Pro Ala Val Thr
915 920 925

Ser Thr Thr Val Pro Arg Thr Thr Pro Asn Tyr Ser His Ser Glu Pro
930 935 940

Asp Thr Thr Pro Ser Ile Ala Thr Ser Pro Gly Ala Glu Ala Thr Ser
945 950 955 960

Asp Phe Pro Thr Ile Thr Val Ser Pro Asp Val Pro Asp Met Val Thr
965 970 975

Ser Gln Val Thr Ser Ser Gly Thr Asp Thr Ser Ile Thr Ile Pro Thr
980 985 990

Leu Thr Leu Ser Ser Gly Glu Pro Glu Thr Thr Thr Ser Phe Ile Thr
995 1000 1005

Tyr Ser Glu Thr His Thr Ser Ser Ala Ile Pro Thr Leu Pro Val
1010 1015 1020

Ser Pro Gly Ala Ser Lys Met Leu Thr Ser Leu Val Ile Ser Ser
1025 1030 1035

Gly Thr Asp Ser Thr Thr Thr Phe Pro Thr Leu Thr Glu Thr Pro
1040 1045 1050

Tyr Glu Pro Glu Thr Thr Ala Ile Gln Leu Ile His Pro Ala Glu
1055 1060 1065

Thr Asn Thr Met Val Pro Arg Thr Thr Pro Lys Phe Ser His Ser
1070 1075 1080

Lys Ser Asp Thr Thr Leu Pro Val Ala Ile Thr Ser Pro Gly Pro
1085 1090 1095

Glu Ala Ser Ser Ala Val Ser Thr Thr Thr Ile Ser Pro Asp Met
1100 1105 1110

Ser Asp Leu Val Thr Ser Leu Val Pro Ser Ser Gly Thr Asp Thr
1115 1120 1125

Ser Thr Thr Phe Pro Thr Leu Ser Glu Thr Pro Tyr Glu Pro Glu
1130 1135 1140

Thr Thr Ala Thr Trp Leu Thr His Pro Ala Glu Thr Ser Thr Thr
1145 1150 1155

Val Ser Gly Thr Ile Pro Asn Phe Ser His Arg Gly Ser Asp Thr
1160 1165 1170

Ala Pro Ser Met Val Thr Ser Pro Gly Val Asp Thr Arg Ser Gly
1175 1180 1185

Val Pro Thr Thr Thr Ile Pro Pro Ser Ile Pro Gly Val Val Thr
1190 1195 1200

Ser Gln Val Thr Ser Ser Ala Thr Asp Thr Ser Thr Ala Ile Pro
1205 1210 1215

Thr Leu Thr Pro Ser Pro Gly Glu Pro Glu Thr Thr Ala Ser Ser
1220 1225 1230

Ala Thr His Pro Gly Thr Gln Thr Gly Phe Thr Val Pro Ile Arg
1235 1240 1245

Thr Val Pro Ser Ser Glu Pro Asp Thr Met Ala Ser Trp Val Thr
1250 1255 1260

His Pro Pro Gln Thr Ser Thr Pro Val Ser Arg Thr Thr Ser Ser
1265 1270 1275

Phe Ser His Ser Ser Pro Asp Ala Thr Pro Val Met Ala Thr Ser
1280 1285 1290

Pro Arg Thr Glu Ala Ser Ser Ala Val Leu Thr Thr Ile Ser Pro
1295 1300 1305

Gly Ala Pro Glu Met Val Thr Ser Gln Ile Thr Ser Ser Gly Ala
1310 1315 1320

Ala Thr Ser Thr Thr Val Pro Thr Leu Thr His Ser Pro Gly Met
1325 1330 1335

Pro Glu Thr Thr Ala Leu Leu Ser Thr His Pro Arg Thr Glu Thr
1340 1345 1350

Ser Lys Thr Phe Pro Ala Ser Thr Val Phe Pro Gln Val Ser Glu
1355 1360 1365

Thr Thr Ala Ser Leu Thr Ile Arg Pro Gly Ala Glu Thr Ser Thr
1370 1375 1380

Ala Leu Pro Thr Gln Thr Thr Ser Ser Leu Phe Thr Leu Leu Val
1385 1390 1395

Thr Gly Thr Ser Arg Val Asp Leu Ser Pro Thr Ala Ser Pro Gly
1400 1405 1410

Val Ser Ala Lys Thr Ala Pro Leu Ser Thr His Pro Gly Thr Glu
1415 1420 1425

Thr Ser Thr Met Ile Pro Thr Ser Thr Leu Ser Leu Gly Leu Leu
1430 1435 1440

Glu Thr Thr Gly Leu Leu Ala Thr Ser Ser Ser Ala Glu Thr Ser
1445 1450 1455

Thr Ser Thr Leu Thr Leu Thr Val Ser Pro Ala Val Ser Gly Leu
1460 1465 1470

Ser Ser Ala Ser Ile Thr Thr Asp Lys Pro Gln Thr Val Thr Ser
1475 1480 1485

Trp Asn Thr Glu Thr Ser Pro Ser Val Thr Ser Val Gly Pro Pro
1490 1495 1500

FIRST COATING LAYER

As indicated above, the first coating layer is substantially non-porous and comprises at least one hydrophilic polymer. Accordingly, the first coating layer has the ability to quickly absorb relatively large amounts of ink, commonly employed in backlit printing, and avoid or minimize bleeding of the dye or pigment in the ink. Organic polymers with good water and solvent absorption are employed in the first coating layer. When the printed image is to be view through the substrate, both the substrate and the first coating layer should be either transparent or translucent. Additionally, the first coating layer should comprise a light-transmissive polymer or resin capable of absorbing the ink and/or a light-transmissive polymer or resin having solubility and swelling properties compatible to the ink. The polymers comprising the first coating layer may not be particularly limited if they function to absorb and capture the ink and/or dye or pigment components of the ink and are capable of forming a substantially non-porous layer. Coating compositions of the first coating layer can be applied to the substrate by means of a roller coater, a knife coater, wire wound rod, or any conventional coating method.

The first coating layer comprises at least one hydrophilic polymer, at least one cationic resin, or a combination thereof. Hydrophilic polymers may be natural or synthetic and include, but are not limited to, polyvinyl pyrrolidone, polyvinyl alcohol, acrylic polymers, copolymers which possess hydrophilic groups such as hydroxy or carboxy, cellulose polymers, starch, gelatin, albumin, casein, cation starch, natural resins such as gum arabic and sodium alginate, polyamide, polyacrylamide, polyethylene imine, polyvinyl pyridylium halide, melamine resin, polyurethane, polyester, and sodium polyacrylate, natural or synthetic hydrophobic polymers modified by making these polymers insoluble in water and water absorbing, and the like. Combinations of such polymers may also be employed in the present invention.

Leu Ala Ser Leu Arg Pro Glu Lys Asp Ser Ser Ala Met Ala Val
1700 1705 1710

Asp Ala Ile Cys Thr His Arg Pro Asp Pro Glu Asp Leu Gly Leu
1715 1720 1725

Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Asn Leu Thr Asn Gly
1730 1735 1740

Ile Gln Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr
1745 1750 1755

Val Asn Gly Phe Thr His Arg Ser Ser Met Pro Thr Thr Ser Thr
1760 1765 1770

Pro Gly Thr Ser Thr Val Asp Val Gly Thr Ser Gly Thr Pro Ser
1775 1780 1785

Ser Ser Pro Ser Pro Thr
1790

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<211> 284

<212> PRT

<213> Homo sapiens

<400> 300

Ile Thr Leu Leu Arg Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys
1 5 10 15

Gly Ser Gln Leu His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu
20 25 30

Thr Met Asp Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn
35 40 45

Leu Asp Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn
50 55 60

Ala Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His
65 70 75 80

Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser Ser
85 90 95

Thr Gln His Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu Pro Tyr Ser
100 105 110

Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg Asn Lys Arg
115 120 125

Asn Ile Glu Asp Ala Leu Asn Gln Leu Phe Arg Asn Ser Ser Ile Lys
130 135 140

Ser Tyr Phe Ser Asp Cys Gln Val Ser Thr Phe Arg Ser Val Pro Asn
145 150 155 160

Arg His His Thr Gly Val Asp Ser Leu Cys Asn Phe Ser Pro Leu Ala
165 170 175

Arg Arg Val Asp Arg Val Ala Ile Tyr Glu Glu Phe Leu Arg Met Thr
180 185 190

Arg Asn Gly Thr Gln Leu Gln Asn Phe Thr Leu Asp Arg Ser Ser Val
195 200 205

Leu Val Asp Gly Tyr Ser Pro Asn Arg Asn Glu Pro Leu Thr Gly Asn
210 215 220

Ser Asp Leu Pro Phe Trp Ala Val Ile Leu Ile Gly Leu Ala Gly Leu
225 230 235 240

Leu Gly Leu Ile Thr Cys Leu Ile Cys Gly Val Leu Val Thr Thr Arg
245 250 255

Arg Arg Lys Lys Glu Gly Glu Tyr Asn Val Gln Gln Gln Cys Pro Gly
260 265 270

Tyr Tyr Gln Ser His Leu Asp Leu Glu Asp Leu Gln
275 280

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gtctctatgt caatggtttc accc 24

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ggacaaggtc accacactct ac 22

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gcagatcctc caggtctagg tgtg 24

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gtctctatgt caatggtttc accc 24

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<212> DNA

<213> Homo sapiens

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actgctggcc ctctcctggt gccattcacc ctcaacttca ccatcaccaa cctgcagtat 60

gaggaggaca tgcatcgccc tggatctagg aagttcaaca ccacagagag ggtcctgcag 120

ggtctgctta gtcccatatt caagaacacc agtgttggcc ctctgtactc tggctgcaga 180

ctgacctctc tcaggtctga gaaggatgga gcagccactg gagtggatgc catctgcatc 240

catcatcttg accccaaaag ccctggactc aacagagagc ggctgtactg ggagctgagc 300

cgactgacca atggcatcaa agagctgggc ccctacaccc tggacaggaa cagtctctat 360

gtcaatggtt tcacccatcg gacctctgtg cccaccacca gcactcctgg gacctccaca 420

gtggaccttg gaacctcagg gactccattc tccctcccaa gccccgca 468

<210> 308

<211> 156

<212> PRT

<213> Homo sapiens

<400> 308

Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr
1 5 10 15

Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe
20 25 30

Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys
35 40 45

Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu
50 55 60

Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Ile
65 70 75 80

His His Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Arg Leu Tyr
85 90 95

Trp Glu Leu Ser Arg Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr
100 105 110

Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Thr
115 120 125

Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly
130 135 140

Thr Ser Gly Thr Pro Phe Ser Leu Pro Ser Pro Ala
145 150 155

<210> 309

<211> 31497

<212> DNA

<213> Homo sapiens

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cccaggtcaa atgcggggac cccagccata tctcccaccc tgagaaattt tggagtttca 120

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gggagctcag aagctctgca gaggccaccc tctctgaggg gattcttctt agacctccat    180

ccagaggcaa atgttgacct gtcc atg ctg aaa ccc tca ggc ctt cct ggg       231
                              Met Leu Lys Pro Ser Gly Leu Pro Gly
                              1               5

tca tct tct ccc acc cgc tcc ttg atg aca ggg agc agg agc act aaa       279
Ser Ser Ser Pro Thr Arg Ser Leu Met Thr Gly Ser Arg Ser Thr Lys
10                  15                  20                  25

gcc aca cca gaa atg gat tca gga ctg aca gga gcc acc ttg tca cct       327
Ala Thr Pro Glu Met Asp Ser Gly Leu Thr Gly Ala Thr Leu Ser Pro
                30                  35                  40

aag aca tct aca ggt gca atc gtg gtg aca gaa cat act ctg ccc ttt       375
Lys Thr Ser Thr Gly Ala Ile Val Val Thr Glu His Thr Leu Pro Phe
            45                  50                  55

act tcc cca gat aag acc ttg gcc agt cct aca tct tcg gtt gtg gga       423
Thr Ser Pro Asp Lys Thr Leu Ala Ser Pro Thr Ser Ser Val Val Gly
        60                  65                  70

aga acc acc cag tct ttg ggg gtg atg tcc tct gct ctc cct gag tca       471
Arg Thr Thr Gln Ser Leu Gly Val Met Ser Ser Ala Leu Pro Glu Ser
    75                  80                  85

acc tct aga gga atg aca cac tcc gag caa aga acc agc cca tcg ctg       519
Thr Ser Arg Gly Met Thr His Ser Glu Gln Arg Thr Ser Pro Ser Leu
90                  95                  100                 105

agt ccc cag gtc aat gga act ccc tct agg aac tac cct gct aca agc       567
Ser Pro Gln Val Asn Gly Thr Pro Ser Arg Asn Tyr Pro Ala Thr Ser
                110                 115                 120

atg gtt tca gga ttg agt tcc cca agg acc agg acc agt tcc aca gaa       615
Met Val Ser Gly Leu Ser Ser Pro Arg Thr Arg Thr Ser Ser Thr Glu
            125                 130                 135

gga aat ttt acc aaa gaa gca tct aca tac aca ctc act gta gag acc       663
Gly Asn Phe Thr Lys Glu Ala Ser Thr Tyr Thr Leu Thr Val Glu Thr
        140                 145                 150

aca agt ggc cca gtc act gag aag tac aca gtc ccc act gag acc tca       711
Thr Ser Gly Pro Val Thr Glu Lys Tyr Thr Val Pro Thr Glu Thr Ser
    155                 160                 165

aca act gaa ggt gac agc aca gag acc ccc tgg gac aca aga tat att       759
Thr Thr Glu Gly Asp Ser Thr Glu Thr Pro Trp Asp Thr Arg Tyr Ile
170                 175                 180                 185

cct gta aaa atc aca tct cca atg aaa aca ttt gca gat tca act gca       807
Pro Val Lys Ile Thr Ser Pro Met Lys Thr Phe Ala Asp Ser Thr Ala
                190                 195                 200
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tcc aag gaa aat gcc cca gtg tct atg act cca gct gag acc aca gtt      855
Ser Lys Glu Asn Ala Pro Val Ser Met Thr Pro Ala Glu Thr Thr Val
            205                 210                 215

act gac tca cat act cca gga agg aca aac cca tca ttt ggg aca ctt      903
Thr Asp Ser His Thr Pro Gly Arg Thr Asn Pro Ser Phe Gly Thr Leu
        220                 225                 230

tat tct tcc ttc ctt gac cta tca cct aaa ggg acc cca aat tcc aga      951
Tyr Ser Ser Phe Leu Asp Leu Ser Pro Lys Gly Thr Pro Asn Ser Arg
    235                 240                 245

ggt gaa aca agc ctg gaa ctg att cta tca acc act gga tat ccc ttc      999
Gly Glu Thr Ser Leu Glu Leu Ile Leu Ser Thr Thr Gly Tyr Pro Phe
250                 255                 260                 265

tcc tct cct gaa cct ggc tct gca gga cac agc aga ata agt acc agt     1047
Ser Ser Pro Glu Pro Gly Ser Ala Gly His Ser Arg Ile Ser Thr Ser
                270                 275                 280

gcg cct ttg tca tca tct gct tca gtt ctc gat aat aaa ata tca gag     1095
Ala Pro Leu Ser Ser Ser Ala Ser Val Leu Asp Asn Lys Ile Ser Glu
            285                 290                 295

acc agc ata ttc tca ggc cag agt ctc acc tcc cct ctg tct cct ggg     1143
Thr Ser Ile Phe Ser Gly Gln Ser Leu Thr Ser Pro Leu Ser Pro Gly
        300                 305                 310

gtg ccc gag gcc aga gcc agc aca atg ccc aac tca gct atc cct ttt     1191
Val Pro Glu Ala Arg Ala Ser Thr Met Pro Asn Ser Ala Ile Pro Phe
    315                 320                 325

tcc atg aca cta agc aat gca gaa aca agt gcc gaa agg gtc aga agc     1239
Ser Met Thr Leu Ser Asn Ala Glu Thr Ser Ala Glu Arg Val Arg Ser
330                 335                 340                 345

aca att tcc tct ctg ggg act cca tca ata tcc aca aag cag aca gca     1287
Thr Ile Ser Ser Leu Gly Thr Pro Ser Ile Ser Thr Lys Gln Thr Ala
                350                 355                 360

gag act atc ctt acc ttc cat gcc ttc gct gag acc atg gat ata ccc     1335
Glu Thr Ile Leu Thr Phe His Ala Phe Ala Glu Thr Met Asp Ile Pro
            365                 370                 375

agc acc cac ata gcc aag act ttg gct tca gaa tgg ttg gga agt cca     1383
Ser Thr His Ile Ala Lys Thr Leu Ala Ser Glu Trp Leu Gly Ser Pro
        380                 385                 390

ggt acc ctt ggt ggc acc agc act tca gcg ctg aca acc aca tct cca     1431
Gly Thr Leu Gly Gly Thr Ser Thr Ser Ala Leu Thr Thr Thr Ser Pro
    395                 400                 405

tct acc act tta gtc tca gag gag acc aac acc cat cac tcc acg agt     1479
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Ser Thr Thr Leu Val Ser Glu Glu Thr Asn Thr His His Ser Thr Ser
410                 415                 420                 425

gga aag gaa aca gaa gga act ttg aat aca tct atg act cca ctt gag     1527
Gly Lys Glu Thr Glu Gly Thr Leu Asn Thr Ser Met Thr Pro Leu Glu
                430                 435                 440

acc tct gct cct gga gaa gag tcc gaa atg act gcc acc ttg gtc ccc     1575
Thr Ser Ala Pro Gly Glu Glu Ser Glu Met Thr Ala Thr Leu Val Pro
            445                 450                 455

act cta ggt ttt aca act ctt gac agc aag atc aga agt cca tct cag     1623
Thr Leu Gly Phe Thr Thr Leu Asp Ser Lys Ile Arg Ser Pro Ser Gln
        460                 465                 470

gtc tct tca tcc cac cca aca aga gag ctc aga acc aca ggc agc acc     1671
Val Ser Ser Ser His Pro Thr Arg Glu Leu Arg Thr Thr Gly Ser Thr
    475                 480                 485

tct ggg agg cag agt tcc agc aca gct gcc cac ggg agc tct gac atc     1719
Ser Gly Arg Gln Ser Ser Ser Thr Ala Ala His Gly Ser Ser Asp Ile
490                 495                 500                 505

ctg agg gca acc act tcc agc acc tca aaa gca tca tca tgg acc agt     1767
Leu Arg Ala Thr Thr Ser Ser Thr Ser Lys Ala Ser Ser Trp Thr Ser
                510                 515                 520

gaa agc aca gct cag caa ttt agt gaa ccc cag cac aca cag tgg gtg     1815
Glu Ser Thr Ala Gln Gln Phe Ser Glu Pro Gln His Thr Gln Trp Val
            525                 530                 535

gag aca agt cct agc atg aaa aca gag aga ccc cca gca tca acc agt     1863
Glu Thr Ser Pro Ser Met Lys Thr Glu Arg Pro Pro Ala Ser Thr Ser
        540                 545                 550

gtg gca gcc cct atc acc act tct gtt ccc tca gtg gtc tct ggc ttc     1911
Val Ala Ala Pro Ile Thr Thr Ser Val Pro Ser Val Val Ser Gly Phe
    555                 560                 565

acc acc ctg aag acc agc tcc aca aaa ggg att tgg ctt gaa gaa aca     1959
Thr Thr Leu Lys Thr Ser Ser Thr Lys Gly Ile Trp Leu Glu Glu Thr
570                 575                 580                 585

tct gca gac aca ctc atc gga gaa tcc aca gct ggc cca acc acc cat     2007
Ser Ala Asp Thr Leu Ile Gly Glu Ser Thr Ala Gly Pro Thr Thr His
                590                 595                 600

cag ttt gct gtt ccc act ggg att tca atg aca gga ggc agc agc acc     2055
Gln Phe Ala Val Pro Thr Gly Ile Ser Met Thr Gly Gly Ser Ser Thr
            605                 610                 615

agg gga agc cag ggc aca acc cac cta ctc acc aga gcc aca gca tca     2103
Arg Gly Ser Gln Gly Thr Thr His Leu Leu Thr Arg Ala Thr Ala Ser
        620                 625                 630
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tct gag aca tcc gca gat ttg act ctg gcc acg aac ggt gtc cca gtc      2151
Ser Glu Thr Ser Ala Asp Leu Thr Leu Ala Thr Asn Gly Val Pro Val
    635                 640                 645

tcc gtg tct cca gca gtg agc aag acg gct gct ggc tca agt cct cca      2199
Ser Val Ser Pro Ala Val Ser Lys Thr Ala Ala Gly Ser Ser Pro Pro
650                 655                 660                 665

gga ggg aca aag cca tca tat aca atg gtt tct tct gtc atc cct gag      2247
Gly Gly Thr Lys Pro Ser Tyr Thr Met Val Ser Ser Val Ile Pro Glu
                670                 675                 680

aca tca tct cta cag tcc tca gct ttc agg gaa gga acc agc ctg gga      2295
Thr Ser Ser Leu Gln Ser Ser Ala Phe Arg Glu Gly Thr Ser Leu Gly
            685                 690                 695

ctg act cca tta aac act aga cat ccc ttc tct tcc cct gaa cca gac      2343
Leu Thr Pro Leu Asn Thr Arg His Pro Phe Ser Ser Pro Glu Pro Asp
        700                 705                 710

tct gca gga cac acc aag ata agc acc agc att cct ctg ttg tca tct      2391
Ser Ala Gly His Thr Lys Ile Ser Thr Ser Ile Pro Leu Leu Ser Ser
    715                 720                 725

gct tca gtt ctt gag gat aaa gtg tca gcg acc agc aca ttc tca cac      2439
Ala Ser Val Leu Glu Asp Lys Val Ser Ala Thr Ser Thr Phe Ser His
730                 735                 740                 745

cac aaa gcc acc tca tct att acc aca ggg act cct gaa atc tca aca      2487
His Lys Ala Thr Ser Ser Ile Thr Thr Gly Thr Pro Glu Ile Ser Thr
                750                 755                 760

aag aca aag ccc agc tca gcc gtt ctt tcc tcc atg acc cta agc aat      2535
Lys Thr Lys Pro Ser Ser Ala Val Leu Ser Ser Met Thr Leu Ser Asn
            765                 770                 775

gca gca aca agt cct gaa aga gtc aga aat gca act tcc cct ctg act      2583
Ala Ala Thr Ser Pro Glu Arg Val Arg Asn Ala Thr Ser Pro Leu Thr
        780                 785                 790

cat cca tct cca tca ggg gaa gag aca gca ggg agt gtc ctc act ctc      2631
His Pro Ser Pro Ser Gly Glu Glu Thr Ala Gly Ser Val Leu Thr Leu
    795                 800                 805

agc acc tct gct gag act aca gac tca cct aac atc cac cca act ggg      2679
Ser Thr Ser Ala Glu Thr Thr Asp Ser Pro Asn Ile His Pro Thr Gly
810                 815                 820                 825

aca ctg act tca gaa tcg tca gag agt cct agc act ctc agc ctc cca      2727
Thr Leu Thr Ser Glu Ser Ser Glu Ser Pro Ser Thr Leu Ser Leu Pro
                830                 835                 840

agt gtc tct gga gtc aaa acc aca ttt tct tca tct act cct tcc act      2775
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Ser Val Ser Gly Val Lys Thr Thr Phe Ser Ser Ser Thr Pro Ser Thr
            845                 850                 855

cat cta ttt act agt gga gaa gaa aca gag gaa act tcg aat cca tct     2823
His Leu Phe Thr Ser Gly Glu Glu Thr Glu Glu Thr Ser Asn Pro Ser
        860                 865                 870

gtg tct caa cct gag act tct gtt tcc aga gta agg acc acc ttg gcc     2871
Val Ser Gln Pro Glu Thr Ser Val Ser Arg Val Arg Thr Thr Leu Ala
    875                 880                 885

agc acc tct gtc cct acc cca gta ttc ccc acc atg gac acc tgg cct     2919
Ser Thr Ser Val Pro Thr Pro Val Phe Pro Thr Met Asp Thr Trp Pro
890                 895                 900                 905

aca cgt tca gct cag ttc tct tca tcc cac cta gtg agt gag ctc aga     2967
Thr Arg Ser Ala Gln Phe Ser Ser Ser His Leu Val Ser Glu Leu Arg
                910                 915                 920

gct acg agc agt acc tca gtt aca aac tca act ggt tca gct ctt cct     3015
Ala Thr Ser Ser Thr Ser Val Thr Asn Ser Thr Gly Ser Ala Leu Pro
            925                 930                 935

aaa ata tct cac ctc act ggg acg gca aca atg tca cag acc aat aga     3063
Lys Ile Ser His Leu Thr Gly Thr Ala Thr Met Ser Gln Thr Asn Arg
        940                 945                 950

gac acg ttt aat gac tct gct gca ccc caa agc aca act tgg cca gag     3111
Asp Thr Phe Asn Asp Ser Ala Ala Pro Gln Ser Thr Thr Trp Pro Glu
    955                 960                 965

act agt ccc aga ttc aag aca ggg tta cct tca gca aca acc act gtt     3159
Thr Ser Pro Arg Phe Lys Thr Gly Leu Pro Ser Ala Thr Thr Thr Val
970                 975                 980                 985

tca acc tct gcc act tct ctc tct gct act gta atg gtc tct aaa  ttc    3207
Ser Thr Ser Ala Thr Ser Leu Ser Ala Thr Val Met Val Ser Lys  Phe
                990                 995                1000

act tct cca gca  act agt tcc atg gaa  gca act tct atc agg  gaa      3252
Thr Ser Pro Ala  Thr Ser Ser Met Glu  Ala Thr Ser Ile Arg  Glu
            1005                1010                1015

cca tca aca acc  atc ctc aca aca gag  acc acg aat ggc cca  ggc      3297
Pro Ser Thr Thr  Ile Leu Thr Thr Glu  Thr Thr Asn Gly Pro  Gly
        1020                1025                1030

tct atg gct gtg  gct tct acc aac atc  cca att gga aag ggc  tac      3342
Ser Met Ala Val  Ala Ser Thr Asn Ile  Pro Ile Gly Lys Gly  Tyr
    1035                1040                1045

att act gaa gga  aga ttg gac aca agc  cat ctg ccc att gga  acc      3387
Ile Thr Glu Gly  Arg Leu Asp Thr Ser  His Leu Pro Ile Gly  Thr
1050                1055                1060
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aca gct tcc tct  gag aca tct atg gat  ttt acc atg gcc aaa  gaa      3432
Thr Ala Ser Ser  Glu Thr Ser Met Asp  Phe Thr Met Ala Lys  Glu
            1065                 1070                 1075

agt gtc tca atg  tca gta tct cca tct  cag tcc atg gat gct  gct      3477
Ser Val Ser Met  Ser Val Ser Pro Ser  Gln Ser Met Asp Ala  Ala
            1080                 1085                 1090

ggc tca agc act  cca gga agg aca agc  caa ttc gtt gac aca  ttt      3522
Gly Ser Ser Thr  Pro Gly Arg Thr Ser  Gln Phe Val Asp Thr  Phe
            1095                 1100                 1105

tct gat gat gtc  tat cat tta aca tcc  aga gaa att aca ata  cct      3567
Ser Asp Asp Val  Tyr His Leu Thr Ser  Arg Glu Ile Thr Ile  Pro
            1110                 1115                 1120

aga gat gga aca  agc tca gct ctg act  cca caa atg act gca  act      3612
Arg Asp Gly Thr  Ser Ser Ala Leu Thr  Pro Gln Met Thr Ala  Thr
            1125                 1130                 1135

cac cct cca tct  cct gat cct ggc tct  gct aga agc acc tgg  ctt      3657
His Pro Pro Ser  Pro Asp Pro Gly Ser  Ala Arg Ser Thr Trp  Leu
            1140                 1145                 1150

ggc atc ttg tcc  tca tct cct tct tct  cct act ccc aaa gtc  aca      3702
Gly Ile Leu Ser  Ser Ser Pro Ser Ser  Pro Thr Pro Lys Val  Thr
            1155                 1160                 1165

atg agc tcc aca  ttt tca act cag aga  gtc acc aca agc atg  ata      3747
Met Ser Ser Thr  Phe Ser Thr Gln Arg  Val Thr Thr Ser Met  Ile
            1170                 1175                 1180

atg gac aca gtt  gaa act agt cgg tgg  aac atg ccc aac tta  cct      3792
Met Asp Thr Val  Glu Thr Ser Arg Trp  Asn Met Pro Asn Leu  Pro
            1185                 1190                 1195

tcc acg act tcc  ctg aca cca agt aat  att cca aca agt ggt  gcc      3837
Ser Thr Thr Ser  Leu Thr Pro Ser Asn  Ile Pro Thr Ser Gly  Ala
            1200                 1205                 1210

ata gga aaa agc  acc ctg gtt ccc ttg  gac act cca tct cca  gcc      3882
Ile Gly Lys Ser  Thr Leu Val Pro Leu  Asp Thr Pro Ser Pro  Ala
            1215                 1220                 1225

aca tca ttg gag  gca tca gaa ggg gga  ctt cca acc ctc agc  acc      3927
Thr Ser Leu Glu  Ala Ser Glu Gly Gly  Leu Pro Thr Leu Ser  Thr
            1230                 1235                 1240

tac cct gaa tca  aca aac aca ccc agc  atc cac ctc gga gca  cac      3972
Tyr Pro Glu Ser  Thr Asn Thr Pro Ser  Ile His Leu Gly Ala  His
            1245                 1250                 1255

gct agt tca gaa  agt cca agc acc atc  aaa ctt acc atg gct  tca      4017
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Ala Ser Ser Glu  Ser Pro Ser Thr Ile  Lys Leu Thr Met Ala  Ser
            1260                 1265                 1270

gta gta aaa cct  ggc tct tac aca cct  ctc acc ttc ccc tca  ata      4062
Val Val Lys Pro  Gly Ser Tyr Thr Pro  Leu Thr Phe Pro Ser  Ile
            1275                 1280                 1285

gag acc cac att  cat gta tca aca gcc  aga atg gct tac tct  tct      4107
Glu Thr His Ile  His Val Ser Thr Ala  Arg Met Ala Tyr Ser  Ser
            1290                 1295                 1300

ggg tct tca cct  gag atg aca gct cct  gga gag act aac act  ggt      4152
Gly Ser Ser Pro  Glu Met Thr Ala Pro  Gly Glu Thr Asn Thr  Gly
            1305                 1310                 1315

agt acc tgg gac  ccc acc acc tac atc  acc act acg gat cct  aag      4197
Ser Thr Trp Asp  Pro Thr Thr Tyr Ile  Thr Thr Thr Asp Pro  Lys
            1320                 1325                 1330

gat aca agt tca  gct cag gtc tct aca  ccc cac tca gtg agg  aca      4242
Asp Thr Ser Ser  Ala Gln Val Ser Thr  Pro His Ser Val Arg  Thr
            1335                 1340                 1345

ctc aga acc aca  gaa aac cat cca aag  aca gag tcc gcc acc  cca      4287
Leu Arg Thr Thr  Glu Asn His Pro Lys  Thr Glu Ser Ala Thr  Pro
            1350                 1355                 1360

gct gct tac tct  gga agt cct aaa atc  tca agt tca ccc aat  ctc      4332
Ala Ala Tyr Ser  Gly Ser Pro Lys Ile  Ser Ser Ser Pro Asn  Leu
            1365                 1370                 1375

acc agt ccg gcc  aca aaa gca tgg acc  atc aca gac aca act  gaa      4377
Thr Ser Pro Ala  Thr Lys Ala Trp Thr  Ile Thr Asp Thr Thr  Glu
            1380                 1385                 1390

cac tcc act caa  tta cat tac aca aaa  ttg gca gaa aaa tca  tct      4422
His Ser Thr Gln  Leu His Tyr Thr Lys  Leu Ala Glu Lys Ser  Ser
            1395                 1400                 1405

gga ttt gag aca  cag tca gct cca gga  cct gtc tct gta gta  atc      4467
Gly Phe Glu Thr  Gln Ser Ala Pro Gly  Pro Val Ser Val Val  Ile
            1410                 1415                 1420

cct acc tcc cct  acc att gga agc agc  aca ttg gaa cta act  tct      4512
Pro Thr Ser Pro  Thr Ile Gly Ser Ser  Thr Leu Glu Leu Thr  Ser
            1425                 1430                 1435

gat gtc cca ggg  gaa ccc ctg gtc ctt  gct ccc agt gag cag  acc      4557
Asp Val Pro Gly  Glu Pro Leu Val Leu  Ala Pro Ser Glu Gln  Thr
            1440                 1445                 1450

aca atc act ctc  ccc atg gca aca tgg  ctg agt acc agt ttg  aca      4602
Thr Ile Thr Leu  Pro Met Ala Thr Trp  Leu Ser Thr Ser Leu  Thr
            1455                 1460                 1465
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gag gaa atg gct  tca aca gac ctt gat  att tca agt cca agt  tca      4647
Glu Glu Met Ala  Ser Thr Asp Leu Asp  Ile Ser Ser Pro Ser  Ser
            1470                 1475                 1480

ccc atg agt aca  ttt gct att ttt cca  cct atg tcc aca cct  tct      4692
Pro Met Ser Thr  Phe Ala Ile Phe Pro  Pro Met Ser Thr Pro  Ser
            1485                 1490                 1495

cat gaa ctt tca  aag tca gag gca gat  acc agt gcc att aga  aat      4737
His Glu Leu Ser  Lys Ser Glu Ala Asp  Thr Ser Ala Ile Arg  Asn
            1500                 1505                 1510

aca gat tca aca  acg ttg gat cag cac  cta gga atc agg agt  ttg      4782
Thr Asp Ser Thr  Thr Leu Asp Gln His  Leu Gly Ile Arg Ser  Leu
            1515                 1520                 1525

ggc aga act ggg  gac tta aca act gtt  cct atc acc cca ctg  aca      4827
Gly Arg Thr Gly  Asp Leu Thr Thr Val  Pro Ile Thr Pro Leu  Thr
            1530                 1535                 1540

acc acg tgg acc  agt gtg att gaa cac  tca aca caa gca cag  gac      4872
Thr Thr Trp Thr  Ser Val Ile Glu His  Ser Thr Gln Ala Gln  Asp
            1545                 1550                 1555

acc ctt tct gca  acg atg agt cct act  cac gtg aca cag tca  ctc      4917
Thr Leu Ser Ala  Thr Met Ser Pro Thr  His Val Thr Gln Ser  Leu
            1560                 1565                 1570

aaa gat caa aca  tct ata cca gcc tca  gca tcc cct tcc cat  ctt      4962
Lys Asp Gln Thr  Ser Ile Pro Ala Ser  Ala Ser Pro Ser His  Leu
            1575                 1580                 1585

act gaa gtc tac  cct gag ctc ggg aca  caa ggg aga agc tcc  tct      5007
Thr Glu Val Tyr  Pro Glu Leu Gly Thr  Gln Gly Arg Ser Ser  Ser
            1590                 1595                 1600

gag gca acc act  ttt tgg aaa cca tct  aca gac aca ctg tcc  aga      5052
Glu Ala Thr Thr  Phe Trp Lys Pro Ser  Thr Asp Thr Leu Ser  Arg
            1605                 1610                 1615

gag att gag act  ggc cca aca aac att  caa tcc act cca ccc  atg      5097
Glu Ile Glu Thr  Gly Pro Thr Asn Ile  Gln Ser Thr Pro Pro  Met
            1620                 1625                 1630

gac aac aca aca  aca ggg agc agt agt  agt gga gtc acc ctg  ggc      5142
Asp Asn Thr Thr  Thr Gly Ser Ser Ser  Ser Gly Val Thr Leu  Gly
            1635                 1640                 1645

ata gcc cac ctt  ccc ata gga aca tcc  tcc cca gct gag aca  tcc      5187
Ile Ala His Leu  Pro Ile Gly Thr Ser  Ser Pro Ala Glu Thr  Ser
            1650                 1655                 1660

aca aac atg gca  ctg gaa aga aga agt  tct aca gcc act gtc  tct      5232
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Thr Asn Met Ala  Leu Glu Arg Arg Ser  Ser Thr Ala Thr Val  Ser
            1665                1670                1675

atg gct ggg aca  atg gga ctc ctt gtt  act agt gct cca gga  aga      5277
Met Ala Gly Thr  Met Gly Leu Leu Val  Thr Ser Ala Pro Gly  Arg
            1680                1685                1690

agc atc agc cag  tca tta gga aga gtt  tcc tct gtc ctt tct  gag      5322
Ser Ile Ser Gln  Ser Leu Gly Arg Val  Ser Ser Val Leu Ser  Glu
            1695                1700                1705

tca act act gaa  gga gtc aca gat tct  agt aag gga agc agc  cca      5367
Ser Thr Thr Glu  Gly Val Thr Asp Ser  Ser Lys Gly Ser Ser  Pro
            1710                1715                1720

agg ctg aac aca  cag gga aat aca gct  ctc tcc tcc tct ctt  gaa      5412
Arg Leu Asn Thr  Gln Gly Asn Thr Ala  Leu Ser Ser Ser Leu  Glu
            1725                1730                1735

ccc agc tat gct  gaa gga agc cag atg  agc aca agc atc cct  cta      5457
Pro Ser Tyr Ala  Glu Gly Ser Gln Met  Ser Thr Ser Ile Pro  Leu
            1740                1745                1750

acc tca tct cct  aca act cct gat gtg  gaa ttc ata ggg ggc  agc      5502
Thr Ser Ser Pro  Thr Thr Pro Asp Val  Glu Phe Ile Gly Gly  Ser
            1755                1760                1765

aca ttt tgg acc  aag gag gtc acc aca  gtt atg acc tca gac  atc      5547
Thr Phe Trp Thr  Lys Glu Val Thr Thr  Val Met Thr Ser Asp  Ile
            1770                1775                1780

tcc aag tct tca  gca agg aca gag tcc  agc tca gct acc ctt  atg      5592
Ser Lys Ser Ser  Ala Arg Thr Glu Ser  Ser Ser Ala Thr Leu  Met
            1785                1790                1795

tcc aca gct ttg  gga agc act gaa aat  aca gga aaa gaa aaa  ctc      5637
Ser Thr Ala Leu  Gly Ser Thr Glu Asn  Thr Gly Lys Glu Lys  Leu
            1800                1805                1810

aga act gcc tct  atg gat ctt cca tct  cca act cca tca atg  gag      5682
Arg Thr Ala Ser  Met Asp Leu Pro Ser  Pro Thr Pro Ser Met  Glu
            1815                1820                1825

gtg aca cca tgg  att tct ctc act ctc  agt aat gcc ccc aat  acc      5727
Val Thr Pro Trp  Ile Ser Leu Thr Leu  Ser Asn Ala Pro Asn  Thr
            1830                1835                1840

aca gat tca ctt  gac ctc agc cat ggg  gtg cac acc agc tct  gca      5772
Thr Asp Ser Leu  Asp Leu Ser His Gly  Val His Thr Ser Ser  Ala
            1845                1850                1855

ggg act ttg gcc  act gac agg tca ttg  aat act ggt gtc act  aga      5817
Gly Thr Leu Ala  Thr Asp Arg Ser Leu  Asn Thr Gly Val Thr  Arg
            1860                1865                1870
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gcc tcc aga ttg  gaa aac ggc tct gat  acc tct tct aag tcc  ctg      5862
Ala Ser Arg Leu  Glu Asn Gly Ser Asp  Thr Ser Ser Lys Ser  Leu
            1875                 1880                 1885

tct atg gga aac  agc act cac act tcc  atg act gac aca gag  aag      5907
Ser Met Gly Asn  Ser Thr His Thr Ser  Met Thr Asp Thr Glu  Lys
            1890                 1895                 1900

agt gaa gtg tct  tct tca atc cat ccc  cga cct gag acc tca  gct      5952
Ser Glu Val Ser  Ser Ser Ile His Pro  Arg Pro Glu Thr Ser  Ala
            1905                 1910                 1915

cct gga gca gag  acc act ttg act tcc  act cct gga aac agg  gcc      5997
Pro Gly Ala Glu  Thr Thr Leu Thr Ser  Thr Pro Gly Asn Arg  Ala
            1920                 1925                 1930

ata agc tta aca  ttg cct ttt tca tcc  att cca gtg gaa gaa  gtc      6042
Ile Ser Leu Thr  Leu Pro Phe Ser Ser  Ile Pro Val Glu Glu  Val
            1935                 1940                 1945

att tct aca ggc  ata acc tca gga cca  gac atc aac tca gca  ccc      6087
Ile Ser Thr Gly  Ile Thr Ser Gly Pro  Asp Ile Asn Ser Ala  Pro
            1950                 1955                 1960

atg aca cat tct  ccc atc acc cca cca  aca att gta tgg acc  agt      6132
Met Thr His Ser  Pro Ile Thr Pro Pro  Thr Ile Val Trp Thr  Ser
            1965                 1970                 1975

aca ggc aca att  gaa cag tcc act caa  cca cta cat gca gtt  tct      6177
Thr Gly Thr Ile  Glu Gln Ser Thr Gln  Pro Leu His Ala Val  Ser
            1980                 1985                 1990

tca gaa aaa gtt  tct gtg cag aca cag  tca act cca tat gtc  aac      6222
Ser Glu Lys Val  Ser Val Gln Thr Gln  Ser Thr Pro Tyr Val  Asn
            1995                 2000                 2005

tct gtg gca gtg  tct gct tcc cct acc  cat gag aat tca gtc  tct      6267
Ser Val Ala Val  Ser Ala Ser Pro Thr  His Glu Asn Ser Val  Ser
            2010                 2015                 2020

tct gga agc agc  aca tcc tct cca tat  tcc tca gcc tca ctt  gaa      6312
Ser Gly Ser Ser  Thr Ser Ser Pro Tyr  Ser Ser Ala Ser Leu  Glu
            2025                 2030                 2035

tcc ttg gat tcc  aca atc agt agg agg  aat gca atc act tcc  tgg      6357
Ser Leu Asp Ser  Thr Ile Ser Arg Arg  Asn Ala Ile Thr Ser  Trp
            2040                 2045                 2050

cta tgg gac ctc  act aca tct ctc ccc  act aca act tgg cca  agt      6402
Leu Trp Asp Leu  Thr Thr Ser Leu Pro  Thr Thr Thr Trp Pro  Ser
            2055                 2060                 2065

act agt tta tct  gag gca ctg tcc tca  ggc cat tct ggg gtt  tca      6447
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Thr Ser Leu Ser  Glu Ala Leu Ser Ser  Gly His Ser Gly Val  Ser
            2070                 2075                 2080

aac cca agt tca  act acg act gaa ttt  cca ctc ttt tca gct  gca      6492
Asn Pro Ser Ser  Thr Thr Thr Glu Phe  Pro Leu Phe Ser Ala  Ala
            2085                 2090                 2095

tcc aca tct gct  gct aag caa aga aat  cca gaa aca gag acc  cat      6537
Ser Thr Ser Ala  Ala Lys Gln Arg Asn  Pro Glu Thr Glu Thr  His
            2100                 2105                 2110

ggt ccc cag aat  aca gcc gcg agt act  ttg aac act gat gca  tcc      6582
Gly Pro Gln Asn  Thr Ala Ala Ser Thr  Leu Asn Thr Asp Ala  Ser
            2115                 2120                 2125

tcg gtc aca ggt  ctt tct gag act cct  gtg ggg gca agt atc  agc      6627
Ser Val Thr Gly  Leu Ser Glu Thr Pro  Val Gly Ala Ser Ile  Ser
            2130                 2135                 2140

tct gaa gtc cct  ctt cca atg gcc ata  act tct aga tca gat  gtt      6672
Ser Glu Val Pro  Leu Pro Met Ala Ile  Thr Ser Arg Ser Asp  Val
            2145                 2150                 2155

tct ggc ctt aca  tct gag agt act gct  aac ccg agt tta ggc  aca      6717
Ser Gly Leu Thr  Ser Glu Ser Thr Ala  Asn Pro Ser Leu Gly  Thr
            2160                 2165                 2170

gcc tct tca gca  ggg acc aaa tta act  agg aca ata tcc ctg  ccc      6762
Ala Ser Ser Ala  Gly Thr Lys Leu Thr  Arg Thr Ile Ser Leu  Pro
            2175                 2180                 2185

act tca gag tct  ttg gtt tcc ttt aga  atg aac aag gat cca  tgg      6807
Thr Ser Glu Ser  Leu Val Ser Phe Arg  Met Asn Lys Asp Pro  Trp
            2190                 2195                 2200

aca gtg tca atc  cct ttg ggg tcc cat  cca act act aat aca  gaa      6852
Thr Val Ser Ile  Pro Leu Gly Ser His  Pro Thr Thr Asn Thr  Glu
            2205                 2210                 2215

aca agc atc cca  gta aac agc gca ggt  cca cct ggc ttg tcc  aca      6897
Thr Ser Ile Pro  Val Asn Ser Ala Gly  Pro Pro Gly Leu Ser  Thr
            2220                 2225                 2230

gta gca tca gat  gta att gac aca cct  tca gat ggg gct gag  agt      6942
Val Ala Ser Asp  Val Ile Asp Thr Pro  Ser Asp Gly Ala Glu  Ser
            2235                 2240                 2245

att ccc act gtc  tcc ttt tcc ccc tcc  cct gat act gaa gtg  aca      6987
Ile Pro Thr Val  Ser Phe Ser Pro Ser  Pro Asp Thr Glu Val  Thr
            2250                 2255                 2260

act atc tca cat  ttc cca gaa aag aca  act cat tca ttt aga  acc      7032
Thr Ile Ser His  Phe Pro Glu Lys Thr  Thr His Ser Phe Arg  Thr
            2265                 2270                 2275
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att tca tct ctc  act cat gag ttg act  tca aga gtg aca cct  att      7077
Ile Ser Ser Leu  Thr His Glu Leu Thr  Ser Arg Val Thr Pro  Ile
            2280                 2285                 2290

cct ggg gat tgg  atg agt tca gct atg  tct aca aag ccc aca  gga      7122
Pro Gly Asp Trp  Met Ser Ser Ala Met  Ser Thr Lys Pro Thr  Gly
            2295                 2300                 2305

gcc agt ccc tcc  att aca ctg gga gag  aga agg aca atc acc  tct      7167
Ala Ser Pro Ser  Ile Thr Leu Gly Glu  Arg Arg Thr Ile Thr  Ser
            2310                 2315                 2320

gct gct cca acc  act tcc ccc ata gtt  ctc act gct agt ttc  aca      7212
Ala Ala Pro Thr  Thr Ser Pro Ile Val  Leu Thr Ala Ser Phe  Thr
            2325                 2330                 2335

gag acc agc aca  gtt tca ctg gat aat  gaa act aca gta aaa  acc      7257
Glu Thr Ser Thr  Val Ser Leu Asp Asn  Glu Thr Thr Val Lys  Thr
            2340                 2345                 2350

tca gat atc ctt  gac gca cgg aaa aca  aat gag ctc ccc tca  gat      7302
Ser Asp Ile Leu  Asp Ala Arg Lys Thr  Asn Glu Leu Pro Ser  Asp
            2355                 2360                 2365

agc agt tct tct  tct gat ctg atc aac  acc tcc ata gct tct  tca      7347
Ser Ser Ser Ser  Ser Asp Leu Ile Asn  Thr Ser Ile Ala Ser  Ser
            2370                 2375                 2380

act atg gat gtc  act aaa aca gcc tcc  atc agt ccc act agc  atc      7392
Thr Met Asp Val  Thr Lys Thr Ala Ser  Ile Ser Pro Thr Ser  Ile
            2385                 2390                 2395

tca gga atg aca  gca agt tcc tcc cca  tct ctc ttc tct tca  gat      7437
Ser Gly Met Thr  Ala Ser Ser Ser Pro  Ser Leu Phe Ser Ser  Asp
            2400                 2405                 2410

aga ccc cag gtt  ccc aca tct aca aca  gag aca aat aca gcc  acc      7482
Arg Pro Gln Val  Pro Thr Ser Thr Thr  Glu Thr Asn Thr Ala  Thr
            2415                 2420                 2425

tct cca tct gtt  tcc agt aac acc tat  tct ctt gat ggg ggc  tcc      7527
Ser Pro Ser Val  Ser Ser Asn Thr Tyr  Ser Leu Asp Gly Gly  Ser
            2430                 2435                 2440

aat gtg ggt ggc  act cca tcc act tta  cca ccc ttt aca atc  acc      7572
Asn Val Gly Gly  Thr Pro Ser Thr Leu  Pro Pro Phe Thr Ile  Thr
            2445                 2450                 2455

cac cct gtc gag  aca agc tcg gcc cta  tta gcc tgg tct aga  cca      7617
His Pro Val Glu  Thr Ser Ser Ala Leu  Leu Ala Trp Ser Arg  Pro
            2460                 2465                 2470

gta aga act ttc  agc acc atg gtc agc  act gac act gcc tcc  gga      7662
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Val Arg Thr Phe  Ser Thr Met Val Ser  Thr Asp Thr Ala Ser  Gly
            2475                2480                2485

gaa aat cct acc  tct agc aat tct gtg  gtg act tct gtt cca  gca      7707
Glu Asn Pro Thr  Ser Ser Asn Ser Val  Val Thr Ser Val Pro  Ala
            2490                2495                2500

cca ggt aca tgg  acc agt gta ggc agt  act act gac tta cct  gcc      7752
Pro Gly Thr Trp  Thr Ser Val Gly Ser  Thr Thr Asp Leu Pro  Ala
            2505                2510                2515

atg ggc ttt ctc  aag aca agt cct gca  gga gag gca cac tca  ctt      7797
Met Gly Phe Leu  Lys Thr Ser Pro Ala  Gly Glu Ala His Ser  Leu
            2520                2525                2530

cta gca tca act  att gaa cca gcc act  gcc ttc act ccc cat  ctc      7842
Leu Ala Ser Thr  Ile Glu Pro Ala Thr  Ala Phe Thr Pro His  Leu
            2535                2540                2545

tca gca gca gtg  gtc act gga tcc agt  gct aca tca gaa gcc  agt      7887
Ser Ala Ala Val  Val Thr Gly Ser Ser  Ala Thr Ser Glu Ala  Ser
            2550                2555                2560

ctt ctc act acg  agt gaa agc aaa gcc  att cat tct tca cca  cag      7932
Leu Leu Thr Thr  Ser Glu Ser Lys Ala  Ile His Ser Ser Pro  Gln
            2565                2570                2575

acc cca act aca  ccc acc tct gga gca  aac tgg gaa act tca  gct      7977
Thr Pro Thr Thr  Pro Thr Ser Gly Ala  Asn Trp Glu Thr Ser  Ala
            2580                2585                2590

act cct gag agc  ctt ttg gta gtc act  gag act tca gac aca  aca      8022
Thr Pro Glu Ser  Leu Leu Val Val Thr  Glu Thr Ser Asp Thr  Thr
            2595                2600                2605

ctt acc tca aag  att ttg gtc aca gat  acc atc ttg ttt tca  act      8067
Leu Thr Ser Lys  Ile Leu Val Thr Asp  Thr Ile Leu Phe Ser  Thr
            2610                2615                2620

gtg tcc acg cca  cct tct aaa ttt cca  agt acg ggg act ctg  tct      8112
Val Ser Thr Pro  Pro Ser Lys Phe Pro  Ser Thr Gly Thr Leu  Ser
            2625                2630                2635

gga gct tcc ttc  cct act tta ctc ccg  gac act cca gcc atc  cct      8157
Gly Ala Ser Phe  Pro Thr Leu Leu Pro  Asp Thr Pro Ala Ile  Pro
            2640                2645                2650

ctc act gcc act  gag cca aca agt tca  tta gct aca tcc ttt  gat      8202
Leu Thr Ala Thr  Glu Pro Thr Ser Ser  Leu Ala Thr Ser Phe  Asp
            2655                2660                2665

tcc acc cca ctg  gtg act ata gct tcg  gat agt ctt ggc aca  gtc      8247
Ser Thr Pro Leu  Val Thr Ile Ala Ser  Asp Ser Leu Gly Thr  Val
            2670                2675                2680
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cca gag act acc  ctg acc atg tca gag  acc tca aat ggt gat  gca      8292
Pro Glu Thr Thr  Leu Thr Met Ser Glu  Thr Ser Asn Gly Asp  Ala
            2685                 2690                 2695

ctg gtt ctt aag  aca gta agt aac cca  gat agg agc atc cct  gga      8337
Leu Val Leu Lys  Thr Val Ser Asn Pro  Asp Arg Ser Ile Pro  Gly
            2700                 2705                 2710

atc act atc caa  gga gta aca gaa agt  cca ctc cat cct tct  tcc      8382
Ile Thr Ile Gln  Gly Val Thr Glu Ser  Pro Leu His Pro Ser  Ser
            2715                 2720                 2725

act tcc ccc tct  aag att gtt gct cca  cgg aat aca acc tat  gaa      8427
Thr Ser Pro Ser  Lys Ile Val Ala Pro  Arg Asn Thr Thr Tyr  Glu
            2730                 2735                 2740

ggt tcg atc aca  gtg gca ctt tct act  ttg cct gcg gga act  act      8472
Gly Ser Ile Thr  Val Ala Leu Ser Thr  Leu Pro Ala Gly Thr  Thr
            2745                 2750                 2755

ggt tcc ctt gta  ttc agt cag agt tct  gaa aac tca gag aca  acg      8517
Gly Ser Leu Val  Phe Ser Gln Ser Ser  Glu Asn Ser Glu Thr  Thr
            2760                 2765                 2770

gct ttg gta gac  tca tca gct ggg ctt  gag agg gca tct gtg  atg      8562
Ala Leu Val Asp  Ser Ser Ala Gly Leu  Glu Arg Ala Ser Val  Met
            2775                 2780                 2785

cca cta acc aca  gga agc cag ggt atg  gct agc tct gga gga  atc      8607
Pro Leu Thr Thr  Gly Ser Gln Gly Met  Ala Ser Ser Gly Gly  Ile
            2790                 2795                 2800

aga agt ggg tcc  act cac tca act gga  acc aaa aca ttt tct  tct      8652
Arg Ser Gly Ser  Thr His Ser Thr Gly  Thr Lys Thr Phe Ser  Ser
            2805                 2810                 2815

ctc cct ctg acc  atg aac cca ggt gag  gtt aca gcc atg tct  gaa      8697
Leu Pro Leu Thr  Met Asn Pro Gly Glu  Val Thr Ala Met Ser  Glu
            2820                 2825                 2830

atc acc acg aac  aga ctg aca gct act  caa tca aca gca ccc  aaa      8742
Ile Thr Thr Asn  Arg Leu Thr Ala Thr  Gln Ser Thr Ala Pro  Lys
            2835                 2840                 2845

ggg ata cct gtg  aag ccc acc agt gct  gag tca ggc ctc cta  aca      8787
Gly Ile Pro Val  Lys Pro Thr Ser Ala  Glu Ser Gly Leu Leu  Thr
            2850                 2855                 2860

cct gtc tct gcc  tcc tca agc cca tca  aag gcc ttt gcc tca  ctg      8832
Pro Val Ser Ala  Ser Ser Ser Pro Ser  Lys Ala Phe Ala Ser  Leu
            2865                 2870                 2875

act aca gct ccc  cca act tgg ggg atc  cca cag tct acc ttg  aca      8877
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Thr Thr Ala Pro  Pro Thr Trp Gly Ile  Pro Gln Ser Thr Leu  Thr
            2880                2885                2890

ttt gag ttt tct  gag gtc cca agt ttg  gat act aag tcc gct  tct      8922
Phe Glu Phe Ser  Glu Val Pro Ser Leu  Asp Thr Lys Ser Ala  Ser
            2895                2900                2905

tta cca act cct  gga cag tcc ctg aac  acc att cca gac tca  gat      8967
Leu Pro Thr Pro  Gly Gln Ser Leu Asn  Thr Ile Pro Asp Ser  Asp
            2910                2915                2920

gca agc aca gca  tct tcc tca ctg tcc  aag tct cca gaa aaa  aac      9012
Ala Ser Thr Ala  Ser Ser Ser Leu Ser  Lys Ser Pro Glu Lys  Asn
            2925                2930                2935

cca agg gca agg  atg atg act tcc aca  aag gcc ata agt gca  agc      9057
Pro Arg Ala Arg  Met Met Thr Ser Thr  Lys Ala Ile Ser Ala  Ser
            2940                2945                2950

tca ttt caa tca  aca ggt ttt act gaa  acc cct gag gga tct  gcc      9102
Ser Phe Gln Ser  Thr Gly Phe Thr Glu  Thr Pro Glu Gly Ser  Ala
            2955                2960                2965

tcc cct tct atg  gca ggg cat gaa ccc  aga gtc ccc act tca  gga      9147
Ser Pro Ser Met  Ala Gly His Glu Pro  Arg Val Pro Thr Ser  Gly
            2970                2975                2980

aca ggg gac cct  aga tat gcc tca gag  agc atg tct tat cca  gac      9192
Thr Gly Asp Pro  Arg Tyr Ala Ser Glu  Ser Met Ser Tyr Pro  Asp
            2985                2990                2995

cca agc aag gca  tca tca gct atg aca  tcg acc tct ctt gca  tca      9237
Pro Ser Lys Ala  Ser Ser Ala Met Thr  Ser Thr Ser Leu Ala  Ser
            3000                3005                3010

aaa ctc aca act  ctc ttc agc aca ggt  caa gca gca agg tct  ggt      9282
Lys Leu Thr Thr  Leu Phe Ser Thr Gly  Gln Ala Ala Arg Ser  Gly
            3015                3020                3025

tct agt tcc tct  ccc ata agc cta tcc  act gag aaa gaa aca  agc      9327
Ser Ser Ser Ser  Pro Ile Ser Leu Ser  Thr Glu Lys Glu Thr  Ser
            3030                3035                3040

ttc ctt tcc ccc  act gca tcc acc tcc  aga aag act tca cta  ttt      9372
Phe Leu Ser Pro  Thr Ala Ser Thr Ser  Arg Lys Thr Ser Leu  Phe
            3045                3050                3055

ctt ggg cct tcc  atg gca agg cag ccc  aac ata ttg gtg cat  ctt      9417
Leu Gly Pro Ser  Met Ala Arg Gln Pro  Asn Ile Leu Val His  Leu
            3060                3065                3070

cag act tca gct  ctg aca ctt tct cca  aca tcc act cta aat  atg      9462
Gln Thr Ser Ala  Leu Thr Leu Ser Pro  Thr Ser Thr Leu Asn  Met
            3075                3080                3085
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tcc cag gag gag  cct cct gag tta acc  tca agc cag acc att  gca      9507
Ser Gln Glu Glu  Pro Pro Glu Leu Thr  Ser Ser Gln Thr Ile  Ala
            3090                 3095                 3100

gaa gaa gag gga  aca aca gct gaa aca  cag acg tta acc ttc  aca      9552
Glu Glu Glu Gly  Thr Thr Ala Glu Thr  Gln Thr Leu Thr Phe  Thr
            3105                 3110                 3115

cca tct gag acc  cca aca tcc ttg tta  cct gtc tct tct ccc  aca      9597
Pro Ser Glu Thr  Pro Thr Ser Leu Leu  Pro Val Ser Ser Pro  Thr
            3120                 3125                 3130

gaa ccc aca gcc  aga aga aag agt tct  cca gaa aca tgg gca  agc      9642
Glu Pro Thr Ala  Arg Arg Lys Ser Ser  Pro Glu Thr Trp Ala  Ser
            3135                 3140                 3145

tct att tca gtt  cct gcc aag acc tcc  ttg gtt gaa aca act  gat      9687
Ser Ile Ser Val  Pro Ala Lys Thr Ser  Leu Val Glu Thr Thr  Asp
            3150                 3155                 3160

gga acg cta gtg  acc acc ata aag atg  tca agc cag gca gca  caa      9732
Gly Thr Leu Val  Thr Thr Ile Lys Met  Ser Ser Gln Ala Ala  Gln
            3165                 3170                 3175

gga aat tcc acg  tgg cct gcc cca gca  gag gag acg ggg acc  agt      9777
Gly Asn Ser Thr  Trp Pro Ala Pro Ala  Glu Glu Thr Gly Thr  Ser
            3180                 3185                 3190

cca gca ggc aca  tcc cca gga agc cca  gaa atg tct acc act  ctc      9822
Pro Ala Gly Thr  Ser Pro Gly Ser Pro  Glu Met Ser Thr Thr  Leu
            3195                 3200                 3205

aaa atc atg agc  tcc aag gaa ccc agc  atc agc cca gag atc  agg      9867
Lys Ile Met Ser  Ser Lys Glu Pro Ser  Ile Ser Pro Glu Ile  Arg
            3210                 3215                 3220

tcc act gtg cga  aat tct cct tgg aag  act cca gaa aca act  gtt      9912
Ser Thr Val Arg  Asn Ser Pro Trp Lys  Thr Pro Glu Thr Thr  Val
            3225                 3230                 3235

ccc atg gag acc  aca gtg gaa cca gtc  acc ctt cag tcc aca  gcc      9957
Pro Met Glu Thr  Thr Val Glu Pro Val  Thr Leu Gln Ser Thr  Ala
            3240                 3245                 3250

cta gga agt ggc  agc acc agc atc tct  cac ctg ccc aca gga  acc     10002
Leu Gly Ser Gly  Ser Thr Ser Ile Ser  His Leu Pro Thr Gly  Thr
            3255                 3260                 3265

aca tca cca acc  aag tca cca aca gaa  aat atg ttg gct aca  gaa     10047
Thr Ser Pro Thr  Lys Ser Pro Thr Glu  Asn Met Leu Ala Thr  Glu
            3270                 3275                 3280

agg gtc tcc ctc  tcc cca tcc cca cct  gag gct tgg acc aac  ctt     10092
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Arg Val Ser Leu  Ser Pro Ser Pro Pro  Glu Ala Trp Thr Asn  Leu
            3285                3290                3295

tat tct gga act  cca gga ggg acc agg  cag tca ctg gcc aca  atg     10137
Tyr Ser Gly Thr  Pro Gly Gly Thr Arg  Gln Ser Leu Ala Thr  Met
            3300                3305                3310

tcc tct gtc tcc  cta gag tca cca act  gct aga agc atc aca  ggg     10182
Ser Ser Val Ser  Leu Glu Ser Pro Thr  Ala Arg Ser Ile Thr  Gly
            3315                3320                3325

act ggt cag caa  agc agt cca gaa ctg  gtt tca aag aca act  gga     10227
Thr Gly Gln Gln  Ser Ser Pro Glu Leu  Val Ser Lys Thr Thr  Gly
            3330                3335                3340

atg gaa ttc tct  atg tgg cat ggc tct  act gga ggg acc aca  ggg     10272
Met Glu Phe Ser  Met Trp His Gly Ser  Thr Gly Gly Thr Thr  Gly
            3345                3350                3355

gac aca cat gtc  tct ctg agc aca tct  tcc aat atc ctt gaa  gac     10317
Asp Thr His Val  Ser Leu Ser Thr Ser  Ser Asn Ile Leu Glu  Asp
            3360                3365                3370

cct gta acc agc  cca aac tct gtg agc  tca ttg aca gat aaa  tcc     10362
Pro Val Thr Ser  Pro Asn Ser Val Ser  Ser Leu Thr Asp Lys  Ser
            3375                3380                3385

aaa cat aaa acc  gag aca tgg gta agc  acc aca gcc att ccc  tcc     10407
Lys His Lys Thr  Glu Thr Trp Val Ser  Thr Thr Ala Ile Pro  Ser
            3390                3395                3400

act gtc ctg aat  aat aag ata atg gca  gct gaa caa cag aca  agt     10452
Thr Val Leu Asn  Asn Lys Ile Met Ala  Ala Glu Gln Gln Thr  Ser
            3405                3410                3415

cga tct gtg gat  gag gct tat tca tca  act agt tct tgg tca  gat     10497
Arg Ser Val Asp  Glu Ala Tyr Ser Ser  Thr Ser Ser Trp Ser  Asp
            3420                3425                3430

cag aca tct ggg  agt gac atc acc ctt  ggt gca tct cct gat  gtc     10542
Gln Thr Ser Gly  Ser Asp Ile Thr Leu  Gly Ala Ser Pro Asp  Val
            3435                3440                3445

aca aac aca tta  tac atc acc tcc aca  gca caa acc acc tca  cta     10587
Thr Asn Thr Leu  Tyr Ile Thr Ser Thr  Ala Gln Thr Thr Ser  Leu
            3450                3455                3460

gtg tct ctg ccc  tct gga gac caa ggc  att aca agc ctc acc  aat     10632
Val Ser Leu Pro  Ser Gly Asp Gln Gly  Ile Thr Ser Leu Thr  Asn
            3465                3470                3475

ccc tca gga gga  aaa aca agc tct gcg  tca tct gtc aca tct  cct     10677
Pro Ser Gly Gly  Lys Thr Ser Ser Ala  Ser Ser Val Thr Ser  Pro
            3480                3485                3490
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tca ata ggg ctt  gag act ctg agg gcc  aat gta agt gca gtg  aaa      10722
Ser Ile Gly Leu  Glu Thr Leu Arg Ala  Asn Val Ser Ala Val  Lys
            3495                 3500                 3505

agt gac att gcc  cct act gct ggg cat  cta tct cag act tca  tct      10767
Ser Asp Ile Ala  Pro Thr Ala Gly His  Leu Ser Gln Thr Ser  Ser
            3510                 3515                 3520

cct gcg gaa gtg  agc atc ctg gac gta  acc aca gct cct act  cca      10812
Pro Ala Glu Val  Ser Ile Leu Asp Val  Thr Thr Ala Pro Thr  Pro
            3525                 3530                 3535

ggt atc tcc acc  acc atc acc acc atg  gga acc aac tca atc  tca      10857
Gly Ile Ser Thr  Thr Ile Thr Thr Met  Gly Thr Asn Ser Ile  Ser
            3540                 3545                 3550

act acc aca ccc  aac cca gaa gtg ggt  atg agt acc atg gac  agc      10902
Thr Thr Thr Pro  Asn Pro Glu Val Gly  Met Ser Thr Met Asp  Ser
            3555                 3560                 3565

acc ccg gcc aca  gag agg cgc aca act  tct aca gaa cac cct  tcc      10947
Thr Pro Ala Thr  Glu Arg Arg Thr Thr  Ser Thr Glu His Pro  Ser
            3570                 3575                 3580

acc tgg tct tcc  aca gct gca tca gat  tcc tgg act gtc aca  gac      10992
Thr Trp Ser Ser  Thr Ala Ala Ser Asp  Ser Trp Thr Val Thr  Asp
            3585                 3590                 3595

atg act tca aac  ttg aaa gtt gca aga  tct cct gga aca att  tcc      11037
Met Thr Ser Asn  Leu Lys Val Ala Arg  Ser Pro Gly Thr Ile  Ser
            3600                 3605                 3610

aca atg cat aca  act tca ttc tta gcc  tca agc act gaa tta  gac      11082
Thr Met His Thr  Thr Ser Phe Leu Ala  Ser Ser Thr Glu Leu  Asp
            3615                 3620                 3625

tcc atg tct act  ccc cat ggc cgt ata  act gtc att gga acc  agc      11127
Ser Met Ser Thr  Pro His Gly Arg Ile  Thr Val Ile Gly Thr  Ser
            3630                 3635                 3640

ctg gtc act cca  tcc tct gat gct tca  gct gta aag aca gag  acc      11172
Leu Val Thr Pro  Ser Ser Asp Ala Ser  Ala Val Lys Thr Glu  Thr
            3645                 3650                 3655

agt aca agt gaa  aga aca ttg agt cct  tca gac aca act gca  tct      11217
Ser Thr Ser Glu  Arg Thr Leu Ser Pro  Ser Asp Thr Thr Ala  Ser
            3660                 3665                 3670

act ccc atc tca  act ttt tct cgt gtc  cag agg atg agc atc  tca      11262
Thr Pro Ile Ser  Thr Phe Ser Arg Val  Gln Arg Met Ser Ile  Ser
            3675                 3680                 3685

gtt cct gac att  tta agt aca agt tgg  act ccc agt agt aca  gaa      11307
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Val Pro Asp Ile  Leu Ser Thr Ser Trp  Thr Pro Ser Ser Thr  Glu
            3690                 3695                 3700

gca gaa gat gtg  cct gtt tca atg gtt  tct aca gat cat gct  agt     11352
Ala Glu Asp Val  Pro Val Ser Met Val  Ser Thr Asp His Ala  Ser
            3705                 3710                 3715

aca aag act gac  cca aat acg ccc ctg  tcc act ttt ctg ttt  gat     11397
Thr Lys Thr Asp  Pro Asn Thr Pro Leu  Ser Thr Phe Leu Phe  Asp
            3720                 3725                 3730

tct ctg tcc act  ctt gac tgg gac act  ggg aga tct ctg tca  tca     11442
Ser Leu Ser Thr  Leu Asp Trp Asp Thr  Gly Arg Ser Leu Ser  Ser
            3735                 3740                 3745

gcc aca gcc act  acc tca gct cct cag  ggg gcc aca act ccc  cag     11487
Ala Thr Ala Thr  Thr Ser Ala Pro Gln  Gly Ala Thr Thr Pro  Gln
            3750                 3755                 3760

gaa ctc act ttg  gaa acc atg atc agc  cca gct acc tca cag  ttg     11532
Glu Leu Thr Leu  Glu Thr Met Ile Ser  Pro Ala Thr Ser Gln  Leu
            3765                 3770                 3775

ccc ttc tct ata  ggg cac att aca agt  gca gtc aca cca gct  gca     11577
Pro Phe Ser Ile  Gly His Ile Thr Ser  Ala Val Thr Pro Ala  Ala
            3780                 3785                 3790

atg gca agg agc  tct gga gtt act ttt  tca aga cca gat ccc  aca     11622
Met Ala Arg Ser  Ser Gly Val Thr Phe  Ser Arg Pro Asp Pro  Thr
            3795                 3800                 3805

agc aaa aag gca  gag cag act tcc act  cag ctt ccc acc acc  act     11667
Ser Lys Lys Ala  Glu Gln Thr Ser Thr  Gln Leu Pro Thr Thr  Thr
            3810                 3815                 3820

tct gca cat cca  ggg cag gtg ccc aga  tca gca gca aca act  ctg     11712
Ser Ala His Pro  Gly Gln Val Pro Arg  Ser Ala Ala Thr Thr  Leu
            3825                 3830                 3835

gat gtg atc cca  cac aca gca aaa act  cca gat gca act ttt  cag     11757
Asp Val Ile Pro  His Thr Ala Lys Thr  Pro Asp Ala Thr Phe  Gln
            3840                 3845                 3850

aga caa ggg cag  aca gct ctt aca aca  gag gca aga gct aca  tct     11802
Arg Gln Gly Gln  Thr Ala Leu Thr Thr  Glu Ala Arg Ala Thr  Ser
            3855                 3860                 3865

gac tcc tgg aat  gag aaa gaa aaa tca  acc cca agt gca cct  tgg     11847
Asp Ser Trp Asn  Glu Lys Glu Lys Ser  Thr Pro Ser Ala Pro  Trp
            3870                 3875                 3880

atc act gag atg  atg aat tct gtc tca  gaa gat acc atc aag  gag     11892
Ile Thr Glu Met  Met Asn Ser Val Ser  Glu Asp Thr Ile Lys  Glu
            3885                 3890                 3895
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gtt acc agc tcc  tcc agt gta tta aag  gac cct gaa tac gct  gga      11937
Val Thr Ser Ser  Ser Ser Val Leu Lys  Asp Pro Glu Tyr Ala  Gly
            3900                 3905                 3910

cat aaa ctt gga  atc tgg gac gac ttc  atc ccc aag ttt gga  aaa      11982
His Lys Leu Gly  Ile Trp Asp Asp Phe  Ile Pro Lys Phe Gly  Lys
            3915                 3920                 3925

gca gcc cat atg  aga gag ttg ccc ctt  ctg agt cca cca cag  gac      12027
Ala Ala His Met  Arg Glu Leu Pro Leu  Leu Ser Pro Pro Gln  Asp
            3930                 3935                 3940

aaa gag gca att  cac cct tct aca aac  aca gta gag acc aca  ggc      12072
Lys Glu Ala Ile  His Pro Ser Thr Asn  Thr Val Glu Thr Thr  Gly
            3945                 3950                 3955

tgg gtc aca agt  tcc gaa cat gct tct  cat tcc act atc cca  gcc      12117
Trp Val Thr Ser  Ser Glu His Ala Ser  His Ser Thr Ile Pro  Ala
            3960                 3965                 3970

cac tca gcg tca  tcc aaa ctc aca tct  cca gtg gtt aca acc  tcc      12162
His Ser Ala Ser  Ser Lys Leu Thr Ser  Pro Val Val Thr Thr  Ser
            3975                 3980                 3985

acc agg gaa caa  gca ata gtt tct atg  tca aca acc aca tgg  cca      12207
Thr Arg Glu Gln  Ala Ile Val Ser Met  Ser Thr Thr Thr Trp  Pro
            3990                 3995                 4000

gag tct aca agg  gct aga aca gag cct  aat tcc ttc ttg act  att      12252
Glu Ser Thr Arg  Ala Arg Thr Glu Pro  Asn Ser Phe Leu Thr  Ile
            4005                 4010                 4015

gaa ctg agg gac  gtc agc cct tac atg  gac acc agc tca acc  aca      12297
Glu Leu Arg Asp  Val Ser Pro Tyr Met  Asp Thr Ser Ser Thr  Thr
            4020                 4025                 4030

caa aca agt att  atc tct tcc cca ggt  tcc act gcg atc acc  aag      12342
Gln Thr Ser Ile  Ile Ser Ser Pro Gly  Ser Thr Ala Ile Thr  Lys
            4035                 4040                 4045

ggg cct aga aca  gaa att acc tcc tct  aag aga ata tcc agc  tca      12387
Gly Pro Arg Thr  Glu Ile Thr Ser Ser  Lys Arg Ile Ser Ser  Ser
            4050                 4055                 4060

ttc ctt gcc cag  tct atg agg tcg tca  gac agc ccc tca gaa  gcc      12432
Phe Leu Ala Gln  Ser Met Arg Ser Ser  Asp Ser Pro Ser Glu  Ala
            4065                 4070                 4075

atc acc agg ctg  tct aac ttt cct gcc  atg aca gaa tct gga  gga      12477
Ile Thr Arg Leu  Ser Asn Phe Pro Ala  Met Thr Glu Ser Gly  Gly
            4080                 4085                 4090

atg atc ctt gct  atg caa aca agt cca  cct ggc gct aca tca  cta      12522
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Met Ile Leu Ala  Met Gln Thr Ser Pro  Pro Gly Ala Thr Ser  Leu
            4095                 4100                 4105

agt gca cct act  ttg gat aca tca gcc  aca gcc tcc tgg aca  ggg     12567
Ser Ala Pro Thr  Leu Asp Thr Ser Ala  Thr Ala Ser Trp Thr  Gly
            4110                 4115                 4120

act cca ctg gct  acg act cag aga ttt  aca tac tca gag aag  acc     12612
Thr Pro Leu Ala  Thr Thr Gln Arg Phe  Thr Tyr Ser Glu Lys  Thr
            4125                 4130                 4135

act ctc ttt agc  aaa ggt cct gag gat  aca tca cag cca agc  cct     12657
Thr Leu Phe Ser  Lys Gly Pro Glu Asp  Thr Ser Gln Pro Ser  Pro
            4140                 4145                 4150

ccc tct gtg gaa  gaa acc agc tct tcc  tct tcc ctg gta cct  atc     12702
Pro Ser Val Glu  Glu Thr Ser Ser Ser  Ser Ser Leu Val Pro  Ile
            4155                 4160                 4165

cat gct aca acc  tcg cct tcc aat att  ttg ttg aca tca caa  ggg     12747
His Ala Thr Thr  Ser Pro Ser Asn Ile  Leu Leu Thr Ser Gln  Gly
            4170                 4175                 4180

cac agt ccc tcc  tct act cca cct gtg  acc tca gtt ttc ttg  tct     12792
His Ser Pro Ser  Ser Thr Pro Pro Val  Thr Ser Val Phe Leu  Ser
            4185                 4190                 4195

gag acc tct ggc  ctg ggg aag acc aca  gac atg tcg agg ata  agc     12837
Glu Thr Ser Gly  Leu Gly Lys Thr Thr  Asp Met Ser Arg Ile  Ser
            4200                 4205                 4210

ttg gaa cct ggc  aca agt tta cct ccc  aat ttg agc agt aca  gca     12882
Leu Glu Pro Gly  Thr Ser Leu Pro Pro  Asn Leu Ser Ser Thr  Ala
            4215                 4220                 4225

ggt gag gcg tta  tcc act tat gaa gcc  tcc aga gat aca aag  gca     12927
Gly Glu Ala Leu  Ser Thr Tyr Glu Ala  Ser Arg Asp Thr Lys  Ala
            4230                 4235                 4240

att cat cat tct  gca gac aca gca gtg  acg aat atg gag gca  acc     12972
Ile His His Ser  Ala Asp Thr Ala Val  Thr Asn Met Glu Ala  Thr
            4245                 4250                 4255

agt tct gaa tat  tct cct atc cca ggc  cat aca aag cca tcc  aaa     13017
Ser Ser Glu Tyr  Ser Pro Ile Pro Gly  His Thr Lys Pro Ser  Lys
            4260                 4265                 4270

gcc aca tct cca  ttg gtt acc tcc cac  atc atg ggg gac atc  act     13062
Ala Thr Ser Pro  Leu Val Thr Ser His  Ile Met Gly Asp Ile  Thr
            4275                 4280                 4285

tct tcc aca tca  gta ttt ggc tcc tcc  gag acc aca gag att  gag     13107
Ser Ser Thr Ser  Val Phe Gly Ser Ser  Glu Thr Thr Glu Ile  Glu
            4290                 4295                 4300
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aca gtg tcc tct  gtg aac cag gga ctt  cag gag aga agc aca  tcc     13152
Thr Val Ser Ser  Val Asn Gln Gly Leu  Gln Glu Arg Ser Thr  Ser
            4305                 4310                 4315

cag gtg gcc agc  tct gct aca gag aca  agc act gtc att acc  cat     13197
Gln Val Ala Ser  Ser Ala Thr Glu Thr  Ser Thr Val Ile Thr  His
            4320                 4325                 4330

gtg tct agt ggt  gat gct act act cat  gtc acc aag aca caa  gcc     13242
Val Ser Ser Gly  Asp Ala Thr Thr His  Val Thr Lys Thr Gln  Ala
            4335                 4340                 4345

act ttc tct agc  gga aca tcc atc tca  agc cct cat cag ttt  ata     13287
Thr Phe Ser Ser  Gly Thr Ser Ile Ser  Ser Pro His Gln Phe  Ile
            4350                 4355                 4360

act tct acc aac  aca ttt aca gat gtg  agc acc aac ccc tcc  acc     13332
Thr Ser Thr Asn  Thr Phe Thr Asp Val  Ser Thr Asn Pro Ser  Thr
            4365                 4370                 4375

tct ctg ata atg  aca gaa tct tca gga  gtg acc atc acc acc  caa     13377
Ser Leu Ile Met  Thr Glu Ser Ser Gly  Val Thr Ile Thr Thr  Gln
            4380                 4385                 4390

aca ggt cct act  gga gct gca aca cag  ggt cca tat ctc ttg  gac     13422
Thr Gly Pro Thr  Gly Ala Ala Thr Gln  Gly Pro Tyr Leu Leu  Asp
            4395                 4400                 4405

aca tca acc atg  cct tac ttg aca gag  act cca tta gct gtg  act     13467
Thr Ser Thr Met  Pro Tyr Leu Thr Glu  Thr Pro Leu Ala Val  Thr
            4410                 4415                 4420

cca gat ttt atg  caa tca gag aag acc  act ctc ata agc aaa  ggt     13512
Pro Asp Phe Met  Gln Ser Glu Lys Thr  Thr Leu Ile Ser Lys  Gly
            4425                 4430                 4435

ccc aag gat gtg  acc tgg aca agc cct  ccc tct gtg gca gaa  acc     13557
Pro Lys Asp Val  Thr Trp Thr Ser Pro  Pro Ser Val Ala Glu  Thr
            4440                 4445                 4450

agc tat ccc tct  tcc ctg aca cct ttc  ttg gtc aca acc ata  cct     13602
Ser Tyr Pro Ser  Ser Leu Thr Pro Phe  Leu Val Thr Thr Ile  Pro
            4455                 4460                 4465

cct gcc act tcc  acg tta caa ggg caa  cat aca tcc tct cct  gtt     13647
Pro Ala Thr Ser  Thr Leu Gln Gly Gln  His Thr Ser Ser Pro  Val
            4470                 4475                 4480

tct gcg act tca  gtt ctt acc tct gga  ctg gtg aag acc aca  gat     13692
Ser Ala Thr Ser  Val Leu Thr Ser Gly  Leu Val Lys Thr Thr  Asp
            4485                 4490                 4495

atg ttg aac aca  agc atg gaa cct gtg  acc aat tca cct caa  aat     13737
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Met Leu Asn Thr  Ser Met Glu Pro Val  Thr Asn Ser Pro Gln  Asn
            4500                4505                4510

ttg aac aat cca  tca aat gag ata ctg  gcc act ttg gca gcc  acc     13782
Leu Asn Asn Pro  Ser Asn Glu Ile Leu  Ala Thr Leu Ala Ala  Thr
            4515                4520                4525

aca gat ata gag  act att cat cct tcc  ata aac aaa gca gtg  acc     13827
Thr Asp Ile Glu  Thr Ile His Pro Ser  Ile Asn Lys Ala Val  Thr
            4530                4535                4540

aat atg ggg act  gcc agt tca gca cat  gta ctg cat tcc act  ctc     13872
Asn Met Gly Thr  Ala Ser Ser Ala His  Val Leu His Ser Thr  Leu
            4545                4550                4555

cca gtc agc tca  gaa cca tct aca gcc  aca tct cca atg gtt  cct     13917
Pro Val Ser Ser  Glu Pro Ser Thr Ala  Thr Ser Pro Met Val  Pro
            4560                4565                4570

gcc tcc agc atg  ggg gac gct ctt gct  tct ata tca ata cct  ggt     13962
Ala Ser Ser Met  Gly Asp Ala Leu Ala  Ser Ile Ser Ile Pro  Gly
            4575                4580                4585

tct gag acc aca  gac att gag gga gag  cca aca tcc tcc ctg  act     14007
Ser Glu Thr Thr  Asp Ile Glu Gly Glu  Pro Thr Ser Ser Leu  Thr
            4590                4595                4600

gct gga cga aaa  gag aac agc acc ctc  cag gag atg aac tca  act     14052
Ala Gly Arg Lys  Glu Asn Ser Thr Leu  Gln Glu Met Asn Ser  Thr
            4605                4610                4615

aca gag tca aac  atc atc ctc tcc aat  gtg tct gtg ggg gct  att     14097
Thr Glu Ser Asn  Ile Ile Leu Ser Asn  Val Ser Val Gly Ala  Ile
            4620                4625                4630

act gaa gcc aca  aaa atg gaa gtc ccc  tct ttt gat gca aca  ttc     14142
Thr Glu Ala Thr  Lys Met Glu Val Pro  Ser Phe Asp Ala Thr  Phe
            4635                4640                4645

ata cca act cct  gct cag tca aca aag  ttc cca gat att ttc  tca     14187
Ile Pro Thr Pro  Ala Gln Ser Thr Lys  Phe Pro Asp Ile Phe  Ser
            4650                4655                4660

gta gcc agc agt  aga ctt tca aac tct  cct ccc atg aca ata  tct     14232
Val Ala Ser Ser  Arg Leu Ser Asn Ser  Pro Pro Met Thr Ile  Ser
            4665                4670                4675

acc cac atg acc  acc acc cag aca ggg  tct tct gga gct aca  tca     14277
Thr His Met Thr  Thr Thr Gln Thr Gly  Ser Ser Gly Ala Thr  Ser
            4680                4685                4690

aag att cca ctt  gcc tta gac aca tca  acc ttg gaa acc tca  gca     14322
Lys Ile Pro Leu  Ala Leu Asp Thr Ser  Thr Leu Glu Thr Ser  Ala
            4695                4700                4705
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ggg act cca tca  gtg gtg act gag ggg  ttt gcc cac tca aaa  ata      14367
Gly Thr Pro Ser  Val Val Thr Glu Gly  Phe Ala His Ser Lys  Ile
            4710                 4715                 4720

acc act gca atg  aac aat gat gtc aag  gac gtg tca cag aca  aac      14412
Thr Thr Ala Met  Asn Asn Asp Val Lys  Asp Val Ser Gln Thr  Asn
            4725                 4730                 4735

cct ccc ttt cag  gat gaa gcc agc tct  ccc tct tct caa gca  cct      14457
Pro Pro Phe Gln  Asp Glu Ala Ser Ser  Pro Ser Ser Gln Ala  Pro
            4740                 4745                 4750

gtc ctt gtc aca  acc tta cct tct tct  gtt gct ttc aca ccg  caa      14502
Val Leu Val Thr  Thr Leu Pro Ser Ser  Val Ala Phe Thr Pro  Gln
            4755                 4760                 4765

tgg cac agt acc  tcc tct cct gtt tct  atg tcc tca gtt ctt  act      14547
Trp His Ser Thr  Ser Ser Pro Val Ser  Met Ser Ser Val Leu  Thr
            4770                 4775                 4780

tct tca ctg gta  aag acc gca ggc aag  gtg gat aca agc tta  gaa      14592
Ser Ser Leu Val  Lys Thr Ala Gly Lys  Val Asp Thr Ser Leu  Glu
            4785                 4790                 4795

aca gtg acc agt  tca cct caa agt atg  agc aac act ttg gat  gac      14637
Thr Val Thr Ser  Ser Pro Gln Ser Met  Ser Asn Thr Leu Asp  Asp
            4800                 4805                 4810

ata tcg gtc act  tca gca gcc acc aca  gat ata gag aca acg  cat      14682
Ile Ser Val Thr  Ser Ala Ala Thr Thr  Asp Ile Glu Thr Thr  His
            4815                 4820                 4825

cct tcc ata aac  aca gta gtt acc aat  gtg ggg acc acc ggt  tca      14727
Pro Ser Ile Asn  Thr Val Val Thr Asn  Val Gly Thr Thr Gly  Ser
            4830                 4835                 4840

gca ttt gaa tca  cat tct act gtc tca  gct tac cca gag cca  tct      14772
Ala Phe Glu Ser  His Ser Thr Val Ser  Ala Tyr Pro Glu Pro  Ser
            4845                 4850                 4855

aaa agt cac att  ctc cca atg tta cca  cct cca cca tgg aag  aca      14817
Lys Ser His Ile  Leu Pro Met Leu Pro  Pro Pro Pro Trp Lys  Thr
            4860                 4865                 4870

cca caa ttt cca  cga tca ata cct aaa  tcc tct aag act aca  aga      14862
Pro Gln Phe Pro  Arg Ser Ile Pro Lys  Ser Ser Lys Thr Thr  Arg
            4875                 4880                 4885

act gag act gag  aca act tcc tcc ctg  act cct aaa ctg agg  gag      14907
Thr Glu Thr Glu  Thr Thr Ser Ser Leu  Thr Pro Lys Leu Arg  Glu
            4890                 4895                 4900

acc agc atc tcc  cag gag atc acc tcg  tcc aca gag aca agc  act      14952
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Thr Ser Ile Ser  Gln Glu Ile Thr Ser  Ser Thr Glu Thr Ser  Thr
            4905                 4910                 4915

gtt cct tac aaa  gag ctc act ggt gcc  act acc gag gta tcc  agg     14997
Val Pro Tyr Lys  Glu Leu Thr Gly Ala  Thr Thr Glu Val Ser  Arg
            4920                 4925                 4930

aca gat gtc act  tcc tct agc agt aca  tcc ttc cct ggc cct  gat     15042
Thr Asp Val Thr  Ser Ser Ser Ser Thr  Ser Phe Pro Gly Pro  Asp
            4935                 4940                 4945

cag tcc aca gtg  tca cta gac atc tcc  aca gaa acc aac acc  agg     15087
Gln Ser Thr Val  Ser Leu Asp Ile Ser  Thr Glu Thr Asn Thr  Arg
            4950                 4955                 4960

ctg tct acc tcc  cca ata atg aca gaa  tct gca gaa ata acc  atc     15132
Leu Ser Thr Ser  Pro Ile Met Thr Glu  Ser Ala Glu Ile Thr  Ile
            4965                 4970                 4975

acc acc caa aca  ggt cct cat ggg gct  aca tca cag gat act  ttt     15177
Thr Thr Gln Thr  Gly Pro His Gly Ala  Thr Ser Gln Asp Thr  Phe
            4980                 4985                 4990

acc atg gac cca  tca aat aca acc ccc  cag gca ggg atc cac  tca     15222
Thr Met Asp Pro  Ser Asn Thr Thr Pro  Gln Ala Gly Ile His  Ser
            4995                 5000                 5005

gct atg act cat  gga ttt tca caa ttg  gat gtg acc act ctt  atg     15267
Ala Met Thr His  Gly Phe Ser Gln Leu  Asp Val Thr Thr Leu  Met
            5010                 5015                 5020

agc aga att cca  cag gat gta tca tgg  aca agt cct ccc tct  gtg     15312
Ser Arg Ile Pro  Gln Asp Val Ser Trp  Thr Ser Pro Pro Ser  Val
            5025                 5030                 5035

gat aaa acc agc  tcc ccc tct tcc ttt  ctg tcc tca cct gca  atg     15357
Asp Lys Thr Ser  Ser Pro Ser Ser Phe  Leu Ser Ser Pro Ala  Met
            5040                 5045                 5050

acc aca cct tcc  ctg att tct tct acc  tta cca gag gat aag  ctc     15402
Thr Thr Pro Ser  Leu Ile Ser Ser Thr  Leu Pro Glu Asp Lys  Leu
            5055                 5060                 5065

tcc tct cct atg  act tca ctt ctc acc  tct ggc cta gtg aag  att     15447
Ser Ser Pro Met  Thr Ser Leu Leu Thr  Ser Gly Leu Val Lys  Ile
            5070                 5075                 5080

aca gac ata tta  cgt aca cgc ttg gaa  cct gtg acc agc tca  ctt     15492
Thr Asp Ile Leu  Arg Thr Arg Leu Glu  Pro Val Thr Ser Ser  Leu
            5085                 5090                 5095

cca aat ttc agc  agc acc tca gat aag  ata ctg gcc act tct  aaa     15537
Pro Asn Phe Ser  Ser Thr Ser Asp Lys  Ile Leu Ala Thr Ser  Lys
            5100                 5105                 5110
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gac agt aaa gac  aca aag gaa att ttt  cct tct ata aac aca  gaa     15582
Asp Ser Lys Asp  Thr Lys Glu Ile Phe  Pro Ser Ile Asn Thr  Glu
            5115                 5120                 5125

gag acc aat gtg  aaa gcc aac aac tct  gga cat gaa tcc cat  tcc     15627
Glu Thr Asn Val  Lys Ala Asn Asn Ser  Gly His Glu Ser His  Ser
            5130                 5135                 5140

cct gca ctg gct  gac tca gag aca ccc  aaa gcc aca act caa  atg     15672
Pro Ala Leu Ala  Asp Ser Glu Thr Pro  Lys Ala Thr Thr Gln  Met
            5145                 5150                 5155

gtt atc acc acc  act gtg gga gat cca  gct cct tcc aca tca  atg     15717
Val Ile Thr Thr  Thr Val Gly Asp Pro  Ala Pro Ser Thr Ser  Met
            5160                 5165                 5170

cca gtg cat ggt  tcc tct gag act aca  aac att aag aga gag  cca     15762
Pro Val His Gly  Ser Ser Glu Thr Thr  Asn Ile Lys Arg Glu  Pro
            5175                 5180                 5185

aca tat ttc ttg  act cct aga ctg aga  gag acc agt acc tct  cag     15807
Thr Tyr Phe Leu  Thr Pro Arg Leu Arg  Glu Thr Ser Thr Ser  Gln
            5190                 5195                 5200

gag tcc agc ttt  ccc acg gac aca agt  ttt cta ctt tcc aaa  gtc     15852
Glu Ser Ser Phe  Pro Thr Asp Thr Ser  Phe Leu Leu Ser Lys  Val
            5205                 5210                 5215

ccc act ggt act  att act gag gtc tcc  agt aca ggg gtc aac  tct     15897
Pro Thr Gly Thr  Ile Thr Glu Val Ser  Ser Thr Gly Val Asn  Ser
            5220                 5225                 5230

tct agc aaa att  tcc acc cca gac cat  gat aag tcc aca gtg  cca     15942
Ser Ser Lys Ile  Ser Thr Pro Asp His  Asp Lys Ser Thr Val  Pro
            5235                 5240                 5245

cct gac acc ttc  aca gga gag atc ccc  agg gtc ttc acc tcc  tct     15987
Pro Asp Thr Phe  Thr Gly Glu Ile Pro  Arg Val Phe Thr Ser  Ser
            5250                 5255                 5260

att aag aca aaa  tct gca gaa atg acg  atc acc acc caa gca  agt     16032
Ile Lys Thr Lys  Ser Ala Glu Met Thr  Ile Thr Thr Gln Ala  Ser
            5265                 5270                 5275

cct cct gag tct  gca tcg cac agt acc  ctt ccc ttg gac aca  tca     16077
Pro Pro Glu Ser  Ala Ser His Ser Thr  Leu Pro Leu Asp Thr  Ser
            5280                 5285                 5290

acc aca ctt tcc  cag gga ggg act cat  tca act gtg act cag  gga     16122
Thr Thr Leu Ser  Gln Gly Gly Thr His  Ser Thr Val Thr Gln  Gly
            5295                 5300                 5305

ttc cca tac tca  gag gtg acc act ctc  atg ggc atg ggt cct  ggg     16167
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Phe Pro Tyr Ser  Glu Val Thr Thr Leu  Met Gly Met Gly Pro  Gly
            5310                 5315                 5320

aat gtg tca tgg  atg aca act ccc cct  gtg gaa gaa acc agc  tct     16212
Asn Val Ser Trp  Met Thr Thr Pro Pro  Val Glu Glu Thr Ser  Ser
            5325                 5330                 5335

gtg tct tcc ctg  atg tct tca cct gcc  atg aca tcc cct tct  cct     16257
Val Ser Ser Leu  Met Ser Ser Pro Ala  Met Thr Ser Pro Ser  Pro
            5340                 5345                 5350

gtt tcc tcc aca  tca cca cag agc atc  ccc tcc tct cct ctt  cct     16302
Val Ser Ser Thr  Ser Pro Gln Ser Ile  Pro Ser Ser Pro Leu  Pro
            5355                 5360                 5365

gtg act gca ctt  cct act tct gtt ctg  gtg aca acc aca gat  gtg     16347
Val Thr Ala Leu  Pro Thr Ser Val Leu  Val Thr Thr Thr Asp  Val
            5370                 5375                 5380

ttg ggc aca aca  agc cca gag tct gta  acc agt tca cct cca  aat     16392
Leu Gly Thr Thr  Ser Pro Glu Ser Val  Thr Ser Ser Pro Pro  Asn
            5385                 5390                 5395

ttg agc agc atc  act cat gag aga ccg  gcc act tac aaa gac  act     16437
Leu Ser Ser Ile  Thr His Glu Arg Pro  Ala Thr Tyr Lys Asp  Thr
            5400                 5405                 5410

gca cac aca gaa  gcc gcc atg cat cat  tcc aca aac acc gca  gtg     16482
Ala His Thr Glu  Ala Ala Met His His  Ser Thr Asn Thr Ala  Val
            5415                 5420                 5425

acc aat gta ggg  act tcc ggg tct gga  cat aaa tca caa tcc  tct     16527
Thr Asn Val Gly  Thr Ser Gly Ser Gly  His Lys Ser Gln Ser  Ser
            5430                 5435                 5440

gtc cta gct gac  tca gag aca tcg aaa  gcc aca cct ctg atg  agt     16572
Val Leu Ala Asp  Ser Glu Thr Ser Lys  Ala Thr Pro Leu Met  Ser
            5445                 5450                 5455

acc acc tcc acc  ctg ggg gac aca agt  gtt tcc aca tca act  cct     16617
Thr Thr Ser Thr  Leu Gly Asp Thr Ser  Val Ser Thr Ser Thr  Pro
            5460                 5465                 5470

aat atc tct cag  act aac caa att caa  aca gag cca aca gca  tcc     16662
Asn Ile Ser Gln  Thr Asn Gln Ile Gln  Thr Glu Pro Thr Ala  Ser
            5475                 5480                 5485

ctg agc cct aga  ctg agg gag agc agc  acg tct gag aag acc  agc     16707
Leu Ser Pro Arg  Leu Arg Glu Ser Ser  Thr Ser Glu Lys Thr  Ser
            5490                 5495                 5500

tca aca aca gag  aca aat act gcc ttt  tct tat gtg ccc aca  ggt     16752
Ser Thr Thr Glu  Thr Asn Thr Ala Phe  Ser Tyr Val Pro Thr  Gly
            5505                 5510                 5515
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gct att act cag  gcc tcc aga aca gaa  atc tcc tct agc aga  aca      16797
Ala Ile Thr Gln  Ala Ser Arg Thr Glu  Ile Ser Ser Ser Arg  Thr
            5520                 5525                 5530

tcc atc tca gac  ctt gat cgg ccc aca  ata gca ccc gac atc  tcc      16842
Ser Ile Ser Asp  Leu Asp Arg Pro Thr  Ile Ala Pro Asp Ile  Ser
            5535                 5540                 5545

aca gga atg atc  acc agg ctc ttc acc  tcc ccc atc atg aca  aaa      16887
Thr Gly Met Ile  Thr Arg Leu Phe Thr  Ser Pro Ile Met Thr  Lys
            5550                 5555                 5560

tct gca gaa atg  acc gtc acc act caa  aca act act cct ggg  gct      16932
Ser Ala Glu Met  Thr Val Thr Thr Gln  Thr Thr Thr Pro Gly  Ala
            5565                 5570                 5575

aca tca cag ggt  atc ctt cct tgg gac  aca tca acc aca ctt  ttc      16977
Thr Ser Gln Gly  Ile Leu Pro Trp Asp  Thr Ser Thr Thr Leu  Phe
            5580                 5585                 5590

cag gga ggg act  cat tca acc gtg tct  cag gga ttc cca cac  tca      17022
Gln Gly Gly Thr  His Ser Thr Val Ser  Gln Gly Phe Pro His  Ser
            5595                 5600                 5605

gag ata acc act  ctt cgg agc aga acc  cct gga gat gtg tca  tgg      17067
Glu Ile Thr Thr  Leu Arg Ser Arg Thr  Pro Gly Asp Val Ser  Trp
            5610                 5615                 5620

atg aca act ccc  cct gtg gaa gaa acc  agc tct ggg ttt tcc  ctg      17112
Met Thr Thr Pro  Pro Val Glu Glu Thr  Ser Ser Gly Phe Ser  Leu
            5625                 5630                 5635

atg tca cct tcc  atg aca tcc cct tct  cct gtt tcc tcc aca  tca      17157
Met Ser Pro Ser  Met Thr Ser Pro Ser  Pro Val Ser Ser Thr  Ser
            5640                 5645                 5650

cca gag agc atc  ccc tcc tct cct ctc  cct gtg act gca ctt  ctt      17202
Pro Glu Ser Ile  Pro Ser Ser Pro Leu  Pro Val Thr Ala Leu  Leu
            5655                 5660                 5665

act tct gtt ctg  gtg aca acc acc aat  gta ttg ggc aca aca  agc      17247
Thr Ser Val Leu  Val Thr Thr Thr Asn  Val Leu Gly Thr Thr  Ser
            5670                 5675                 5680

cca gag acc gta  acg agt tca cct cca  aat tta agc agc ccc  aca      17292
Pro Glu Thr Val  Thr Ser Ser Pro Pro  Asn Leu Ser Ser Pro  Thr
            5685                 5690                 5695

cag gag aga ctg  acc act tac aaa gac  act gcg cac aca gaa  gcc      17337
Gln Glu Arg Leu  Thr Thr Tyr Lys Asp  Thr Ala His Thr Glu  Ala
            5700                 5705                 5710

atg cat gct tcc  atg cat aca aac act  gca gtg gcc aac gtc  ggg      17382
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Met His Ala Ser  Met His Thr Asn Thr  Ala Val Ala Asn Val  Gly
            5715                 5720                 5725

acc tcc att tct  gga cat gaa tca caa  tct tct gtc cca gct  gat     17427
Thr Ser Ile Ser  Gly His Glu Ser Gln  Ser Ser Val Pro Ala  Asp
            5730                 5735                 5740

tca cac aca tcc  aaa gcc aca tct cca  atg ggt atc acc ttc  gcc     17472
Ser His Thr Ser  Lys Ala Thr Ser Pro  Met Gly Ile Thr Phe  Ala
            5745                 5750                 5755

atg ggg gat aca  agt gtt tct aca tca  act cct gcc ttc ttt  gag     17517
Met Gly Asp Thr  Ser Val Ser Thr Ser  Thr Pro Ala Phe Phe  Glu
            5760                 5765                 5770

act aga att cag  act gaa tca aca tcc  tct ttg att cct gga  tta     17562
Thr Arg Ile Gln  Thr Glu Ser Thr Ser  Ser Leu Ile Pro Gly  Leu
            5775                 5780                 5785

agg gac acc agg  acg tct gag gag atc  aac act gtg aca gag  acc     17607
Arg Asp Thr Arg  Thr Ser Glu Glu Ile  Asn Thr Val Thr Glu  Thr
            5790                 5795                 5800

agc act gtc ctt  tca gaa gtg ccc act  act act act act gag  gtc     17652
Ser Thr Val Leu  Ser Glu Val Pro Thr  Thr Thr Thr Thr Glu  Val
            5805                 5810                 5815

tcc agg aca gaa  gtt atc act tcc agc  aga aca acc atc tca  ggg     17697
Ser Arg Thr Glu  Val Ile Thr Ser Ser  Arg Thr Thr Ile Ser  Gly
            5820                 5825                 5830

cct gat cat tcc  aaa atg tca ccc tac  atc tcc aca gaa acc  atc     17742
Pro Asp His Ser  Lys Met Ser Pro Tyr  Ile Ser Thr Glu Thr  Ile
            5835                 5840                 5845

acc agg ctc tcc  act ttt cct ttt gta  aca gga tcc aca gaa  atg     17787
Thr Arg Leu Ser  Thr Phe Pro Phe Val  Thr Gly Ser Thr Glu  Met
            5850                 5855                 5860

gcc atc acc aac  caa aca ggt cct ata  ggg act atc tca cag  gct     17832
Ala Ile Thr Asn  Gln Thr Gly Pro Ile  Gly Thr Ile Ser Gln  Ala
            5865                 5870                 5875

acc ctt acc ctg  gac aca tca agc aca  gct tcc tgg gaa ggg  act     17877
Thr Leu Thr Leu  Asp Thr Ser Ser Thr  Ala Ser Trp Glu Gly  Thr
            5880                 5885                 5890

cac tca cct gtg  act cag aga ttt cca  cac tca gag gag acc  act     17922
His Ser Pro Val  Thr Gln Arg Phe Pro  His Ser Glu Glu Thr  Thr
            5895                 5900                 5905

act atg agc aga  agt act aag ggc gtg  tca tgg caa agc cct  ccc     17967
Thr Met Ser Arg  Ser Thr Lys Gly Val  Ser Trp Gln Ser Pro  Pro
            5910                 5915                 5920
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tct gtg gaa gaa  acc agt tct cct tct  tcc cca gtg cct tta  cct      18012
Ser Val Glu Glu  Thr Ser Ser Pro Ser  Ser Pro Val Pro Leu  Pro
            5925                 5930                 5935

gca ata acc tca  cat tca tct ctt tat  tcc gca gta tca gga  agt      18057
Ala Ile Thr Ser  His Ser Ser Leu Tyr  Ser Ala Val Ser Gly  Ser
            5940                 5945                 5950

agc ccc act tct  gct ctc cct gtg act  tcc ctt ctc acc tct  ggc      18102
Ser Pro Thr Ser  Ala Leu Pro Val Thr  Ser Leu Leu Thr Ser  Gly
            5955                 5960                 5965

agg agg aag acc  ata gac atg ttg gac  aca cac tca gaa ctt  gtg      18147
Arg Arg Lys Thr  Ile Asp Met Leu Asp  Thr His Ser Glu Leu  Val
            5970                 5975                 5980

acc agc tcc tta  cca agt gca agt agc  ttc tca ggt gag ata  ctc      18192
Thr Ser Ser Leu  Pro Ser Ala Ser Ser  Phe Ser Gly Glu Ile  Leu
            5985                 5990                 5995

act tct gaa gcc  tcc aca aat aca gag  aca att cac ttt tca  gag      18237
Thr Ser Glu Ala  Ser Thr Asn Thr Glu  Thr Ile His Phe Ser  Glu
            6000                 6005                 6010

aac aca gca gaa  acc aat atg ggg acc  acc aat tct atg cat  aaa      18282
Asn Thr Ala Glu  Thr Asn Met Gly Thr  Thr Asn Ser Met His  Lys
            6015                 6020                 6025

cta cat tcc tct  gtc tca atc cac tcc  cag cca tcc gga cac  aca      18327
Leu His Ser Ser  Val Ser Ile His Ser  Gln Pro Ser Gly His  Thr
            6030                 6035                 6040

cct cca aag gtt  act gga tct atg atg  gag gac gct att gtt  tcc      18372
Pro Pro Lys Val  Thr Gly Ser Met Met  Glu Asp Ala Ile Val  Ser
            6045                 6050                 6055

aca tca aca cct  ggt tct cct gag act  aaa aat gtt gac aga  gac      18417
Thr Ser Thr Pro  Gly Ser Pro Glu Thr  Lys Asn Val Asp Arg  Asp
            6060                 6065                 6070

tca aca tcc cct  ctg act cct gaa ctg  aaa gag gac agc acc  gcc      18462
Ser Thr Ser Pro  Leu Thr Pro Glu Leu  Lys Glu Asp Ser Thr  Ala
            6075                 6080                 6085

ctg gtg atg aac  tca act aca gag tca  aac act gtt ttc tcc  agt      18507
Leu Val Met Asn  Ser Thr Thr Glu Ser  Asn Thr Val Phe Ser  Ser
            6090                 6095                 6100

gtg tcc ctg gat  gct gct act gag gtc  tcc agg gca gaa gtc  acc      18552
Val Ser Leu Asp  Ala Ala Thr Glu Val  Ser Arg Ala Glu Val  Thr
            6105                 6110                 6115

tac tat gat cct  aca ttc atg cca gct  tct gct cag tca aca  aag      18597
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Tyr Tyr Asp Pro  Thr Phe Met Pro Ala  Ser Ala Gln Ser Thr  Lys
            6120                 6125                 6130

tcc cca gac att  tca cct gaa gcc agc  agc agt cat tct aac  tct     18642
Ser Pro Asp Ile  Ser Pro Glu Ala Ser  Ser Ser His Ser Asn  Ser
            6135                 6140                 6145

cct ccc ttg aca  ata tct aca cac aag  acc atc gcc aca caa  aca     18687
Pro Pro Leu Thr  Ile Ser Thr His Lys  Thr Ile Ala Thr Gln  Thr
            6150                 6155                 6160

ggt cct tct ggg  gtg aca tct ctt ggc  caa ctg acc ctg gac  aca     18732
Gly Pro Ser Gly  Val Thr Ser Leu Gly  Gln Leu Thr Leu Asp  Thr
            6165                 6170                 6175

tca acc ata gcc  acc tca gca gga act  cca tca gcc aga act  cag     18777
Ser Thr Ile Ala  Thr Ser Ala Gly Thr  Pro Ser Ala Arg Thr  Gln
            6180                 6185                 6190

gat ttt gta gat  tca gaa aca acc agt  gtc atg aac aat gat  ctc     18822
Asp Phe Val Asp  Ser Glu Thr Thr Ser  Val Met Asn Asn Asp  Leu
            6195                 6200                 6205

aat gat gtg ttg  aag aca agc cct ttc  tct gca gaa gaa gcc  aac     18867
Asn Asp Val Leu  Lys Thr Ser Pro Phe  Ser Ala Glu Glu Ala  Asn
            6210                 6215                 6220

tct ctc tct tct  cag gca cct ctc ctt  gtg aca acc tca cct  tct     18912
Ser Leu Ser Ser  Gln Ala Pro Leu Leu  Val Thr Thr Ser Pro  Ser
            6225                 6230                 6235

cct gta act tcc  aca ttg caa gag cac  agt acc tcc tct ctt  gtt     18957
Pro Val Thr Ser  Thr Leu Gln Glu His  Ser Thr Ser Ser Leu  Val
            6240                 6245                 6250

tct gtg acc tca  gta ccc acc cct aca  ctg gcg aag atc aca  gac     19002
Ser Val Thr Ser  Val Pro Thr Pro Thr  Leu Ala Lys Ile Thr  Asp
            6255                 6260                 6265

atg gac aca aac  tta gaa cct gtg act  cgt tca cct caa aat  tta     19047
Met Asp Thr Asn  Leu Glu Pro Val Thr  Arg Ser Pro Gln Asn  Leu
            6270                 6275                 6280

agg aac acc ttg  gcc act tca gaa gcc  acc aca gat aca cac  aca     19092
Arg Asn Thr Leu  Ala Thr Ser Glu Ala  Thr Thr Asp Thr His  Thr
            6285                 6290                 6295

atg cat cct tct  ata aac aca gca atg  gcc aat gtg ggg acc  acc     19137
Met His Pro Ser  Ile Asn Thr Ala Met  Ala Asn Val Gly Thr  Thr
            6300                 6305                 6310

agt tca cca aat  gaa ttc tat ttt act  gtc tca cct gac tca  gac     19182
Ser Ser Pro Asn  Glu Phe Tyr Phe Thr  Val Ser Pro Asp Ser  Asp
            6315                 6320                 6325
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cca tat aaa gcc  aca tcc gca gta gtt  atc act tcc acc tcg  ggg     19227
Pro Tyr Lys Ala  Thr Ser Ala Val Val  Ile Thr Ser Thr Ser  Gly
            6330                 6335                 6340

gac tca ata gtt  tcc aca tca atg cct  aga tcc tct gcg atg  aaa     19272
Asp Ser Ile Val  Ser Thr Ser Met Pro  Arg Ser Ser Ala Met  Lys
            6345                 6350                 6355

aag att gag tct  gag aca act ttc tcc  ctg ata ttt aga ctg  agg     19317
Lys Ile Glu Ser  Glu Thr Thr Phe Ser  Leu Ile Phe Arg Leu  Arg
            6360                 6365                 6370

gag act agc acc  tcc cag aaa att ggc  tca tcc tca gac aca  agc     19362
Glu Thr Ser Thr  Ser Gln Lys Ile Gly  Ser Ser Ser Asp Thr  Ser
            6375                 6380                 6385

acg gtc ttt gac  aaa gca ttc act gct  gct act act gag gtc  tcc     19407
Thr Val Phe Asp  Lys Ala Phe Thr Ala  Ala Thr Thr Glu Val  Ser
            6390                 6395                 6400

aga aca gaa ctc  acc tcc tct agc aga  aca tcc atc caa ggc  act     19452
Arg Thr Glu Leu  Thr Ser Ser Ser Arg  Thr Ser Ile Gln Gly  Thr
            6405                 6410                 6415

gaa aag ccc aca  atg tca ccg gac acc  tcc aca aga tct gtc  acc     19497
Glu Lys Pro Thr  Met Ser Pro Asp Thr  Ser Thr Arg Ser Val  Thr
            6420                 6425                 6430

atg ctt tct act  ttt gct ggc ctg aca  aaa tcc gaa gaa agg  acc     19542
Met Leu Ser Thr  Phe Ala Gly Leu Thr  Lys Ser Glu Glu Arg  Thr
            6435                 6440                 6445

att gcc acc caa  aca ggt cct cat agg  gcg aca tca cag ggt  acc     19587
Ile Ala Thr Gln  Thr Gly Pro His Arg  Ala Thr Ser Gln Gly  Thr
            6450                 6455                 6460

ctt acc tgg gac  aca tca atc aca acc  tca cag gca ggg acc  cac     19632
Leu Thr Trp Asp  Thr Ser Ile Thr Thr  Ser Gln Ala Gly Thr  His
            6465                 6470                 6475

tca gct atg act  cat gga ttt tca caa  tta gat ttg tcc act  ctt     19677
Ser Ala Met Thr  His Gly Phe Ser Gln  Leu Asp Leu Ser Thr  Leu
            6480                 6485                 6490

acg agt aga gtt  cct gag tac ata tca  ggg aca agc cca ccc  tct     19722
Thr Ser Arg Val  Pro Glu Tyr Ile Ser  Gly Thr Ser Pro Pro  Ser
            6495                 6500                 6505

gtg gaa aaa acc  agc tct tcc tct tcc  ctt ctg tct tta cca  gca     19767
Val Glu Lys Thr  Ser Ser Ser Ser Ser  Leu Leu Ser Leu Pro  Ala
            6510                 6515                 6520

ata acc tca ccg  tcc cct gta cct act  aca tta cca gaa agt  agg     19812
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Ile Thr Ser Pro  Ser Pro Val Pro Thr  Thr Leu Pro Glu Ser  Arg
            6525                 6530                 6535

ccg tct tct cct  gtt cat ctg act tca  ctc ccc acc tct ggc  cta     19857
Pro Ser Ser Pro  Val His Leu Thr Ser  Leu Pro Thr Ser Gly  Leu
            6540                 6545                 6550

gtg aag acc aca  gat atg ctg gca tct  gtg gcc agt tta cct  cca     19902
Val Lys Thr Thr  Asp Met Leu Ala Ser  Val Ala Ser Leu Pro  Pro
            6555                 6560                 6565

aac ttg ggc agc  acc tca cat aag ata  ccg act act tca gaa  gac     19947
Asn Leu Gly Ser  Thr Ser His Lys Ile  Pro Thr Thr Ser Glu  Asp
            6570                 6575                 6580

att aaa gat aca  gag aaa atg tat cct  tcc aca aac ata gca  gta     19992
Ile Lys Asp Thr  Glu Lys Met Tyr Pro  Ser Thr Asn Ile Ala  Val
            6585                 6590                 6595

acc aat gtg ggg  acc acc act tct gaa  aag gaa tct tat tcg  tct     20037
Thr Asn Val Gly  Thr Thr Thr Ser Glu  Lys Glu Ser Tyr Ser  Ser
            6600                 6605                 6610

gtc cca gcc tac  tca gaa cca ccc aaa  gtc acc tct cca atg  gtt     20082
Val Pro Ala Tyr  Ser Glu Pro Pro Lys  Val Thr Ser Pro Met  Val
            6615                 6620                 6625

acc tct ttc aac  ata agg gac acc att  gtt tcc aca tcc atg  cct     20127
Thr Ser Phe Asn  Ile Arg Asp Thr Ile  Val Ser Thr Ser Met  Pro
            6630                 6635                 6640

ggc tcc tct gag  att aca agg att gag  atg gag tca aca ttc  tcc     20172
Gly Ser Ser Glu  Ile Thr Arg Ile Glu  Met Glu Ser Thr Phe  Ser
            6645                 6650                 6655

gtg gct cat ggg  ctg aag gga acc agc  acc tcc cag gac ccc  atc     20217
Val Ala His Gly  Leu Lys Gly Thr Ser  Thr Ser Gln Asp Pro  Ile
            6660                 6665                 6670

gta tcc aca gag  aaa agt gct gtc ctt  cac aag ttg acc act  ggt     20262
Val Ser Thr Glu  Lys Ser Ala Val Leu  His Lys Leu Thr Thr  Gly
            6675                 6680                 6685

gct act gag acc  tct agg aca gaa gtt  gcc tct tct aga aga  aca     20307
Ala Thr Glu Thr  Ser Arg Thr Glu Val  Ala Ser Ser Arg Arg  Thr
            6690                 6695                 6700

tcc att cca ggc  cct gat cat tcc aca  gag tca cca gac atc  tcc     20352
Ser Ile Pro Gly  Pro Asp His Ser Thr  Glu Ser Pro Asp Ile  Ser
            6705                 6710                 6715

act gaa gtg atc  ccc agc ctg cct atc  tcc ctt ggc att aca  gaa     20397
Thr Glu Val Ile  Pro Ser Leu Pro Ile  Ser Leu Gly Ile Thr  Glu
            6720                 6725                 6730
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tct tca aat atg  acc atc atc act cga  aca ggt cct cct ctt  ggc      20442
Ser Ser Asn Met  Thr Ile Ile Thr Arg  Thr Gly Pro Pro Leu  Gly
            6735                 6740                 6745

tct aca tca cag  ggc aca ttt acc ttg  gac aca cca act aca  tcc      20487
Ser Thr Ser Gln  Gly Thr Phe Thr Leu  Asp Thr Pro Thr Thr  Ser
            6750                 6755                 6760

tcc agg gca gga  aca cac tcg atg gcg  act cag gaa ttt cca  cac      20532
Ser Arg Ala Gly  Thr His Ser Met Ala  Thr Gln Glu Phe Pro  His
            6765                 6770                 6775

tca gaa atg acc  act gtc atg aac aag  gac cct gag att cta  tca      20577
Ser Glu Met Thr  Thr Val Met Asn Lys  Asp Pro Glu Ile Leu  Ser
            6780                 6785                 6790

tgg aca atc cct  cct tct ata gag aaa  acc agc ttc tcc tct  tcc      20622
Trp Thr Ile Pro  Pro Ser Ile Glu Lys  Thr Ser Phe Ser Ser  Ser
            6795                 6800                 6805

ctg atg cct tca  cca gcc atg act tca  cct cct gtt tcc tca  aca      20667
Leu Met Pro Ser  Pro Ala Met Thr Ser  Pro Pro Val Ser Ser  Thr
            6810                 6815                 6820

tta cca aag acc  att cac acc act cct  tct cct atg acc tca  ctg      20712
Leu Pro Lys Thr  Ile His Thr Thr Pro  Ser Pro Met Thr Ser  Leu
            6825                 6830                 6835

ctc acc cct agc  cta gtg atg acc aca  gac aca ttg ggc aca  agc      20757
Leu Thr Pro Ser  Leu Val Met Thr Thr  Asp Thr Leu Gly Thr  Ser
            6840                 6845                 6850

cca gaa cct aca  acc agt tca cct cca  aat ttg agc agt acc  tca      20802
Pro Glu Pro Thr  Thr Ser Ser Pro Pro  Asn Leu Ser Ser Thr  Ser
            6855                 6860                 6865

cat gag ata ctg  aca aca gat gaa gac  acc aca gct ata gaa  gcc      20847
His Glu Ile Leu  Thr Thr Asp Glu Asp  Thr Thr Ala Ile Glu  Ala
            6870                 6875                 6880

atg cat cct tcc  aca agc aca gca gcg  act aat gtg gaa acc  acc      20892
Met His Pro Ser  Thr Ser Thr Ala Ala  Thr Asn Val Glu Thr  Thr
            6885                 6890                 6895

agt tct gga cat  ggg tca caa tcc tct  gtc cta gct gac tca  gaa      20937
Ser Ser Gly His  Gly Ser Gln Ser Ser  Val Leu Ala Asp Ser  Glu
            6900                 6905                 6910

aaa acc aag gcc  aca gct cca atg gat  acc acc tcc acc atg  ggg      20982
Lys Thr Lys Ala  Thr Ala Pro Met Asp  Thr Thr Ser Thr Met  Gly
            6915                 6920                 6925

cat aca act gtt  tcc aca tca atg tct  gtt tcc tct gag act  aca      21027
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His Thr Thr Val  Ser Thr Ser Met Ser  Val Ser Ser Glu Thr  Thr
            6930                 6935                 6940

aaa att aag aga  gag tca aca tat tcc  ttg act cct gga ctg  aga     21072
Lys Ile Lys Arg  Glu Ser Thr Tyr Ser  Leu Thr Pro Gly Leu  Arg
            6945                 6950                 6955

gag acc agc att  tcc caa aat gcc agc  ttt tcc act gac aca  agt     21117
Glu Thr Ser Ile  Ser Gln Asn Ala Ser  Phe Ser Thr Asp Thr  Ser
            6960                 6965                 6970

att gtt ctt tca  gaa gtc ccc act ggt  act act gct gag gtc  tcc     21162
Ile Val Leu Ser  Glu Val Pro Thr Gly  Thr Thr Ala Glu Val  Ser
            6975                 6980                 6985

agg aca gaa gtc  acc tcc tct ggt aga  aca tcc atc cct ggc  cct     21207
Arg Thr Glu Val  Thr Ser Ser Gly Arg  Thr Ser Ile Pro Gly  Pro
            6990                 6995                 7000

tct cag tcc aca  gtt ttg cca gaa ata  tcc aca aga aca atg  aca     21252
Ser Gln Ser Thr  Val Leu Pro Glu Ile  Ser Thr Arg Thr Met  Thr
            7005                 7010                 7015

agg ctc ttt gcc  tcg ccc acc atg aca  gaa tca gca gaa atg  acc     21297
Arg Leu Phe Ala  Ser Pro Thr Met Thr  Glu Ser Ala Glu Met  Thr
            7020                 7025                 7030

atc ccc act caa  aca ggt cct tct ggg  tct acc tca cag gat  acc     21342
Ile Pro Thr Gln  Thr Gly Pro Ser Gly  Ser Thr Ser Gln Asp  Thr
            7035                 7040                 7045

ctt acc ttg gac  aca tcc acc aca aag  tcc cag gca aag act  cat     21387
Leu Thr Leu Asp  Thr Ser Thr Thr Lys  Ser Gln Ala Lys Thr  His
            7050                 7055                 7060

tca act ttg act  cag aga ttt cca cac  tca gag atg acc act  ctc     21432
Ser Thr Leu Thr  Gln Arg Phe Pro His  Ser Glu Met Thr Thr  Leu
            7065                 7070                 7075

atg agc aga ggt  cct gga gat atg tca  tgg caa agc tct ccc  tct     21477
Met Ser Arg Gly  Pro Gly Asp Met Ser  Trp Gln Ser Ser Pro  Ser
            7080                 7085                 7090

ctg gaa aat ccc  agc tct ctc cct tcc  ctg ctg tct tta cct  gcc     21522
Leu Glu Asn Pro  Ser Ser Leu Pro Ser  Leu Leu Ser Leu Pro  Ala
            7095                 7100                 7105

aca acc tca cct  cct ccc att tcc tcc  aca tta cca gtg act  atc     21567
Thr Thr Ser Pro  Pro Pro Ile Ser Ser  Thr Leu Pro Val Thr  Ile
            7110                 7115                 7120

tcc tcc tct cct  ctt cct gtg act tca  ctt ctc acc tct agc  ccg     21612
Ser Ser Ser Pro  Leu Pro Val Thr Ser  Leu Leu Thr Ser Ser  Pro
            7125                 7130                 7135
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gta acg acc aca  gac atg tta cac aca  agc cca gaa ctt gta  acc      21657
Val Thr Thr Thr  Asp Met Leu His Thr  Ser Pro Glu Leu Val  Thr
            7140                 7145                 7150

agt tca cct cca  aag ctg agc cac act  tca gat gag aga ctg  acc      21702
Ser Ser Pro Pro  Lys Leu Ser His Thr  Ser Asp Glu Arg Leu  Thr
            7155                 7160                 7165

act ggc aag gac  acc aca aat aca gaa  gct gtg cat cct tcc  aca      21747
Thr Gly Lys Asp  Thr Thr Asn Thr Glu  Ala Val His Pro Ser  Thr
            7170                 7175                 7180

aac aca gca gcg  tcc aat gtg gag att  ccc agc tct gga cat  gaa      21792
Asn Thr Ala Ala  Ser Asn Val Glu Ile  Pro Ser Ser Gly His  Glu
            7185                 7190                 7195

tcc cct tcc tct  gcc tta gct gac tca  gag aca tcc aaa gcc  aca      21837
Ser Pro Ser Ser  Ala Leu Ala Asp Ser  Glu Thr Ser Lys Ala  Thr
            7200                 7205                 7210

tca cca atg ttt  att acc tcc acc cag  gag gat aca act gtt  gcc      21882
Ser Pro Met Phe  Ile Thr Ser Thr Gln  Glu Asp Thr Thr Val  Ala
            7215                 7220                 7225

ata tca acc cct  cac ttc ttg gag act  agc aga att cag aaa  gag      21927
Ile Ser Thr Pro  His Phe Leu Glu Thr  Ser Arg Ile Gln Lys  Glu
            7230                 7235                 7240

tca att tcc tcc  ctg agc cct aaa ttg  agg gag aca ggc agt  tct      21972
Ser Ile Ser Ser  Leu Ser Pro Lys Leu  Arg Glu Thr Gly Ser  Ser
            7245                 7250                 7255

gtg gag aca agc  tca gcc ata gag aca  agt gct gtc ctt tct  gaa      22017
Val Glu Thr Ser  Ser Ala Ile Glu Thr  Ser Ala Val Leu Ser  Glu
            7260                 7265                 7270

gtg tcc gtt ggt  gct act act gag atc  tcc agg aca gaa gtc  acc      22062
Val Ser Val Gly  Ala Thr Thr Glu Ile  Ser Arg Thr Glu Val  Thr
            7275                 7280                 7285

tcc tct agc aga  aca tcc atc tct ggt  tct gct gag tcc aca  atg      22107
Ser Ser Ser Arg  Thr Ser Ile Ser Gly  Ser Ala Glu Ser Thr  Met
            7290                 7295                 7300

ttg cca gaa ata  tcc acc aca aga aaa  atc att aag ttc cct  act      22152
Leu Pro Glu Ile  Ser Thr Thr Arg Lys  Ile Ile Lys Phe Pro  Thr
            7305                 7310                 7315

tcc ccc atc ctg  gca gaa tca tca gaa  atg acc atc aag acc  caa      22197
Ser Pro Ile Leu  Ala Glu Ser Ser Glu  Met Thr Ile Lys Thr  Gln
            7320                 7325                 7330

aca agt cct cct  ggg tct aca tca gag  agt acc ttt aca tta  gac      22242
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Thr Ser Pro Pro  Gly Ser Thr Ser Glu  Ser Thr Phe Thr Leu  Asp
            7335                 7340                 7345

aca tca acc act  ccc tcc ttg gta ata  acc cat tcg act atg  act     22287
Thr Ser Thr Thr  Pro Ser Leu Val Ile  Thr His Ser Thr Met  Thr
            7350                 7355                 7360

cag aga ttg cca  cac tca gag ata acc  act ctt gtg agt aga  ggt     22332
Gln Arg Leu Pro  His Ser Glu Ile Thr  Thr Leu Val Ser Arg  Gly
            7365                 7370                 7375

gct ggg gat gtg  cca cgg ccc agc tct  ctc cct gtg gaa gaa  aca     22377
Ala Gly Asp Val  Pro Arg Pro Ser Ser  Leu Pro Val Glu Glu  Thr
            7380                 7385                 7390

agc cct cca tct  tcc cag ctg tct tta  tct gcc atg atc tca  cct     22422
Ser Pro Pro Ser  Ser Gln Leu Ser Leu  Ser Ala Met Ile Ser  Pro
            7395                 7400                 7405

tct cct gtt tct  tcc aca tta cca gca  agt agc cac tcc tct  tct     22467
Ser Pro Val Ser  Ser Thr Leu Pro Ala  Ser Ser His Ser Ser  Ser
            7410                 7415                 7420

gct tct gtg act  tca ctt ctc aca cca  ggc caa gtg aag act  act     22512
Ala Ser Val Thr  Ser Leu Leu Thr Pro  Gly Gln Val Lys Thr  Thr
            7425                 7430                 7435

gag gtg ttg gac  gca agt gca gaa cct  gaa acc agt tca cct  cca     22557
Glu Val Leu Asp  Ala Ser Ala Glu Pro  Glu Thr Ser Ser Pro  Pro
            7440                 7445                 7450

agt ttg agc agc  acc tca gtt gaa ata  ctg gcc acc tct gaa  gtc     22602
Ser Leu Ser Ser  Thr Ser Val Glu Ile  Leu Ala Thr Ser Glu  Val
            7455                 7460                 7465

acc aca gat acg  gag aaa att cat cct  ttc tca aac acg gca  gta     22647
Thr Thr Asp Thr  Glu Lys Ile His Pro  Phe Ser Asn Thr Ala  Val
            7470                 7475                 7480

acc aaa gtt gga  act tcc agt tct gga  cat gaa tcc cct tcc  tct     22692
Thr Lys Val Gly  Thr Ser Ser Ser Gly  His Glu Ser Pro Ser  Ser
            7485                 7490                 7495

gtc cta cct gac  tca gag aca acc aaa  gcc aca tcg gca atg  ggt     22737
Val Leu Pro Asp  Ser Glu Thr Thr Lys  Ala Thr Ser Ala Met  Gly
            7500                 7505                 7510

acc atc tcc att  atg ggg gat aca agt  gtt tct aca tta act  cct     22782
Thr Ile Ser Ile  Met Gly Asp Thr Ser  Val Ser Thr Leu Thr  Pro
            7515                 7520                 7525

gcc tta tct aac  act agg aaa att cag  tca gag cca gct tcc  tca     22827
Ala Leu Ser Asn  Thr Arg Lys Ile Gln  Ser Glu Pro Ala Ser  Ser
            7530                 7535                 7540
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ctg acc acc aga  ttg agg gag acc agc  acc tct gaa gag acc  agc      22872
Leu Thr Thr Arg  Leu Arg Glu Thr Ser  Thr Ser Glu Glu Thr  Ser
            7545                 7550                 7555

tta gcc aca gaa  gca aac act gtt ctt  tct aaa gtg tcc act  ggt      22917
Leu Ala Thr Glu  Ala Asn Thr Val Leu  Ser Lys Val Ser Thr  Gly
            7560                 7565                 7570

gct act act gag  gtc tcc agg aca gaa  gcc atc tcc ttt agc  aga      22962
Ala Thr Thr Glu  Val Ser Arg Thr Glu  Ala Ile Ser Phe Ser  Arg
            7575                 7580                 7585

aca tcc atg tca  ggc cct gag cag tcc  aca atg tca caa gac  atc      23007
Thr Ser Met Ser  Gly Pro Glu Gln Ser  Thr Met Ser Gln Asp  Ile
            7590                 7595                 7600

tcc ata gga acc  atc ccc agg att tct  gcc tcc tct gtc ctg  aca      23052
Ser Ile Gly Thr  Ile Pro Arg Ile Ser  Ala Ser Ser Val Leu  Thr
            7605                 7610                 7615

gaa tct gca aaa  atg acc atc aca acc  caa aca ggt cct tcg  gag      23097
Glu Ser Ala Lys  Met Thr Ile Thr Thr  Gln Thr Gly Pro Ser  Glu
            7620                 7625                 7630

tct aca cta gaa  agt acc ctt aat ttg  aac aca gca acc aca  ccc      23142
Ser Thr Leu Glu  Ser Thr Leu Asn Leu  Asn Thr Ala Thr Thr  Pro
            7635                 7640                 7645

tct tgg gtg gaa  acc cac tct ata gta  att cag gga ttt cca  cac      23187
Ser Trp Val Glu  Thr His Ser Ile Val  Ile Gln Gly Phe Pro  His
            7650                 7655                 7660

cca gag atg acc  act tcc atg ggc aga  ggt cct gga ggt gtg  tca      23232
Pro Glu Met Thr  Thr Ser Met Gly Arg  Gly Pro Gly Gly Val  Ser
            7665                 7670                 7675

tgg cct agc cct  ccc ttt gtg aaa gaa  acc agc cct cca tcc  tcc      23277
Trp Pro Ser Pro  Pro Phe Val Lys Glu  Thr Ser Pro Pro Ser  Ser
            7680                 7685                 7690

ccg ctg tct tta  cct gcc gtg acc tca  cct cat cct gtt tcc  acc      23322
Pro Leu Ser Leu  Pro Ala Val Thr Ser  Pro His Pro Val Ser  Thr
            7695                 7700                 7705

aca ttc cta gca  cat atc ccc ccc tct  ccc ctt cct gtg act  tca      23367
Thr Phe Leu Ala  His Ile Pro Pro Ser  Pro Leu Pro Val Thr  Ser
            7710                 7715                 7720

ctt ctc acc tct  ggc ccg gcg aca acc  aca gat atc ttg ggt  aca      23412
Leu Leu Thr Ser  Gly Pro Ala Thr Thr  Thr Asp Ile Leu Gly  Thr
            7725                 7730                 7735

agc aca gaa cct  gga acc agt tca tct  tca agt ttg agc acc  acc      23457
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Ser Thr Glu Pro  Gly Thr Ser Ser Ser  Ser Ser Leu Ser Thr  Thr
            7740                 7745                 7750

tcc cat gag aga  ctg acc act tac aaa  gac act gca cat aca  gaa     23502
Ser His Glu Arg  Leu Thr Thr Tyr Lys  Asp Thr Ala His Thr  Glu
            7755                 7760                 7765

gcc gtg cat cct  tcc aca aac aca gga  ggg acc aat gtg gca  acc     23547
Ala Val His Pro  Ser Thr Asn Thr Gly  Gly Thr Asn Val Ala  Thr
            7770                 7775                 7780

acc agc tct gga  tat aaa tca cag tcc  tct gtc cta gct gac  tca     23592
Thr Ser Ser Gly  Tyr Lys Ser Gln Ser  Ser Val Leu Ala Asp  Ser
            7785                 7790                 7795

tct cca atg tgt  acc acc tcc acc atg  ggg gat aca agt gtt  ctc     23637
Ser Pro Met Cys  Thr Thr Ser Thr Met  Gly Asp Thr Ser Val  Leu
            7800                 7805                 7810

aca tca act cct  gcc ttc ctt gag act  agg agg att cag aca  gag     23682
Thr Ser Thr Pro  Ala Phe Leu Glu Thr  Arg Arg Ile Gln Thr  Glu
            7815                 7820                 7825

cta gct tcc tcc  ctg acc cct gga ttg  agg gag tcc agt ggc  tct     23727
Leu Ala Ser Ser  Leu Thr Pro Gly Leu  Arg Glu Ser Ser Gly  Ser
            7830                 7835                 7840

gaa ggg acc agc  tca ggc acc aag atg  agc act gtc ctc tct  aaa     23772
Glu Gly Thr Ser  Ser Gly Thr Lys Met  Ser Thr Val Leu Ser  Lys
            7845                 7850                 7855

gtg ccc act ggt  gct act act gag atc  tcc aag gaa gac gtc  acc     23817
Val Pro Thr Gly  Ala Thr Thr Glu Ile  Ser Lys Glu Asp Val  Thr
            7860                 7865                 7870

tcc atc cca ggt  ccc gct caa tcc aca  ata tca cca gac atc  tcc     23862
Ser Ile Pro Gly  Pro Ala Gln Ser Thr  Ile Ser Pro Asp Ile  Ser
            7875                 7880                 7885

aca aga acc gtc  agc tgg ttc tct aca  tcc cct gtc atg aca  gaa     23907
Thr Arg Thr Val  Ser Trp Phe Ser Thr  Ser Pro Val Met Thr  Glu
            7890                 7895                 7900

tca gca gaa ata  acc atg aac acc cat  aca agt cct tta ggg  gcc     23952
Ser Ala Glu Ile  Thr Met Asn Thr His  Thr Ser Pro Leu Gly  Ala
            7905                 7910                 7915

aca aca caa ggc  acc agt act ttg gcc  acg tca agc aca acc  tct     23997
Thr Thr Gln Gly  Thr Ser Thr Leu Ala  Thr Ser Ser Thr Thr  Ser
            7920                 7925                 7930

ttg aca atg aca  cac tca act ata tct  caa gga ttt tca cac  tca     24042
Leu Thr Met Thr  His Ser Thr Ile Ser  Gln Gly Phe Ser His  Ser
            7935                 7940                 7945
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cag atg agc act  ctt atg agg agg ggt  cct gag gat gta tca  tgg     24087
Gln Met Ser Thr  Leu Met Arg Arg Gly  Pro Glu Asp Val Ser  Trp
            7950                 7955                 7960

atg agc cct ccc  ctt ctg gaa aaa act  aga cct tcc ttt tct  ctg     24132
Met Ser Pro Pro  Leu Leu Glu Lys Thr  Arg Pro Ser Phe Ser  Leu
            7965                 7970                 7975

atg tct tca cca  gcc aca act tca cct  tct cct gtt tcc tcc  aca     24177
Met Ser Ser Pro  Ala Thr Thr Ser Pro  Ser Pro Val Ser Ser  Thr
            7980                 7985                 7990

tta cca gag agc  atc tct tcc tct cct  ctt cct gtg act tca  ctc     24222
Leu Pro Glu Ser  Ile Ser Ser Ser Pro  Leu Pro Val Thr Ser  Leu
            7995                 8000                 8005

ctc acg tct ggc  ttg gca aaa act aca  gat atg ttg cac aaa  agc     24267
Leu Thr Ser Gly  Leu Ala Lys Thr Thr  Asp Met Leu His Lys  Ser
            8010                 8015                 8020

tca gaa cct gta  acc aac tca cct gca  aat ttg agc agc acc  tca     24312
Ser Glu Pro Val  Thr Asn Ser Pro Ala  Asn Leu Ser Ser Thr  Ser
            8025                 8030                 8035

gtt gaa ata ctg  gcc acc tct gaa gtc  acc aca gat aca gag  aaa     24357
Val Glu Ile Leu  Ala Thr Ser Glu Val  Thr Thr Asp Thr Glu  Lys
            8040                 8045                 8050

act cat cct tct  tca aac aga aca gtg  acc gat gtg ggg acc  tcc     24402
Thr His Pro Ser  Ser Asn Arg Thr Val  Thr Asp Val Gly Thr  Ser
            8055                 8060                 8065

agt tct gga cat  gaa tcc act tcc ttt  gtc cta gct gac tca  cag     24447
Ser Ser Gly His  Glu Ser Thr Ser Phe  Val Leu Ala Asp Ser  Gln
            8070                 8075                 8080

aca tcc aaa gtc  aca tct cca atg gtt  att acc tcc acc atg  gag     24492
Thr Ser Lys Val  Thr Ser Pro Met Val  Ile Thr Ser Thr Met  Glu
            8085                 8090                 8095

gat acg agt gtc  tcc aca tca act cct  ggc ttt ttt gag act  agc     24537
Asp Thr Ser Val  Ser Thr Ser Thr Pro  Gly Phe Phe Glu Thr  Ser
            8100                 8105                 8110

aga att cag aca  gaa cca aca tcc tcc  ctg acc ctt gga ctg  aga     24582
Arg Ile Gln Thr  Glu Pro Thr Ser Ser  Leu Thr Leu Gly Leu  Arg
            8115                 8120                 8125

aag acc agc agc  tct gag ggg acc agc  tta gcc aca gag atg  agc     24627
Lys Thr Ser Ser  Ser Glu Gly Thr Ser  Leu Ala Thr Glu Met  Ser
            8130                 8135                 8140

act gtc ctt tct  gga gtg ccc act ggt  gcc act gct gaa gtc  tcc     24672
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Thr Val Leu Ser  Gly Val Pro Thr Gly  Ala Thr Ala Glu Val  Ser
            8145                8150                8155

agg aca gaa gtc  acc tcc tct agc aga  aca tcc atc tca ggc  ttt     24717
Arg Thr Glu Val  Thr Ser Ser Ser Arg  Thr Ser Ile Ser Gly  Phe
            8160                8165                8170

gct cag ctc aca  gtg tca cca gag act  tcc aca gaa acc atc  acc     24762
Ala Gln Leu Thr  Val Ser Pro Glu Thr  Ser Thr Glu Thr Ile  Thr
            8175                8180                8185

aga ctc cct acc  tcc agc ata atg aca  gaa tca gca gaa atg  atg     24807
Arg Leu Pro Thr  Ser Ser Ile Met Thr  Glu Ser Ala Glu Met  Met
            8190                8195                8200

atc aag aca caa  aca gat cct cct ggg  tct aca cca gag agt  act     24852
Ile Lys Thr Gln  Thr Asp Pro Pro Gly  Ser Thr Pro Glu Ser  Thr
            8205                8210                8215

cat act gtg gac  ata tca aca aca ccc  aac tgg gta gaa acc  cac     24897
His Thr Val Asp  Ile Ser Thr Thr Pro  Asn Trp Val Glu Thr  His
            8220                8225                8230

tcg act gtg act  cag aga ttt tca cac  tca gag atg acc act  ctt     24942
Ser Thr Val Thr  Gln Arg Phe Ser His  Ser Glu Met Thr Thr  Leu
            8235                8240                8245

gtg agc aga agc  cct ggt gat atg tta  tgg cct agt caa tcc  tct     24987
Val Ser Arg Ser  Pro Gly Asp Met Leu  Trp Pro Ser Gln Ser  Ser
            8250                8255                8260

gtg gaa gaa acc  agc tct gcc tct tcc  ctg ctg tct ctg cct  gcc     25032
Val Glu Glu Thr  Ser Ser Ala Ser Ser  Leu Leu Ser Leu Pro  Ala
            8265                8270                8275

acg acc tca cct  tct cct gtt tcc tct  aca tta gta gag gat  ttc     25077
Thr Thr Ser Pro  Ser Pro Val Ser Ser  Thr Leu Val Glu Asp  Phe
            8280                8285                8290

cct tcc gct tct  ctt cct gtg act tct  ctt ctc acc cct ggc  ctg     25122
Pro Ser Ala Ser  Leu Pro Val Thr Ser  Leu Leu Thr Pro Gly  Leu
            8295                8300                8305

gtg ata acc aca  gac agg atg ggc ata  agc aga gaa cct gga  acc     25167
Val Ile Thr Thr  Asp Arg Met Gly Ile  Ser Arg Glu Pro Gly  Thr
            8310                8315                8320

agt tcc act tca  aat ttg agc agc acc  tcc cat gag aga ctg  acc     25212
Ser Ser Thr Ser  Asn Leu Ser Ser Thr  Ser His Glu Arg Leu  Thr
            8325                8330                8335

act ttg gaa gac  act gta gat aca gaa  gac atg cag cct tcc  aca     25257
Thr Leu Glu Asp  Thr Val Asp Thr Glu  Asp Met Gln Pro Ser  Thr
            8340                8345                8350
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cac aca gca gtg  acc aac gtg agg acc  tcc att tct gga cat  gaa      25302
His Thr Ala Val  Thr Asn Val Arg Thr  Ser Ile Ser Gly His  Glu
            8355                 8360                 8365

tca caa tct tct  gtc cta tct gac tca  gag aca ccc aaa gcc  aca      25347
Ser Gln Ser Ser  Val Leu Ser Asp Ser  Glu Thr Pro Lys Ala  Thr
            8370                 8375                 8380

tct cca atg ggt  acc acc tac acc atg  ggg gaa acg agt gtt  tcc      25392
Ser Pro Met Gly  Thr Thr Tyr Thr Met  Gly Glu Thr Ser Val  Ser
            8385                 8390                 8395

ata tcc act tct  gac ttc ttt gag acc  agc aga att cag ata  gaa      25437
Ile Ser Thr Ser  Asp Phe Phe Glu Thr  Ser Arg Ile Gln Ile  Glu
            8400                 8405                 8410

cca aca tcc tcc  ctg act tct gga ttg  agg gag acc agc agc  tct      25482
Pro Thr Ser Ser  Leu Thr Ser Gly Leu  Arg Glu Thr Ser Ser  Ser
            8415                 8420                 8425

gag agg atc agc  tca gcc aca gag gga  agc act gtc ctt tct  gaa      25527
Glu Arg Ile Ser  Ser Ala Thr Glu Gly  Ser Thr Val Leu Ser  Glu
            8430                 8435                 8440

gtg ccc agt ggt  gct acc act gag gtc  tcc agg aca gaa gtg  ata      25572
Val Pro Ser Gly  Ala Thr Thr Glu Val  Ser Arg Thr Glu Val  Ile
            8445                 8450                 8455

tcc tct agg gga  aca tcc atg tca ggg  cct gat cag ttc acc  ata      25617
Ser Ser Arg Gly  Thr Ser Met Ser Gly  Pro Asp Gln Phe Thr  Ile
            8460                 8465                 8470

tca cca gac atc  tct act gaa gcg atc  acc agg ctt tct act  tcc      25662
Ser Pro Asp Ile  Ser Thr Glu Ala Ile  Thr Arg Leu Ser Thr  Ser
            8475                 8480                 8485

ccc att atg aca  gaa tca gca gaa agt  gcc atc act att gag  aca      25707
Pro Ile Met Thr  Glu Ser Ala Glu Ser  Ala Ile Thr Ile Glu  Thr
            8490                 8495                 8500

ggt tct cct ggg  gct aca tca gag ggt  acc ctc acc ttg gac  acc      25752
Gly Ser Pro Gly  Ala Thr Ser Glu Gly  Thr Leu Thr Leu Asp  Thr
            8505                 8510                 8515

tca aca aca acc  ttt tgg tca ggg acc  cac tca act gca tct  cca      25797
Ser Thr Thr Thr  Phe Trp Ser Gly Thr  His Ser Thr Ala Ser  Pro
            8520                 8525                 8530

gga ttt tca cac  tca gag atg acc act  ctt atg agt aga act  cct      25842
Gly Phe Ser His  Ser Glu Met Thr Thr  Leu Met Ser Arg Thr  Pro
            8535                 8540                 8545

gga gat gtg cca  tgg ccg agc ctt ccc  tct gtg gaa gaa gcc  agc      25887
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Gly Asp Val Pro  Trp Pro Ser Leu Pro  Ser Val Glu Glu Ala  Ser
            8550                 8555                 8560

tct gtc tct tcc  tca ctg tct tca cct  gcc atg acc tca act  tct     25932
Ser Val Ser Ser  Ser Leu Ser Ser Pro  Ala Met Thr Ser Thr  Ser
            8565                 8570                 8575

ttt ttc tcc aca  tta cca gag agc atc  tcc tcc tct cct cat  cct     25977
Phe Phe Ser Thr  Leu Pro Glu Ser Ile  Ser Ser Ser Pro His  Pro
            8580                 8585                 8590

gtg act gca ctt  ctc acc ctt ggc cca  gtg aag acc aca gac  atg     26022
Val Thr Ala Leu  Leu Thr Leu Gly Pro  Val Lys Thr Thr Asp  Met
            8595                 8600                 8605

ttg cgc aca agc  tca gaa cct gaa acc  agt tca cct cca aat  ttg     26067
Leu Arg Thr Ser  Ser Glu Pro Glu Thr  Ser Ser Pro Pro Asn  Leu
            8610                 8615                 8620

agc agc acc tca  gct gaa ata tta gcc  acg tct gaa gtc acc  aaa     26112
Ser Ser Thr Ser  Ala Glu Ile Leu Ala  Thr Ser Glu Val Thr  Lys
            8625                 8630                 8635

gat aga gag aaa  att cat ccc tcc tca  aac aca cct gta gtc  aat     26157
Asp Arg Glu Lys  Ile His Pro Ser Ser  Asn Thr Pro Val Val  Asn
            8640                 8645                 8650

gta ggg act gtg  att tat aaa cat cta  tcc cct tcc tct gtt  ttg     26202
Val Gly Thr Val  Ile Tyr Lys His Leu  Ser Pro Ser Ser Val  Leu
            8655                 8660                 8665

gct gac tta gtg  aca aca aaa ccc aca  tct cca atg gct acc  acc     26247
Ala Asp Leu Val  Thr Thr Lys Pro Thr  Ser Pro Met Ala Thr  Thr
            8670                 8675                 8680

tcc act ctg ggg  aat aca agt gtt tcc  aca tca act cct gcc  ttc     26292
Ser Thr Leu Gly  Asn Thr Ser Val Ser  Thr Ser Thr Pro Ala  Phe
            8685                 8690                 8695

cca gaa act atg  atg aca cag cca act  tcc tcc ctg act tct  gga     26337
Pro Glu Thr Met  Met Thr Gln Pro Thr  Ser Ser Leu Thr Ser  Gly
            8700                 8705                 8710

tta agg gag atc  agt acc tct caa gag  acc agc tca gca aca  gag     26382
Leu Arg Glu Ile  Ser Thr Ser Gln Glu  Thr Ser Ser Ala Thr  Glu
            8715                 8720                 8725

aga agt gct tct  ctt tct gga atg ccc  act ggt gct act act  aag     26427
Arg Ser Ala Ser  Leu Ser Gly Met Pro  Thr Gly Ala Thr Thr  Lys
            8730                 8735                 8740

gtc tcc aga aca  gaa gcc ctc tcc tta  ggc aga aca tcc acc  cca     26472
Val Ser Arg Thr  Glu Ala Leu Ser Leu  Gly Arg Thr Ser Thr  Pro
            8745                 8750                 8755
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ggt cct gct caa  tcc aca ata tca cca  gaa atc tcc acg gaa  acc      26517
Gly Pro Ala Gln  Ser Thr Ile Ser Pro  Glu Ile Ser Thr Glu  Thr
            8760                 8765                 8770

atc act aga att  tct act ccc ctc acc  acg aca gga tca gca  gaa      26562
Ile Thr Arg Ile  Ser Thr Pro Leu Thr  Thr Thr Gly Ser Ala  Glu
            8775                 8780                 8785

atg acc atc acc  ccc aaa aca ggt cat  tct ggg gca tcc tca  caa      26607
Met Thr Ile Thr  Pro Lys Thr Gly His  Ser Gly Ala Ser Ser  Gln
            8790                 8795                 8800

ggt acc ttt acc  ttg gac aca tca agc  aga gcc tcc tgg cca  gga      26652
Gly Thr Phe Thr  Leu Asp Thr Ser Ser  Arg Ala Ser Trp Pro  Gly
            8805                 8810                 8815

act cac tca gct  gca act cac aga tct  cca cac tca ggg atg  acc      26697
Thr His Ser Ala  Ala Thr His Arg Ser  Pro His Ser Gly Met  Thr
            8820                 8825                 8830

act cct atg agc  aga ggt cct gag gat  gtg tca tgg cca agc  cgc      26742
Thr Pro Met Ser  Arg Gly Pro Glu Asp  Val Ser Trp Pro Ser  Arg
            8835                 8840                 8845

cca tca gtg gaa  aaa act agc cct cca  tct tcc ctg gtg tct  tta      26787
Pro Ser Val Glu  Lys Thr Ser Pro Pro  Ser Ser Leu Val Ser  Leu
            8850                 8855                 8860

tct gca gta acc  tca cct tcg cca ctt  tat tcc aca cca tct  gag      26832
Ser Ala Val Thr  Ser Pro Ser Pro Leu  Tyr Ser Thr Pro Ser  Glu
            8865                 8870                 8875

agt agc cac tca  tct cct ctc cgg gtg  act tct ctt ttc acc  cct      26877
Ser Ser His Ser  Ser Pro Leu Arg Val  Thr Ser Leu Phe Thr  Pro
            8880                 8885                 8890

gtc atg atg aag  acc aca gac atg ttg  gac aca agc ttg gaa  cct      26922
Val Met Met Lys  Thr Thr Asp Met Leu  Asp Thr Ser Leu Glu  Pro
            8895                 8900                 8905

gtg acc act tca  cct ccc agt atg aat  atc acc tca gat gag  agt      26967
Val Thr Thr Ser  Pro Pro Ser Met Asn  Ile Thr Ser Asp Glu  Ser
            8910                 8915                 8920

ctg gcc act tct  aaa gcc acc atg gag  aca gag gca att cag  ctt      27012
Leu Ala Thr Ser  Lys Ala Thr Met Glu  Thr Glu Ala Ile Gln  Leu
            8925                 8930                 8935

tca gaa aac aca  gct gtg act cag atg  ggc acc atc agc gct  aga      27057
Ser Glu Asn Thr  Ala Val Thr Gln Met  Gly Thr Ile Ser Ala  Arg
            8940                 8945                 8950

caa gaa ttc tat  tcc tct tat cca ggc  ctc cca gag cca tcc  aaa      27102
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Gln Glu Phe Tyr  Ser Ser Tyr Pro Gly  Leu Pro Glu Pro Ser  Lys
                 8955                 8960                 8965

gtg aca tct cca  gtg gtc acc tct tcc  acc ata aaa gac att  gtt     27147
Val Thr Ser Pro  Val Val Thr Ser Ser  Thr Ile Lys Asp Ile  Val
                 8970                 8975                 8980

tct aca acc ata  cct gct tcc tct gag  ata aca aga att gag  atg     27192
Ser Thr Thr Ile  Pro Ala Ser Ser Glu  Ile Thr Arg Ile Glu  Met
                 8985                 8990                 8995

gag tca aca tcc  acc ctg acc ccc aca  cca agg gag acc agc  acc     27237
Glu Ser Thr Ser  Thr Leu Thr Pro Thr  Pro Arg Glu Thr Ser  Thr
                 9000                 9005                 9010

tcc cag gag atc  cac tca gcc aca aag  cca agc act gtt cct  tac     27282
Ser Gln Glu Ile  His Ser Ala Thr Lys  Pro Ser Thr Val Pro  Tyr
                 9015                 9020                 9025

aag gca ctc act  agt gcc acg att gag  gac tcc atg aca caa  gtc     27327
Lys Ala Leu Thr  Ser Ala Thr Ile Glu  Asp Ser Met Thr Gln  Val
                 9030                 9035                 9040

atg tcc tct agc  aga gga cct agc cct  gat cag tcc aca atg  tca     27372
Met Ser Ser Ser  Arg Gly Pro Ser Pro  Asp Gln Ser Thr Met  Ser
                 9045                 9050                 9055

caa gac ata tcc  agt gaa gtg atc acc  agg ctc tct acc tcc  ccc     27417
Gln Asp Ile Ser  Ser Glu Val Ile Thr  Arg Leu Ser Thr Ser  Pro
                 9060                 9065                 9070

atc aag gca gaa  tct aca gaa atg acc  att acc acc caa aca  ggt     27462
Ile Lys Ala Glu  Ser Thr Glu Met Thr  Ile Thr Thr Gln Thr  Gly
                 9075                 9080                 9085

tct cct ggg gct  aca tca agg ggt acc  ctt acc ttg gac act  tca     27507
Ser Pro Gly Ala  Thr Ser Arg Gly Thr  Leu Thr Leu Asp Thr  Ser
                 9090                 9095                 9100

aca act ttt atg  tca ggg acc cac tca  act gca tct caa gga  ttt     27552
Thr Thr Phe Met  Ser Gly Thr His Ser  Thr Ala Ser Gln Gly  Phe
                 9105                 9110                 9115

tca cac tca cag  atg acc gct ctt atg  agt aga act cct gga  gat     27597
Ser His Ser Gln  Met Thr Ala Leu Met  Ser Arg Thr Pro Gly  Asp
                 9120                 9125                 9130

gtg cca tgg cta  agc cat ccc tct gtg  gaa gaa gcc agc tct  gcc     27642
Val Pro Trp Leu  Ser His Pro Ser Val  Glu Glu Ala Ser Ser  Ala
                 9135                 9140                 9145

tct ttc tca ctg  tct tca cct gtc atg  acc tca tct tct ccc  gtt     27687
Ser Phe Ser Leu  Ser Ser Pro Val Met  Thr Ser Ser Ser Pro  Val
                 9150                 9155                 9160
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tct tcc aca tta  cca gac agc atc cac  tct tct tcg ctt cct  gtg      27732
Ser Ser Thr Leu  Pro Asp Ser Ile His  Ser Ser Ser Leu Pro  Val
            9165                 9170                 9175

aca tca ctt ctc  acc tca ggg ctg gtg  aag acc aca gag ctg  ttg      27777
Thr Ser Leu Leu  Thr Ser Gly Leu Val  Lys Thr Thr Glu Leu  Leu
            9180                 9185                 9190

ggc aca agc tca  gaa cct gaa acc agt  tca ccc cca aat ttg  agc      27822
Gly Thr Ser Ser  Glu Pro Glu Thr Ser  Ser Pro Pro Asn Leu  Ser
            9195                 9200                 9205

agc acc tca gct  gaa ata ctg gcc acc  act gaa gtc act aca  gat      27867
Ser Thr Ser Ala  Glu Ile Leu Ala Thr  Thr Glu Val Thr Thr  Asp
            9210                 9215                 9220

aca gag aaa ctg  gag atg acc aat gtg  gta acc tca ggt tat  aca      27912
Thr Glu Lys Leu  Glu Met Thr Asn Val  Val Thr Ser Gly Tyr  Thr
            9225                 9230                 9235

cat gaa tct cct  tcc tct gtc cta gct  gac tca gtg aca aca  aag      27957
His Glu Ser Pro  Ser Ser Val Leu Ala  Asp Ser Val Thr Thr  Lys
            9240                 9245                 9250

gcc aca tct tca  atg ggt atc acc tac  ccc aca gga gat aca  aat      28002
Ala Thr Ser Ser  Met Gly Ile Thr Tyr  Pro Thr Gly Asp Thr  Asn
            9255                 9260                 9265

gtt ctc aca tca  acc cct gcc ttc tct  gac acc agt agg att  caa      28047
Val Leu Thr Ser  Thr Pro Ala Phe Ser  Asp Thr Ser Arg Ile  Gln
            9270                 9275                 9280

aca aag tca aag  ctc tca ctg act cct  ggg ttg atg gag acc  agc      28092
Thr Lys Ser Lys  Leu Ser Leu Thr Pro  Gly Leu Met Glu Thr  Ser
            9285                 9290                 9295

atc tct gaa gag  acc agc tct gcc aca  gaa aaa agc act gtc  ctt      28137
Ile Ser Glu Glu  Thr Ser Ser Ala Thr  Glu Lys Ser Thr Val  Leu
            9300                 9305                 9310

tct agt gtg ccc  act ggt gct act act  gag gtc tcc agg aca  gaa      28182
Ser Ser Val Pro  Thr Gly Ala Thr Thr  Glu Val Ser Arg Thr  Glu
            9315                 9320                 9325

gcc atc tct tct  agc aga aca tcc atc  cca ggc cct gct caa  tcc      28227
Ala Ile Ser Ser  Ser Arg Thr Ser Ile  Pro Gly Pro Ala Gln  Ser
            9330                 9335                 9340

aca atg tca tca  gac acc tcc atg gaa  acc atc act aga att  tct      28272
Thr Met Ser Ser  Asp Thr Ser Met Glu  Thr Ile Thr Arg Ile  Ser
            9345                 9350                 9355

acc ccc ctc aca  agg aaa gaa tca aca  gac atg gcc atc acc  ccc      28317
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Thr Pro Leu Thr  Arg Lys Glu Ser Thr  Asp Met Ala Ile Thr  Pro
            9360                 9365                 9370

aaa aca ggt cct  tct ggg gct acc tcg  cag ggt acc ttt acc  ttg     28362
Lys Thr Gly Pro  Ser Gly Ala Thr Ser  Gln Gly Thr Phe Thr  Leu
            9375                 9380                 9385

gac tca tca agc  aca gcc tcc tgg cca  gga act cac tca gct  aca     28407
Asp Ser Ser Ser  Thr Ala Ser Trp Pro  Gly Thr His Ser Ala  Thr
            9390                 9395                 9400

act cag aga ttt  cca cag tca gtg gtg  aca act cct atg agc  aga     28452
Thr Gln Arg Phe  Pro Gln Ser Val Val  Thr Thr Pro Met Ser  Arg
            9405                 9410                 9415

ggt cct gag gat  gtg tca tgg cca agc  ccg ctg tct gtg gaa  aaa     28497
Gly Pro Glu Asp  Val Ser Trp Pro Ser  Pro Leu Ser Val Glu  Lys
            9420                 9425                 9430

aac agc cct cca  tct tcc ctg gta tct  tca tct tca gta acc  tca     28542
Asn Ser Pro Pro  Ser Ser Leu Val Ser  Ser Ser Ser Val Thr  Ser
            9435                 9440                 9445

cct tcg cca ctt  tat tcc aca cca tct  ggg agt agc cac tcc  tct     28587
Pro Ser Pro Leu  Tyr Ser Thr Pro Ser  Gly Ser Ser His Ser  Ser
            9450                 9455                 9460

cct gtc cct gtc  act tct ctt ttc acc  tct atc atg atg aag  gcc     28632
Pro Val Pro Val  Thr Ser Leu Phe Thr  Ser Ile Met Met Lys  Ala
            9465                 9470                 9475

aca gac atg ttg  gat gca agt ttg gaa  cct gag acc act tca  gct     28677
Thr Asp Met Leu  Asp Ala Ser Leu Glu  Pro Glu Thr Thr Ser  Ala
            9480                 9485                 9490

ccc aat atg aat  atc acc tca gat gag  agt ctg gcc gct tct  aaa     28722
Pro Asn Met Asn  Ile Thr Ser Asp Glu  Ser Leu Ala Ala Ser  Lys
            9495                 9500                 9505

gcc acc acg gag  aca gag gca att cac  gtt ttt gaa aat aca  gca     28767
Ala Thr Thr Glu  Thr Glu Ala Ile His  Val Phe Glu Asn Thr  Ala
            9510                 9515                 9520

gcg tcc cat gtg  gaa acc acc agt gct  aca gag gaa ctc tat  tcc     28812
Ala Ser His Val  Glu Thr Thr Ser Ala  Thr Glu Glu Leu Tyr  Ser
            9525                 9530                 9535

tct tcc cca ggc  ttc tca gag cca aca  aaa gtg ata tct cca  gtg     28857
Ser Ser Pro Gly  Phe Ser Glu Pro Thr  Lys Val Ile Ser Pro  Val
            9540                 9545                 9550

gtc acc tct tcc  tct ata aga gac aac  atg gtt tcc aca aca  atg     28902
Val Thr Ser Ser  Ser Ile Arg Asp Asn  Met Val Ser Thr Thr  Met
            9555                 9560                 9565
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cct ggc tcc tct  ggc att aca agg att  gag ata gag tca atg  tca      28947
Pro Gly Ser Ser  Gly Ile Thr Arg Ile  Glu Ile Glu Ser Met  Ser
            9570                 9575                 9580

tct ctg acc cct  gga ctg agg gag acc  aga acc tcc cag gac  atc      28992
Ser Leu Thr Pro  Gly Leu Arg Glu Thr  Arg Thr Ser Gln Asp  Ile
            9585                 9590                 9595

acc tca tcc aca  gag aca agc act gtc  ctt tac aag atg ccc  tct      29037
Thr Ser Ser Thr  Glu Thr Ser Thr Val  Leu Tyr Lys Met Pro  Ser
            9600                 9605                 9610

ggt gcc act cct  gag gtc tcc agg aca  gaa gtt atg ccc tct  agc      29082
Gly Ala Thr Pro  Glu Val Ser Arg Thr  Glu Val Met Pro Ser  Ser
            9615                 9620                 9625

aga aca tcc att  cct ggc cct gct cag  tcc aca atg tca cta  gac      29127
Arg Thr Ser Ile  Pro Gly Pro Ala Gln  Ser Thr Met Ser Leu  Asp
            9630                 9635                 9640

atc tcc gat gaa  gtt gtc acc agg ctg  tct acc tct ccc atc  atg      29172
Ile Ser Asp Glu  Val Val Thr Arg Leu  Ser Thr Ser Pro Ile  Met
            9645                 9650                 9655

aca gaa tct gca  gaa ata acc atc acc  acc caa aca ggt tat  tct      29217
Thr Glu Ser Ala  Glu Ile Thr Ile Thr  Thr Gln Thr Gly Tyr  Ser
            9660                 9665                 9670

ctg gct aca tcc  cag gtt acc ctt ccc  ttg ggc acc tca atg  acc      29262
Leu Ala Thr Ser  Gln Val Thr Leu Pro  Leu Gly Thr Ser Met  Thr
            9675                 9680                 9685

ttt ttg tca ggg  acc cac tca act atg  tct caa gga ctt tca  cac      29307
Phe Leu Ser Gly  Thr His Ser Thr Met  Ser Gln Gly Leu Ser  His
            9690                 9695                 9700

tca gag atg acc  aat ctt atg agc agg  ggt cct gaa agt ctg  tca      29352
Ser Glu Met Thr  Asn Leu Met Ser Arg  Gly Pro Glu Ser Leu  Ser
            9705                 9710                 9715

tgg acg agc cct  cgc ttt gtg gaa aca  act aga tct tcc tct  tct      29397
Trp Thr Ser Pro  Arg Phe Val Glu Thr  Thr Arg Ser Ser Ser  Ser
            9720                 9725                 9730

ctg aca tca tta  cct ctc acg acc tca  ctt tct cct gtg tcc  tcc      29442
Leu Thr Ser Leu  Pro Leu Thr Thr Ser  Leu Ser Pro Val Ser  Ser
            9735                 9740                 9745

aca tta cta gac  agt agc ccc tcc tct  cct ctt cct gtg act  tca      29487
Thr Leu Leu Asp  Ser Ser Pro Ser Ser  Pro Leu Pro Val Thr  Ser
            9750                 9755                 9760

ctt atc ctc cca  ggc ctg gtg aag act  aca gaa gtg ttg gat  aca      29532
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Leu Ile Leu Pro  Gly Leu Val Lys Thr  Thr Glu Val Leu Asp  Thr
            9765                 9770                 9775

agc tca gag cct  aaa acc agt tca tct  cca aat ttg agc agc  acc     29577
Ser Ser Glu Pro  Lys Thr Ser Ser Ser  Pro Asn Leu Ser Ser  Thr
            9780                 9785                 9790

tca gtt gaa ata  ccg gcc acc tct gaa  atc atg aca gat aca  gag     29622
Ser Val Glu Ile  Pro Ala Thr Ser Glu  Ile Met Thr Asp Thr  Glu
            9795                 9800                 9805

aaa att cat cct  tcc tca aac aca gcg  gtg gcc aaa gtg agg  acc     29667
Lys Ile His Pro  Ser Ser Asn Thr Ala  Val Ala Lys Val Arg  Thr
            9810                 9815                 9820

tcc agt tct gtt  cat gaa tct cat tcc  tct gtc cta gct gac  tca     29712
Ser Ser Ser Val  His Glu Ser His Ser  Ser Val Leu Ala Asp  Ser
            9825                 9830                 9835

gaa aca acc ata  acc ata cct tca atg  ggt atc acc tcc gct  gtg     29757
Glu Thr Thr Ile  Thr Ile Pro Ser Met  Gly Ile Thr Ser Ala  Val
            9840                 9845                 9850

gac gat acc act  gtt ttc aca tca aat  cct gcc ttc tct gag  act     29802
Asp Asp Thr Thr  Val Phe Thr Ser Asn  Pro Ala Phe Ser Glu  Thr
            9855                 9860                 9865

agg agg att ccg  aca gag cca aca ttc  tca ttg act cct gga  ttc     29847
Arg Arg Ile Pro  Thr Glu Pro Thr Phe  Ser Leu Thr Pro Gly  Phe
            9870                 9875                 9880

agg gag act agc  acc tct gaa gag acc  acc tca atc aca gaa  aca     29892
Arg Glu Thr Ser  Thr Ser Glu Glu Thr  Thr Ser Ile Thr Glu  Thr
            9885                 9890                 9895

agt gca gtc ctt  tat gga gtg ccc act  agt gct act act gaa  gtc     29937
Ser Ala Val Leu  Tyr Gly Val Pro Thr  Ser Ala Thr Thr Glu  Val
            9900                 9905                 9910

tcc atg aca gaa  atc atg tcc tct aat  aga aca cac atc cct  gac     29982
Ser Met Thr Glu  Ile Met Ser Ser Asn  Arg Thr His Ile Pro  Asp
            9915                 9920                 9925

tct gat cag tcc  acg atg tct cca gac  atc atc act gaa gtg  atc     30027
Ser Asp Gln Ser  Thr Met Ser Pro Asp  Ile Ile Thr Glu Val  Ile
            9930                 9935                 9940

acc agg ctc tct  tcc tca tcc atg atg  tca gaa tca aca caa  atg     30072
Thr Arg Leu Ser  Ser Ser Ser Met Met  Ser Glu Ser Thr Gln  Met
            9945                 9950                 9955

acc atc acc acc  caa aaa agt tct cct  ggg gct aca gca cag  agt     30117
Thr Ile Thr Thr  Gln Lys Ser Ser Pro  Gly Ala Thr Ala Gln  Ser
            9960                 9965                 9970
```

```
act ctt acc ttg  gcc aca aca aca gcc  ccc ttg gca agg acc  cac      30162
Thr Leu Thr Leu  Ala Thr Thr Thr Ala  Pro Leu Ala Arg Thr  His
            9975                 9980                 9985

tca act gtt cct  cct aga ttt tta cac  tca gag atg aca act  ctt     30207
Ser Thr Val Pro  Pro Arg Phe Leu His  Ser Glu Met Thr Thr  Leu
            9990                 9995                10000

atg agt agg agt   cct gaa aat cca tca   tgg aag agc tct ccc   ttt  30252
Met Ser Arg Ser   Pro Glu Asn Pro Ser   Trp Lys Ser Ser Pro   Phe
            10005                10010                10015

gtg gaa aaa act   agc tct tca tct tct   ctg ttg tcc tta cct   gtc  30297
Val Glu Lys Thr   Ser Ser Ser Ser Ser   Leu Leu Ser Leu Pro   Val
            10020                10025                10030

acg acc tca cct   tct gtt tct tcc aca   tta ccg cag agt atc   cct  30342
Thr Thr Ser Pro   Ser Val Ser Ser Thr   Leu Pro Gln Ser Ile   Pro
            10035                10040                10045

tcc tcc tct ttt   tct gtg act tca ctc   ctc acc cca ggc atg   gtg  30387
Ser Ser Ser Phe   Ser Val Thr Ser Leu   Leu Thr Pro Gly Met   Val
            10050                10055                10060

aag act aca gac   aca agc aca gaa cct   gga acc agt tta tct   cca  30432
Lys Thr Thr Asp   Thr Ser Thr Glu Pro   Gly Thr Ser Leu Ser   Pro
            10065                10070                10075

aat ctg agt ggc   acc tca gtt gaa ata   ctg gct gcc tct gaa   gtc  30477
Asn Leu Ser Gly   Thr Ser Val Glu Ile   Leu Ala Ala Ser Glu   Val
            10080                10085                10090

acc aca gat aca   gag aaa att cat cct   tct tca agc atg gca   gtg  30522
Thr Thr Asp Thr   Glu Lys Ile His Pro   Ser Ser Ser Met Ala   Val
            10095                10100                10105

acc aat gtg gga   acc acc agt tct gga   cat gaa cta tat tcc   tct  30567
Thr Asn Val Gly   Thr Thr Ser Ser Gly   His Glu Leu Tyr Ser   Ser
            10110                10115                10120

gtt tca atc cac   tcg gag cca tcc aag   gct aca tac cca gtg   ggt  30612
Val Ser Ile His   Ser Glu Pro Ser Lys   Ala Thr Tyr Pro Val   Gly
            10125                10130                10135

act ccc tct tcc   atg gct gaa acc tct   att tcc aca tca atg   cct  30657
Thr Pro Ser Ser   Met Ala Glu Thr Ser   Ile Ser Thr Ser Met   Pro
            10140                10145                10150

gct aat ttt gag   acc aca gga ttt gag   gct gag cca ttt tct   cat  30702
Ala Asn Phe Glu   Thr Thr Gly Phe Glu   Ala Glu Pro Phe Ser   His
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ttg act tct gga   ttt agg aag aca aac   atg tcc ctg gac acc   agc  30747
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Leu Thr Ser Gly   Phe Arg Lys Thr Asn   Met Ser Leu Asp Thr   Ser
            10170                 10175                 10180

tca gtc aca cca   aca aat aca cct tct   tct cct ggg tcc act   cac  30792
Ser Val Thr Pro   Thr Asn Thr Pro Ser   Ser Pro Gly Ser Thr   His
            10185                 10190                 10195

ctt tta cag agt   tcc aag act gat ttc   acc tct tct gca aaa   aca  30837
Leu Leu Gln Ser   Ser Lys Thr Asp Phe   Thr Ser Ser Ala Lys   Thr
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tca tcc cca gac   tgg cct cca gcc tca   cag tat act gaa att   cca  30882
Ser Ser Pro Asp   Trp Pro Pro Ala Ser   Gln Tyr Thr Glu Ile   Pro
            10215                 10220                 10225

gtg gac ata atc   acc ccc ttt aat gct   tct cca tct att acg   gag  30927
Val Asp Ile Ile   Thr Pro Phe Asn Ala   Ser Pro Ser Ile Thr   Glu
            10230                 10235                 10240

tcc act ggg ata   acc tcc ttc cca gaa   tcc agg ttt act atg   tct  30972
Ser Thr Gly Ile   Thr Ser Phe Pro Glu   Ser Arg Phe Thr Met   Ser
            10245                 10250                 10255

gta aca gaa agt   act cat cat ctg agt   aca gat ttg ctg cct   tca  31017
Val Thr Glu Ser   Thr His His Leu Ser   Thr Asp Leu Leu Pro   Ser
            10260                 10265                 10270

gct gag act att   tcc act ggc aca gtg   atg cct tct cta tca   gag  31062
Ala Glu Thr Ile   Ser Thr Gly Thr Val   Met Pro Ser Leu Ser   Glu
            10275                 10280                 10285

gcc atg act tca   ttt gcc acc act gga   gtt cca cga gcc atc   tca  31107
Ala Met Thr Ser   Phe Ala Thr Thr Gly   Val Pro Arg Ala Ile   Ser
            10290                 10295                 10300

ggt tca ggt agt   cca ttc tct agg aca   gag tca ggc cct ggg   gat  31152
Gly Ser Gly Ser   Pro Phe Ser Arg Thr   Glu Ser Gly Pro Gly   Asp
            10305                 10310                 10315

gct act ctg tcc   acc att gca gag agc   ctg cct tca tcc act   cct  31197
Ala Thr Leu Ser   Thr Ile Ala Glu Ser   Leu Pro Ser Ser Thr   Pro
            10320                 10325                 10330

gtg cca ttc tcc   tct tca acc ttc act   acc act gat tct tca   acc  31242
Val Pro Phe Ser   Ser Ser Thr Phe Thr   Thr Thr Asp Ser Ser   Thr
            10335                 10340                 10345

atc cca gcc ctc   cat gag ata act tcc   tct tca gct acc cca   tat  31287
Ile Pro Ala Leu   His Glu Ile Thr Ser   Ser Ser Ala Thr Pro   Tyr
            10350                 10355                 10360

aga gtg gac acc   agt ctt ggg aca gag   agc agc act act gaa   gga  31332
Arg Val Asp Thr   Ser Leu Gly Thr Glu   Ser Ser Thr Thr Glu   Gly
            10365                 10370                 10375
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cgc ttg gtt atg   gtc agt act ttg gac   act tca agc caa cca   ggc  31377
Arg Leu Val Met   Val Ser Thr Leu Asp   Thr Ser Ser Gln Pro   Gly
            10380                 10385                 10390

agg aca tct tca   aca ccc att ttg gat   acc aga atg aca gag   agc  31422
Arg Thr Ser Ser   Thr Pro Ile Leu Asp   Thr Arg Met Thr Glu   Ser
            10395                 10400                 10405

gtt gag ctg gga   aca gtg aca agt gct   tat caa gtt cct tca   ctc  31467
Val Glu Leu Gly   Thr Val Thr Ser Ala   Tyr Gln Val Pro Ser   Leu
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Ser Thr Arg Leu   Thr Arg Thr Asp Gly   Ile
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<211> 10431

<212> PRT

<213> Homo sapiens

<400> 310

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Leu Met Thr Gly Ser Arg Ser Thr Lys Ala Thr Pro Glu Met Asp Ser
            20                  25                  30

Gly Leu Thr Gly Ala Thr Leu Ser Pro Lys Thr Ser Thr Gly Ala Ile
        35                  40                  45

Val Val Thr Glu His Thr Leu Pro Phe Thr Ser Pro Asp Lys Thr Leu
    50                  55                  60

Ala Ser Pro Thr Ser Ser Val Val Gly Arg Thr Thr Gln Ser Leu Gly
65                  70                  75                  80

Val Met Ser Ser Ala Leu Pro Glu Ser Thr Ser Arg Gly Met Thr His
                85                  90                  95
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Ser Glu Gln Arg Thr Ser Pro Ser Leu Ser Pro Gln Val Asn Gly Thr
100 105 110

Pro Ser Arg Asn Tyr Pro Ala Thr Ser Met Val Ser Gly Leu Ser Ser
115 120 125

Pro Arg Thr Arg Thr Ser Ser Thr Glu Gly Asn Phe Thr Lys Glu Ala
130 135 140

Ser Thr Tyr Thr Leu Thr Val Glu Thr Thr Ser Gly Pro Val Thr Glu
145 150 155 160

Lys Tyr Thr Val Pro Thr Glu Thr Ser Thr Thr Glu Gly Asp Ser Thr
165 170 175

Glu Thr Pro Trp Asp Thr Arg Tyr Ile Pro Val Lys Ile Thr Ser Pro
180 185 190

Met Lys Thr Phe Ala Asp Ser Thr Ala Ser Lys Glu Asn Ala Pro Val
195 200 205

Ser Met Thr Pro Ala Glu Thr Thr Val Thr Asp Ser His Thr Pro Gly
210 215 220

Arg Thr Asn Pro Ser Phe Gly Thr Leu Tyr Ser Ser Phe Leu Asp Leu
225 230 235 240

Ser Pro Lys Gly Thr Pro Asn Ser Arg Gly Glu Thr Ser Leu Glu Leu
245 250 255

Ile Leu Ser Thr Thr Gly Tyr Pro Phe Ser Ser Pro Glu Pro Gly Ser
260 265 270

Ala Gly His Ser Arg Ile Ser Thr Ser Ala Pro Leu Ser Ser Ser Ala
275 280 285

Ser Val Leu Asp Asn Lys Ile Ser Glu Thr Ser Ile Phe Ser Gly Gln
290 295 300

Ser Leu Thr Ser Pro Leu Ser Pro Gly Val Pro Glu Ala Arg Ala Ser
305 310 315 320

Thr Met Pro Asn Ser Ala Ile Pro Phe Ser Met Thr Leu Ser Asn Ala
325 330 335

Glu Thr Ser Ala Glu Arg Val Arg Ser Thr Ile Ser Ser Leu Gly Thr
340 345 350

Pro Ser Ile Ser Thr Lys Gln Thr Ala Glu Thr Ile Leu Thr Phe His
355 360 365

Ala Phe Ala Glu Thr Met Asp Ile Pro Ser Thr His Ile Ala Lys Thr
370 375 380

Leu Ala Ser Glu Trp Leu Gly Ser Pro Gly Thr Leu Gly Gly Thr Ser
385 390 395 400

Thr Ser Ala Leu Thr Thr Thr Ser Pro Ser Thr Thr Leu Val Ser Glu
405 410 415

Glu Thr Asn Thr His His Ser Thr Ser Gly Lys Glu Thr Glu Gly Thr
420 425 430

Leu Asn Thr Ser Met Thr Pro Leu Glu Thr Ser Ala Pro Gly Glu Glu
435 440 445

Ser Glu Met Thr Ala Thr Leu Val Pro Thr Leu Gly Phe Thr Thr Leu
450 455 460

Asp Ser Lys Ile Arg Ser Pro Ser Gln Val Ser Ser Ser His Pro Thr
465 470 475 480

Arg Glu Leu Arg Thr Thr Gly Ser Thr Ser Gly Arg Gln Ser Ser Ser
485 490 495

Thr Ala Ala His Gly Ser Ser Asp Ile Leu Arg Ala Thr Thr Ser Ser
500 505 510

Thr Ser Lys Ala Ser Ser Trp Thr Ser Glu Ser Thr Ala Gln Gln Phe
515 520 525

Ser Glu Pro Gln His Thr Gln Trp Val Glu Thr Ser Pro Ser Met Lys
530 535 540

Thr Glu Arg Pro Pro Ala Ser Thr Ser Val Ala Ala Pro Ile Thr Thr
545 550 555 560

Ser Val Pro Ser Val Val Ser Gly Phe Thr Thr Leu Lys Thr Ser Ser
565 570 575

Thr Lys Gly Ile Trp Leu Glu Glu Thr Ser Ala Asp Thr Leu Ile Gly
580 585 590

Glu Ser Thr Ala Gly Pro Thr Thr His Gln Phe Ala Val Pro Thr Gly
595 600 605

Ile Ser Met Thr Gly Gly Ser Ser Thr Arg Gly Ser Gln Gly Thr Thr
610 615 620

His Leu Leu Thr Arg Ala Thr Ala Ser Ser Glu Thr Ser Ala Asp Leu
625 630 635 640

Thr Leu Ala Thr Asn Gly Val Pro Val Ser Val Ser Pro Ala Val Ser
645 650 655

Lys Thr Ala Ala Gly Ser Ser Pro Pro Gly Gly Thr Lys Pro Ser Tyr
660 665 670

Thr Met Val Ser Ser Val Ile Pro Glu Thr Ser Ser Leu Gln Ser Ser
675 680 685

Ala Phe Arg Glu Gly Thr Ser Leu Gly Leu Thr Pro Leu Asn Thr Arg
690 695 700

His Pro Phe Ser Ser Pro Glu Pro Asp Ser Ala Gly His Thr Lys Ile
705 710 715 720

Ser Thr Ser Ile Pro Leu Leu Ser Ser Ala Ser Val Leu Glu Asp Lys
725 730 735

Val Ser Ala Thr Ser Thr Phe Ser His His Lys Ala Thr Ser Ser Ile
740 745 750

Thr Thr Gly Thr Pro Glu Ile Ser Thr Lys Thr Lys Pro Ser Ser Ala
755 760 765

Val Leu Ser Ser Met Thr Leu Ser Asn Ala Ala Thr Ser Pro Glu Arg
770 775 780

Val Arg Asn Ala Thr Ser Pro Leu Thr His Pro Ser Pro Ser Gly Glu
785 790 795 800

Glu Thr Ala Gly Ser Val Leu Thr Leu Ser Thr Ser Ala Glu Thr Thr
805 810 815

Asp Ser Pro Asn Ile His Pro Thr Gly Thr Leu Thr Ser Glu Ser Ser
820 825 830

Glu Ser Pro Ser Thr Leu Ser Leu Pro Ser Val Ser Gly Val Lys Thr
835 840 845

Thr Phe Ser Ser Ser Thr Pro Ser Thr His Leu Phe Thr Ser Gly Glu
850 855 860

Glu Thr Glu Glu Thr Ser Asn Pro Ser Val Ser Gln Pro Glu Thr Ser
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Val Ser Arg Val Arg Thr Thr Leu Ala Ser Thr Ser Val Pro Thr Pro
885 890 895

Val Phe Pro Thr Met Asp Thr Trp Pro Thr Arg Ser Ala Gln Phe Ser
900 905 910

Ser Ser His Leu Val Ser Glu Leu Arg Ala Thr Ser Ser Thr Ser Val
915 920 925

Thr Asn Ser Thr Gly Ser Ala Leu Pro Lys Ile Ser His Leu Thr Gly
930 935 940

Thr Ala Thr Met Ser Gln Thr Asn Arg Asp Thr Phe Asn Asp Ser Ala
945 950 955 960

Ala Pro Gln Ser Thr Thr Trp Pro Glu Thr Ser Pro Arg Phe Lys Thr
965 970 975

Gly Leu Pro Ser Ala Thr Thr Thr Val Ser Thr Ser Ala Thr Ser Leu
980 985 990

Ser Ala Thr Val Met Val Ser Lys Phe Thr Ser Pro Ala Thr Ser Ser
995 1000 1005

Met Glu Ala Thr Ser Ile Arg Glu Pro Ser Thr Thr Ile Leu Thr
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Thr Glu Thr Thr Asn Gly Pro Gly Ser Met Ala Val Ala Ser Thr
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Asn Ile Pro Ile Gly Lys Gly Tyr Ile Thr Glu Gly Arg Leu Asp
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Met Asp Phe Thr Met Ala Lys Glu Ser Val Ser Met Ser Val Ser
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Pro Ser Gln Ser Met Asp Ala Ala Gly Ser Ser Thr Pro Gly Arg
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Ser Ser Pro Thr Pro Lys Val Thr Met Ser Ser Thr Phe Ser Thr
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Arg Trp Asn Met Pro Asn Leu Pro Ser Thr Thr Ser Leu Thr Pro
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Ser Asn Ile Pro Thr Ser Gly Ala Ile Gly Lys Ser Thr Leu Val
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Pro Ser Ile His Leu Gly Ala His Ala Ser Ser Glu Ser Pro Ser
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Thr Ala Arg Met Ala Tyr Ser Ser Gly Ser Ser Pro Glu Met Thr
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Ala Pro Gly Glu Thr Asn Thr Gly Ser Thr Trp Asp Pro Thr Thr
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Tyr Ile Thr Thr Thr Asp Pro Lys Asp Thr Ser Ser Ala Gln Val
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Ser Thr Pro His Ser Val Arg Thr Leu Arg Thr Thr Glu Asn His
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Pro Lys Thr Glu Ser Ala Thr Pro Ala Ala Tyr Ser Gly Ser Pro
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Lys Ile Ser Ser Ser Pro Asn Leu Thr Ser Pro Ala Thr Lys Ala
1370 1375 1380

Trp Thr Ile Thr Asp Thr Thr Glu His Ser Thr Gln Leu His Tyr
1385 1390 1395

Thr Lys Leu Ala Glu Lys Ser Ser Gly Phe Glu Thr Gln Ser Ala
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Pro Gly Pro Val Ser Val Val Ile Pro Thr Ser Pro Thr Ile Gly
1415 1420 1425

Ser Ser Thr Leu Glu Leu Thr Ser Asp Val Pro Gly Glu Pro Leu
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Val Leu Ala Pro Ser Glu Gln Thr Thr Ile Thr Leu Pro Met Ala
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Thr Trp Leu Ser Thr Ser Leu Thr Glu Glu Met Ala Ser Thr Asp
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Leu Asp Ile Ser Ser Pro Ser Ser Pro Met Ser Thr Phe Ala Ile
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Phe Pro Pro Met Ser Thr Pro Ser His Glu Leu Ser Lys Ser Glu
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Ala Asp Thr Ser Ala Ile Arg Asn Thr Asp Ser Thr Thr Leu Asp
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Gln His Leu Gly Ile Arg Ser Leu Gly Arg Thr Gly Asp Leu Thr
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Thr Val Pro Ile Thr Pro Leu Thr Thr Thr Trp Thr Ser Val Ile
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Glu His Ser Thr Gln Ala Gln Asp Thr Leu Ser Ala Thr Met Ser
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Pro Thr His Val Thr Gln Ser Leu Lys Asp Gln Thr Ser Ile Pro
1565 1570 1575

Ala Ser Ala Ser Pro Ser His Leu Thr Glu Val Tyr Pro Glu Leu
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Gly Thr Gln Gly Arg Ser Ser Ser Glu Ala Thr Thr Phe Trp Lys
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Pro Ser Thr Asp Thr Leu Ser Arg Glu Ile Glu Thr Gly Pro Thr
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Asn Ile Gln Ser Thr Pro Pro Met Asp Asn Thr Thr Thr Gly Ser
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Ser Ser Ser Gly Val Thr Leu Gly Ile Ala His Leu Pro Ile Gly
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Arg Ser Ser Thr Ala Thr Val Ser Met Ala Gly Thr Met Gly Leu
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Asp Ser Ser Lys Gly Ser Ser Pro Arg Leu Asn Thr Gln Gly Asn
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Gln Met Ser Thr Ser Ile Pro Leu Thr Ser Ser Pro Thr Thr Pro
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1775 1780 1785

Glu Ser Ser Ser Ala Thr Leu Met Ser Thr Ala Leu Gly Ser Thr
1790 1795 1800

Glu Asn Thr Gly Lys Glu Lys Leu Arg Thr Ala Ser Met Asp Leu
1805 1810 1815

Pro Ser Pro Thr Pro Ser Met Glu Val Thr Pro Trp Ile Ser Leu
1820 1825 1830

Thr Leu Ser Asn Ala Pro Asn Thr Thr Asp Ser Leu Asp Leu Ser
1835 1840 1845

His Gly Val His Thr Ser Ser Ala Gly Thr Leu Ala Thr Asp Arg
1850 1855 1860

Ser Leu Asn Thr Gly Val Thr Arg Ala Ser Arg Leu Glu Asn Gly
1865 1870 1875

Ser Asp Thr Ser Ser Lys Ser Leu Ser Met Gly Asn Ser Thr His
1880 1885 1890

Thr Ser Met Thr Asp Thr Glu Lys Ser Glu Val Ser Ser Ser Ile
1895 1900 1905

His Pro Arg Pro Glu Thr Ser Ala Pro Gly Ala Glu Thr Thr Leu
1910 1915 1920

Thr Ser Thr Pro Gly Asn Arg Ala Ile Ser Leu Thr Leu Pro Phe
1925 1930 1935

Ser Ser Ile Pro Val Glu Glu Val Ile Ser Thr Gly Ile Thr Ser
1940 1945 1950

Gly Pro Asp Ile Asn Ser Ala Pro Met Thr His Ser Pro Ile Thr
1955 1960 1965

Pro Pro Thr Ile Val Trp Thr Ser Thr Gly Thr Ile Glu Gln Ser
1970 1975 1980

Thr Gln Pro Leu His Ala Val Ser Ser Glu Lys Val Ser Val Gln
1985 1990 1995

Thr Gln Ser Thr Pro Tyr Val Asn Ser Val Ala Val Ser Ala Ser
2000 2005 2010

Pro Thr His Glu Asn Ser Val Ser Ser Gly Ser Ser Thr Ser Ser
2015 2020 2025

Pro Tyr Ser Ser Ala Ser Leu Glu Ser Leu Asp Ser Thr Ile Ser
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Pro Ser Pro Asp Thr Glu Val Thr Thr Ile Ser His Phe Pro Glu
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Lys Thr Thr His Ser Phe Arg Thr Ile Ser Ser Leu Thr His Glu
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Leu Thr Ser Arg Val Thr Pro Ile Pro Gly Asp Trp Met Ser Ser
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Ala Met Ser Thr Lys Pro Thr Gly Ala Ser Pro Ser Ile Thr Leu
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Pro Ser Lys Ala Phe Ala Ser Leu Thr Thr Ala Pro Pro Thr Trp
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2990 2995 3000

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Gln Pro Asn Ile Leu Val His Leu Gln Thr Ser Ala Leu Thr Leu
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Ser Pro Thr Ser Thr Leu Asn Met Ser Gln Glu Glu Pro Pro Glu
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Glu Thr Gln Thr Leu Thr Phe Thr Pro Ser Glu Thr Pro Thr Ser
3110 3115 3120

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3125 3130 3135

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Lys Met Ser Ser Gln Ala Ala Gln Gly Asn Ser Thr Trp Pro Ala
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Pro Ala Glu Glu Thr Gly Thr Ser Pro Ala Gly Thr Ser Pro Gly
3185 3190 3195

Ser Pro Glu Met Ser Thr Thr Leu Lys Ile Met Ser Ser Lys Glu
3200 3205 3210

Pro Ser Ile Ser Pro Glu Ile Arg Ser Thr Val Arg Asn Ser Pro
3215 3220 3225

Trp Lys Thr Pro Glu Thr Thr Val Pro Met Glu Thr Thr Val Glu
3230 3235 3240

Pro Val Thr Leu Gln Ser Thr Ala Leu Gly Ser Gly Ser Thr Ser
3245 3250 3255

Ile Ser His Leu Pro Thr Gly Thr Thr Ser Pro Thr Lys Ser Pro
3260 3265 3270

Thr Glu Asn Met Leu Ala Thr Glu Arg Val Ser Leu Ser Pro Ser
3275 3280 3285

Pro Pro Glu Ala Trp Thr Asn Leu Tyr Ser Gly Thr Pro Gly Gly
3290 3295 3300

Thr Arg Gln Ser Leu Ala Thr Met Ser Ser Val Ser Leu Glu Ser
3305 3310 3315

Pro Thr Ala Arg Ser Ile Thr Gly Thr Gly Gln Gln Ser Ser Pro
3320 3325 3330

Glu Leu Val Ser Lys Thr Thr Gly Met Glu Phe Ser Met Trp His
3335 3340 3345

Gly Ser Thr Gly Gly Thr Thr Gly Asp Thr His Val Ser Leu Ser
3350 3355 3360

Thr Ser Ser Asn Ile Leu Glu Asp Pro Val Thr Ser Pro Asn Ser
3365 3370 3375

Val Ser Ser Leu Thr Asp Lys Ser Lys His Lys Thr Glu Thr Trp
3380 3385 3390

Val Ser Thr Thr Ala Ile Pro Ser Thr Val Leu Asn Asn Lys Ile
3395 3400 3405

Met Ala Ala Glu Gln Gln Thr Ser Arg Ser Val Asp Glu Ala Tyr
3410 3415 3420

Ser Ser Thr Ser Ser Trp Ser Asp Gln Thr Ser Gly Ser Asp Ile
3425 3430 3435

Thr Leu Gly Ala Ser Pro Asp Val Thr Asn Thr Leu Tyr Ile Thr
3440 3445 3450

Ser Thr Ala Gln Thr Thr Ser Leu Val Ser Leu Pro Ser Gly Asp
3455 3460 3465

Gln Gly Ile Thr Ser Leu Thr Asn Pro Ser Gly Gly Lys Thr Ser
3470 3475 3480

Ser Ala Ser Ser Val Thr Ser Pro Ser Ile Gly Leu Glu Thr Leu
3485 3490 3495

Arg Ala Asn Val Ser Ala Val Lys Ser Asp Ile Ala Pro Thr Ala
3500 3505 3510

Gly His Leu Ser Gln Thr Ser Ser Pro Ala Glu Val Ser Ile Leu
3515 3520 3525

Asp Val Thr Thr Ala Pro Thr Pro Gly Ile Ser Thr Thr Ile Thr
3530 3535 3540

Thr Met Gly Thr Asn Ser Ile Ser Thr Thr Thr Pro Asn Pro Glu
3545 3550 3555

Val Gly Met Ser Thr Met Asp Ser Thr Pro Ala Thr Glu Arg Arg
3560 3565 3570

Thr Thr Ser Thr Glu His Pro Ser Thr Trp Ser Ser Thr Ala Ala
3575 3580 3585

Ser Asp Ser Trp Thr Val Thr Asp Met Thr Ser Asn Leu Lys Val
3590 3595 3600

Ala Arg Ser Pro Gly Thr Ile Ser Thr Met His Thr Thr Ser Phe
3605 3610 3615

Leu Ala Ser Ser Thr Glu Leu Asp Ser Met Ser Thr Pro His Gly
3620 3625 3630

Arg Ile Thr Val Ile Gly Thr Ser Leu Val Thr Pro Ser Ser Asp
3635 3640 3645

Ala Ser Ala Val Lys Thr Glu Thr Ser Thr Ser Glu Arg Thr Leu
3650 3655 3660

Ser Pro Ser Asp Thr Thr Ala Ser Thr Pro Ile Ser Thr Phe Ser
3665 3670 3675

Arg Val Gln Arg Met Ser Ile Ser Val Pro Asp Ile Leu Ser Thr
3680 3685 3690

Ser Trp Thr Pro Ser Ser Thr Glu Ala Glu Asp Val Pro Val Ser
3695 3700 3705

Met Val Ser Thr Asp His Ala Ser Thr Lys Thr Asp Pro Asn Thr
3710 3715 3720

Pro Leu Ser Thr Phe Leu Phe Asp Ser Leu Ser Thr Leu Asp Trp
3725 3730 3735

Asp Thr Gly Arg Ser Leu Ser Ser Ala Thr Ala Thr Thr Ser Ala
3740 3745 3750

Pro Gln Gly Ala Thr Thr Pro Gln Glu Leu Thr Leu Glu Thr Met
3755 3760 3765

Ile Ser Pro Ala Thr Ser Gln Leu Pro Phe Ser Ile Gly His Ile
3770 3775 3780

Thr Ser Ala Val Thr Pro Ala Ala Met Ala Arg Ser Ser Gly Val
3785 3790 3795

Thr Phe Ser Arg Pro Asp Pro Thr Ser Lys Lys Ala Glu Gln Thr
3800 3805 3810

Ser Thr Gln Leu Pro Thr Thr Thr Ser Ala His Pro Gly Gln Val
3815 3820 3825

Pro Arg Ser Ala Ala Thr Thr Leu Asp Val Ile Pro His Thr Ala
3830 3835 3840

Lys Thr Pro Asp Ala Thr Phe Gln Arg Gln Gly Gln Thr Ala Leu
3845 3850 3855

Thr Thr Glu Ala Arg Ala Thr Ser Asp Ser Trp Asn Glu Lys Glu
3860 3865 3870

Lys Ser Thr Pro Ser Ala Pro Trp Ile Thr Glu Met Met Asn Ser
3875 3880 3885

Val Ser Glu Asp Thr Ile Lys Glu Val Thr Ser Ser Ser Ser Val
3890 3895 3900

Leu Lys Asp Pro Glu Tyr Ala Gly His Lys Leu Gly Ile Trp Asp
3905 3910 3915

Asp Phe Ile Pro Lys Phe Gly Lys Ala Ala His Met Arg Glu Leu
3920 3925 3930

Pro Leu Leu Ser Pro Pro Gln Asp Lys Glu Ala Ile His Pro Ser
3935 3940 3945

Thr Asn Thr Val Glu Thr Thr Gly Trp Val Thr Ser Ser Glu His
3950 3955 3960

Ala Ser His Ser Thr Ile Pro Ala His Ser Ala Ser Ser Lys Leu
3965 3970 3975

Thr Ser Pro Val Val Thr Thr Ser Thr Arg Glu Gln Ala Ile Val
3980 3985 3990

Ser Met Ser Thr Thr Thr Trp Pro Glu Ser Thr Arg Ala Arg Thr
3995 4000 4005

Glu Pro Asn Ser Phe Leu Thr Ile Glu Leu Arg Asp Val Ser Pro
4010 4015 4020

Tyr Met Asp Thr Ser Ser Thr Thr Gln Thr Ser Ile Ile Ser Ser
4025 4030 4035

Pro Gly Ser Thr Ala Ile Thr Lys Gly Pro Arg Thr Glu Ile Thr
4040 4045 4050

Ser Ser Lys Arg Ile Ser Ser Ser Phe Leu Ala Gln Ser Met Arg
4055 4060 4065

Ser Ser Asp Ser Pro Ser Glu Ala Ile Thr Arg Leu Ser Asn Phe
4070 4075 4080

Pro Ala Met Thr Glu Ser Gly Gly Met Ile Leu Ala Met Gln Thr
4085 4090 4095

Ser Pro Pro Gly Ala Thr Ser Leu Ser Ala Pro Thr Leu Asp Thr
4100 4105 4110

Ser Ala Thr Ala Ser Trp Thr Gly Thr Pro Leu Ala Thr Thr Gln
4115 4120 4125

Arg Phe Thr Tyr Ser Glu Lys Thr Thr Leu Phe Ser Lys Gly Pro
4130 4135 4140

Glu Asp Thr Ser Gln Pro Ser Pro Pro Ser Val Glu Glu Thr Ser
4145 4150 4155

Ser Ser Ser Ser Leu Val Pro Ile His Ala Thr Thr Ser Pro Ser
4160 4165 4170

Asn Ile Leu Leu Thr Ser Gln Gly His Ser Pro Ser Ser Thr Pro
4175 4180 4185

Pro Val Thr Ser Val Phe Leu Ser Glu Thr Ser Gly Leu Gly Lys
4190 4195 4200

Thr Thr Asp Met Ser Arg Ile Ser Leu Glu Pro Gly Thr Ser Leu
4205 4210 4215

Pro Pro Asn Leu Ser Ser Thr Ala Gly Glu Ala Leu Ser Thr Tyr
4220 4225 4230

Glu Ala Ser Arg Asp Thr Lys Ala Ile His His Ser Ala Asp Thr
4235 4240 4245

Ala Val Thr Asn Met Glu Ala Thr Ser Ser Glu Tyr Ser Pro Ile
4250 4255 4260

Pro Gly His Thr Lys Pro Ser Lys Ala Thr Ser Pro Leu Val Thr
4265 4270 4275

Ser His Ile Met Gly Asp Ile Thr Ser Ser Thr Ser Val Phe Gly
4280 4285 4290

Ser Ser Glu Thr Thr Glu Ile Glu Thr Val Ser Ser Val Asn Gln
4295 4300 4305

Gly Leu Gln Glu Arg Ser Thr Ser Gln Val Ala Ser Ser Ala Thr
4310 4315 4320

Glu Thr Ser Thr Val Ile Thr His Val Ser Ser Gly Asp Ala Thr
4325 4330 4335

Thr His Val Thr Lys Thr Gln Ala Thr Phe Ser Ser Gly Thr Ser
4340 4345 4350

Ile Ser Ser Pro His Gln Phe Ile Thr Ser Thr Asn Thr Phe Thr
4355 4360 4365

Asp Val Ser Thr Asn Pro Ser Thr Ser Leu Ile Met Thr Glu Ser
4370 4375 4380

Ser Gly Val Thr Ile Thr Thr Gln Thr Gly Pro Thr Gly Ala Ala
4385 4390 4395

Thr Gln Gly Pro Tyr Leu Leu Asp Thr Ser Thr Met Pro Tyr Leu
4400 4405 4410

Thr Glu Thr Pro Leu Ala Val Thr Pro Asp Phe Met Gln Ser Glu
4415 4420 4425

Lys Thr Thr Leu Ile Ser Lys Gly Pro Lys Asp Val Thr Trp Thr
4430 4435 4440

Ser Pro Pro Ser Val Ala Glu Thr Ser Tyr Pro Ser Ser Leu Thr
4445 4450 4455

Pro Phe Leu Val Thr Thr Ile Pro Pro Ala Thr Ser Thr Leu Gln
4460 4465 4470

Gly Gln His Thr Ser Ser Pro Val Ser Ala Thr Ser Val Leu Thr
4475 4480 4485

Ser Gly Leu Val Lys Thr Thr Asp Met Leu Asn Thr Ser Met Glu
4490 4495 4500

Pro Val Thr Asn Ser Pro Gln Asn Leu Asn Asn Pro Ser Asn Glu
4505 4510 4515

Ile Leu Ala Thr Leu Ala Ala Thr Thr Asp Ile Glu Thr Ile His
4520 4525 4530

Pro Ser Ile Asn Lys Ala Val Thr Asn Met Gly Thr Ala Ser Ser
4535 4540 4545

Ala His Val Leu His Ser Thr Leu Pro Val Ser Ser Glu Pro Ser
4550 4555 4560

Thr Ala Thr Ser Pro Met Val Pro Ala Ser Ser Met Gly Asp Ala
4565 4570 4575

Leu Ala Ser Ile Ser Ile Pro Gly Ser Glu Thr Thr Asp Ile Glu
4580 4585 4590

Gly Glu Pro Thr Ser Ser Leu Thr Ala Gly Arg Lys Glu Asn Ser
4595 4600 4605

Thr Leu Gln Glu Met Asn Ser Thr Thr Glu Ser Asn Ile Ile Leu
4610 4615 4620

Ser Asn Val Ser Val Gly Ala Ile Thr Glu Ala Thr Lys Met Glu
4625 4630 4635

Val Pro Ser Phe Asp Ala Thr Phe Ile Pro Thr Pro Ala Gln Ser
4640 4645 4650

Thr Lys Phe Pro Asp Ile Phe Ser Val Ala Ser Ser Arg Leu Ser
4655 4660 4665

Asn Ser Pro Pro Met Thr Ile Ser Thr His Met Thr Thr Thr Gln
4670 4675 4680

Thr Gly Ser Ser Gly Ala Thr Ser Lys Ile Pro Leu Ala Leu Asp
4685 4690 4695

Thr Ser Thr Leu Glu Thr Ser Ala Gly Thr Pro Ser Val Val Thr
4700 4705 4710

Glu Gly Phe Ala His Ser Lys Ile Thr Thr Ala Met Asn Asn Asp
4715 4720 4725

Val Lys Asp Val Ser Gln Thr Asn Pro Pro Phe Gln Asp Glu Ala
4730 4735 4740

Ser Ser Pro Ser Ser Gln Ala Pro Val Leu Val Thr Thr Leu Pro
4745 4750 4755

Ser Ser Val Ala Phe Thr Pro Gln Trp His Ser Thr Ser Ser Pro
4760 4765 4770

Val Ser Met Ser Ser Val Leu Thr Ser Ser Leu Val Lys Thr Ala
4775 4780 4785

Gly Lys Val Asp Thr Ser Leu Glu Thr Val Thr Ser Ser Pro Gln
4790 4795 4800

Ser Met Ser Asn Thr Leu Asp Asp Ile Ser Val Thr Ser Ala Ala
4805 4810 4815

Thr Thr Asp Ile Glu Thr Thr His Pro Ser Ile Asn Thr Val Val
4820 4825 4830

Thr Asn Val Gly Thr Thr Gly Ser Ala Phe Glu Ser His Ser Thr
4835 4840 4845

Val Ser Ala Tyr Pro Glu Pro Ser Lys Ser His Ile Leu Pro Met
4850 4855 4860

Leu Pro Pro Pro Pro Trp Lys Thr Pro Gln Phe Pro Arg Ser Ile
4865 4870 4875

Pro Lys Ser Ser Lys Thr Thr Arg Thr Glu Thr Glu Thr Thr Ser
4880 4885 4890

Ser Leu Thr Pro Lys Leu Arg Glu Thr Ser Ile Ser Gln Glu Ile
4895 4900 4905

Thr Ser Ser Thr Glu Thr Ser Thr Val Pro Tyr Lys Glu Leu Thr
4910 4915 4920

Gly Ala Thr Thr Glu Val Ser Arg Thr Asp Val Thr Ser Ser Ser
4925 4930 4935

Ser Thr Ser Phe Pro Gly Pro Asp Gln Ser Thr Val Ser Leu Asp
4940 4945 4950

Ile Ser Thr Glu Thr Asn Thr Arg Leu Ser Thr Ser Pro Ile Met
4955 4960 4965

Thr Glu Ser Ala Glu Ile Thr Ile Thr Thr Gln Thr Gly Pro His
4970 4975 4980

Gly Ala Thr Ser Gln Asp Thr Phe Thr Met Asp Pro Ser Asn Thr
4985 4990 4995

Thr Pro Gln Ala Gly Ile His Ser Ala Met Thr His Gly Phe Ser
5000 5005 5010

Gln Leu Asp Val Thr Thr Leu Met Ser Arg Ile Pro Gln Asp Val
5015 5020 5025

Ser Trp Thr Ser Pro Pro Ser Val Asp Lys Thr Ser Ser Pro Ser
5030 5035 5040

Ser Phe Leu Ser Ser Pro Ala Met Thr Thr Pro Ser Leu Ile Ser
5045 5050 5055

Ser Thr Leu Pro Glu Asp Lys Leu Ser Ser Pro Met Thr Ser Leu
5060 5065 5070

Leu Thr Ser Gly Leu Val Lys Ile Thr Asp Ile Leu Arg Thr Arg
5075 5080 5085

Leu Glu Pro Val Thr Ser Ser Leu Pro Asn Phe Ser Ser Thr Ser
5090 5095 5100

Asp Lys Ile Leu Ala Thr Ser Lys Asp Ser Lys Asp Thr Lys Glu
5105 5110 5115

Ile Phe Pro Ser Ile Asn Thr Glu Glu Thr Asn Val Lys Ala Asn
5120 5125 5130

Asn Ser Gly His Glu Ser His Ser Pro Ala Leu Ala Asp Ser Glu
5135 5140 5145

Thr Pro Lys Ala Thr Thr Gln Met Val Ile Thr Thr Thr Val Gly
5150 5155 5160

Asp Pro Ala Pro Ser Thr Ser Met Pro Val His Gly Ser Ser Glu
5165 5170 5175

Thr Thr Asn Ile Lys Arg Glu Pro Thr Tyr Phe Leu Thr Pro Arg
5180 5185 5190

Leu Arg Glu Thr Ser Thr Ser Gln Glu Ser Ser Phe Pro Thr Asp
5195 5200 5205

Thr Ser Phe Leu Leu Ser Lys Val Pro Thr Gly Thr Ile Thr Glu
5210 5215 5220

Val Ser Ser Thr Gly Val Asn Ser Ser Ser Lys Ile Ser Thr Pro
5225 5230 5235

Asp His Asp Lys Ser Thr Val Pro Pro Asp Thr Phe Thr Gly Glu
5240 5245 5250

Ile Pro Arg Val Phe Thr Ser Ser Ile Lys Thr Lys Ser Ala Glu
5255 5260 5265

Met Thr Ile Thr Thr Gln Ala Ser Pro Pro Glu Ser Ala Ser His
5270 5275 5280

Ser Thr Leu Pro Leu Asp Thr Ser Thr Thr Leu Ser Gln Gly Gly
5285 5290 5295

Thr His Ser Thr Val Thr Gln Gly Phe Pro Tyr Ser Glu Val Thr
5300 5305 5310

Thr Leu Met Gly Met Gly Pro Gly Asn Val Ser Trp Met Thr Thr
5315 5320 5325

Pro Pro Val Glu Glu Thr Ser Ser Val Ser Ser Leu Met Ser Ser
5330 5335 5340

Pro Ala Met Thr Ser Pro Ser Pro Val Ser Ser Thr Ser Pro Gln
5345 5350 5355

Ser Ile Pro Ser Ser Pro Leu Pro Val Thr Ala Leu Pro Thr Ser
5360 5365 5370

Val Leu Val Thr Thr Thr Asp Val Leu Gly Thr Thr Ser Pro Glu
5375 5380 5385

Ser Val Thr Ser Ser Pro Pro Asn Leu Ser Ser Ile Thr His Glu
5390 5395 5400

Arg Pro Ala Thr Tyr Lys Asp Thr Ala His Thr Glu Ala Ala Met
5405 5410 5415

His His Ser Thr Asn Thr Ala Val Thr Asn Val Gly Thr Ser Gly
5420 5425 5430

Ser Gly His Lys Ser Gln Ser Ser Val Leu Ala Asp Ser Glu Thr
5435 5440 5445

Ser Lys Ala Thr Pro Leu Met Ser Thr Thr Ser Thr Leu Gly Asp
5450 5455 5460

Thr Ser Val Ser Thr Ser Thr Pro Asn Ile Ser Gln Thr Asn Gln
5465 5470 5475

Ile Gln Thr Glu Pro Thr Ala Ser Leu Ser Pro Arg Leu Arg Glu
5480 5485 5490

Ser Ser Thr Ser Glu Lys Thr Ser Ser Thr Thr Glu Thr Asn Thr
5495 5500 5505

Ala Phe Ser Tyr Val Pro Thr Gly Ala Ile Thr Gln Ala Ser Arg
5510 5515 5520

Thr Glu Ile Ser Ser Ser Arg Thr Ser Ile Ser Asp Leu Asp Arg
5525 5530 5535

Pro Thr Ile Ala Pro Asp Ile Ser Thr Gly Met Ile Thr Arg Leu
5540 5545 5550

Phe Thr Ser Pro Ile Met Thr Lys Ser Ala Glu Met Thr Val Thr
5555 5560 5565

Thr Gln Thr Thr Thr Pro Gly Ala Thr Ser Gln Gly Ile Leu Pro
5570 5575 5580

Trp Asp Thr Ser Thr Thr Leu Phe Gln Gly Gly Thr His Ser Thr
5585 5590 5595

Val Ser Gln Gly Phe Pro His Ser Glu Ile Thr Thr Leu Arg Ser
5600 5605 5610

Arg Thr Pro Gly Asp Val Ser Trp Met Thr Thr Pro Pro Val Glu
5615 5620 5625

Glu Thr Ser Ser Gly Phe Ser Leu Met Ser Pro Ser Met Thr Ser
5630 5635 5640

Pro Ser Pro Val Ser Ser Thr Ser Pro Glu Ser Ile Pro Ser Ser
5645 5650 5655

Pro Leu Pro Val Thr Ala Leu Leu Thr Ser Val Leu Val Thr Thr
5660 5665 5670

Thr Asn Val Leu Gly Thr Thr Ser Pro Glu Thr Val Thr Ser Ser
5675 5680 5685

Pro Pro Asn Leu Ser Ser Pro Thr Gln Glu Arg Leu Thr Thr Tyr
5690 5695 5700

Lys Asp Thr Ala His Thr Glu Ala Met His Ala Ser Met His Thr
5705 5710 5715

Asn Thr Ala Val Ala Asn Val Gly Thr Ser Ile Ser Gly His Glu
5720 5725 5730

Ser Gln Ser Ser Val Pro Ala Asp Ser His Thr Ser Lys Ala Thr
5735 5740 5745

Ser Pro Met Gly Ile Thr Phe Ala Met Gly Asp Thr Ser Val Ser
5750 5755 5760

Thr Ser Thr Pro Ala Phe Phe Glu Thr Arg Ile Gln Thr Glu Ser
5765 5770 5775

Thr Ser Ser Leu Ile Pro Gly Leu Arg Asp Thr Arg Thr Ser Glu
5780 5785 5790

Glu Ile Asn Thr Val Thr Glu Thr Ser Thr Val Leu Ser Glu Val
5795 5800 5805

Pro Thr Thr Thr Thr Thr Glu Val Ser Arg Thr Glu Val Ile Thr
5810 5815 5820

Ser Ser Arg Thr Thr Ile Ser Gly Pro Asp His Ser Lys Met Ser
5825 5830 5835

Pro Tyr Ile Ser Thr Glu Thr Ile Thr Arg Leu Ser Thr Phe Pro
5840 5845 5850

Phe Val Thr Gly Ser Thr Glu Met Ala Ile Thr Asn Gln Thr Gly
5855 5860 5865

Pro Ile Gly Thr Ile Ser Gln Ala Thr Leu Thr Leu Asp Thr Ser
5870 5875 5880

Ser Thr Ala Ser Trp Glu Gly Thr His Ser Pro Val Thr Gln Arg
5885 5890 5895

Phe Pro His Ser Glu Glu Thr Thr Thr Met Ser Arg Ser Thr Lys
5900 5905 5910

Gly Val Ser Trp Gln Ser Pro Pro Ser Val Glu Glu Thr Ser Ser
5915 5920 5925

Pro Ser Ser Pro Val Pro Leu Pro Ala Ile Thr Ser His Ser Ser
5930 5935 5940

Leu Tyr Ser Ala Val Ser Gly Ser Ser Pro Thr Ser Ala Leu Pro
5945 5950 5955

Val Thr Ser Leu Leu Thr Ser Gly Arg Arg Lys Thr Ile Asp Met
5960 5965 5970

Leu Asp Thr His Ser Glu Leu Val Thr Ser Ser Leu Pro Ser Ala
5975 5980 5985

Ser Ser Phe Ser Gly Glu Ile Leu Thr Ser Glu Ala Ser Thr Asn
5990 5995 6000

Thr Glu Thr Ile His Phe Ser Glu Asn Thr Ala Glu Thr Asn Met
6005 6010 6015

Gly Thr Thr Asn Ser Met His Lys Leu His Ser Ser Val Ser Ile
6020 6025 6030

His Ser Gln Pro Ser Gly His Thr Pro Pro Lys Val Thr Gly Ser
6035 6040 6045

Met Met Glu Asp Ala Ile Val Ser Thr Ser Thr Pro Gly Ser Pro
6050 6055 6060

Glu Thr Lys Asn Val Asp Arg Asp Ser Thr Ser Pro Leu Thr Pro
6065 6070 6075

Glu Leu Lys Glu Asp Ser Thr Ala Leu Val Met Asn Ser Thr Thr
6080 6085 6090

Glu Ser Asn Thr Val Phe Ser Ser Val Ser Leu Asp Ala Ala Thr
6095 6100 6105

Glu Val Ser Arg Ala Glu Val Thr Tyr Tyr Asp Pro Thr Phe Met
6110 6115 6120

Pro Ala Ser Ala Gln Ser Thr Lys Ser Pro Asp Ile Ser Pro Glu
6125 6130 6135

Ala Ser Ser Ser His Ser Asn Ser Pro Pro Leu Thr Ile Ser Thr
6140 6145 6150

His Lys Thr Ile Ala Thr Gln Thr Gly Pro Ser Gly Val Thr Ser
6155 6160 6165

Leu Gly Gln Leu Thr Leu Asp Thr Ser Thr Ile Ala Thr Ser Ala
6170 6175 6180

Gly Thr Pro Ser Ala Arg Thr Gln Asp Phe Val Asp Ser Glu Thr
6185 6190 6195

Thr Ser Val Met Asn Asn Asp Leu Asn Asp Val Leu Lys Thr Ser
6200 6205 6210

Pro Phe Ser Ala Glu Glu Ala Asn Ser Leu Ser Ser Gln Ala Pro
6215 6220 6225

Leu Leu Val Thr Thr Ser Pro Ser Pro Val Thr Ser Thr Leu Gln
6230 6235 6240

Glu His Ser Thr Ser Ser Leu Val Ser Val Thr Ser Val Pro Thr
6245 6250 6255

Pro Thr Leu Ala Lys Ile Thr Asp Met Asp Thr Asn Leu Glu Pro
6260 6265 6270

Val Thr Arg Ser Pro Gln Asn Leu Arg Asn Thr Leu Ala Thr Ser
6275 6280 6285

Glu Ala Thr Thr Asp Thr His Thr Met His Pro Ser Ile Asn Thr
6290 6295 6300

Ala Met Ala Asn Val Gly Thr Thr Ser Ser Pro Asn Glu Phe Tyr
6305 6310 6315

Phe Thr Val Ser Pro Asp Ser Asp Pro Tyr Lys Ala Thr Ser Ala
6320 6325 6330

Val Val Ile Thr Ser Thr Ser Gly Asp Ser Ile Val Ser Thr Ser
6335 6340 6345

Met Pro Arg Ser Ser Ala Met Lys Lys Ile Glu Ser Glu Thr Thr
6350 6355 6360

Phe Ser Leu Ile Phe Arg Leu Arg Glu Thr Ser Thr Ser Gln Lys
6365 6370 6375

Ile Gly Ser Ser Ser Asp Thr Ser Thr Val Phe Asp Lys Ala Phe
6380 6385 6390

Thr Ala Ala Thr Thr Glu Val Ser Arg Thr Glu Leu Thr Ser Ser
6395 6400 6405

Ser Arg Thr Ser Ile Gln Gly Thr Glu Lys Pro Thr Met Ser Pro
6410 6415 6420

Asp Thr Ser Thr Arg Ser Val Thr Met Leu Ser Thr Phe Ala Gly
6425 6430 6435

Leu Thr Lys Ser Glu Glu Arg Thr Ile Ala Thr Gln Thr Gly Pro
6440 6445 6450

His Arg Ala Thr Ser Gln Gly Thr Leu Thr Trp Asp Thr Ser Ile
6455 6460 6465

Thr Thr Ser Gln Ala Gly Thr His Ser Ala Met Thr His Gly Phe
6470 6475 6480

Ser Gln Leu Asp Leu Ser Thr Leu Thr Ser Arg Val Pro Glu Tyr
6485 6490 6495

Ile Ser Gly Thr Ser Pro Pro Ser Val Glu Lys Thr Ser Ser Ser
6500 6505 6510

Ser Ser Leu Leu Ser Leu Pro Ala Ile Thr Ser Pro Ser Pro Val
6515 6520 6525

Pro Thr Thr Leu Pro Glu Ser Arg Pro Ser Ser Pro Val His Leu
6530 6535 6540

Thr Ser Leu Pro Thr Ser Gly Leu Val Lys Thr Thr Asp Met Leu
6545 6550 6555

Ala Ser Val Ala Ser Leu Pro Pro Asn Leu Gly Ser Thr Ser His
6560 6565 6570

Lys Ile Pro Thr Thr Ser Glu Asp Ile Lys Asp Thr Glu Lys Met
6575 6580 6585

Tyr Pro Ser Thr Asn Ile Ala Val Thr Asn Val Gly Thr Thr Thr
6590 6595 6600

Ser Glu Lys Glu Ser Tyr Ser Ser Val Pro Ala Tyr Ser Glu Pro
6605 6610 6615

Pro Lys Val Thr Ser Pro Met Val Thr Ser Phe Asn Ile Arg Asp
6620 6625 6630

Thr Ile Val Ser Thr Ser Met Pro Gly Ser Ser Glu Ile Thr Arg
6635 6640 6645

Ile Glu Met Glu Ser Thr Phe Ser Val Ala His Gly Leu Lys Gly
6650 6655 6660

Thr Ser Thr Ser Gln Asp Pro Ile Val Ser Thr Glu Lys Ser Ala
6665 6670 6675

Val Leu His Lys Leu Thr Thr Gly Ala Thr Glu Thr Ser Arg Thr
6680 6685 6690

Glu Val Ala Ser Ser Arg Arg Thr Ser Ile Pro Gly Pro Asp His
6695 6700 6705

Ser Thr Glu Ser Pro Asp Ile Ser Thr Glu Val Ile Pro Ser Leu
6710 6715 6720

Pro Ile Ser Leu Gly Ile Thr Glu Ser Ser Asn Met Thr Ile Ile
6725 6730 6735

Thr Arg Thr Gly Pro Pro Leu Gly Ser Thr Ser Gln Gly Thr Phe
6740 6745 6750

Thr Leu Asp Thr Pro Thr Thr Ser Ser Arg Ala Gly Thr His Ser
6755 6760 6765

Met Ala Thr Gln Glu Phe Pro His Ser Glu Met Thr Thr Val Met
6770 6775 6780

Asn Lys Asp Pro Glu Ile Leu Ser Trp Thr Ile Pro Pro Ser Ile
6785 6790 6795

Glu Lys Thr Ser Phe Ser Ser Ser Leu Met Pro Ser Pro Ala Met
6800 6805 6810

Thr Ser Pro Pro Val Ser Ser Thr Leu Pro Lys Thr Ile His Thr
6815 6820 6825

Thr Pro Ser Pro Met Thr Ser Leu Leu Thr Pro Ser Leu Val Met
6830 6835 6840

Thr Thr Asp Thr Leu Gly Thr Ser Pro Glu Pro Thr Thr Ser Ser
6845 6850 6855

Pro Pro Asn Leu Ser Ser Thr Ser His Glu Ile Leu Thr Thr Asp
6860 6865 6870

Glu Asp Thr Thr Ala Ile Glu Ala Met His Pro Ser Thr Ser Thr
6875 6880 6885

Ala Ala Thr Asn Val Glu Thr Thr Ser Ser Gly His Gly Ser Gln
6890 6895 6900

Ser Ser Val Leu Ala Asp Ser Glu Lys Thr Lys Ala Thr Ala Pro
6905 6910 6915

Met Asp Thr Thr Ser Thr Met Gly His Thr Thr Val Ser Thr Ser
6920 6925 6930

Met Ser Val Ser Ser Glu Thr Thr Lys Ile Lys Arg Glu Ser Thr
6935 6940 6945

Tyr Ser Leu Thr Pro Gly Leu Arg Glu Thr Ser Ile Ser Gln Asn
6950 6955 6960

Ala Ser Phe Ser Thr Asp Thr Ser Ile Val Leu Ser Glu Val Pro
6965 6970 6975

Thr Gly Thr Thr Ala Glu Val Ser Arg Thr Glu Val Thr Ser Ser
6980 6985 6990

Gly Arg Thr Ser Ile Pro Gly Pro Ser Gln Ser Thr Val Leu Pro
6995 7000 7005

Glu Ile Ser Thr Arg Thr Met Thr Arg Leu Phe Ala Ser Pro Thr
7010 7015 7020

Met Thr Glu Ser Ala Glu Met Thr Ile Pro Thr Gln Thr Gly Pro
7025 7030 7035

Ser Gly Ser Thr Ser Gln Asp Thr Leu Thr Leu Asp Thr Ser Thr
7040 7045 7050

Thr Lys Ser Gln Ala Lys Thr His Ser Thr Leu Thr Gln Arg Phe
7055 7060 7065

Pro His Ser Glu Met Thr Thr Leu Met Ser Arg Gly Pro Gly Asp
7070 7075 7080

Met Ser Trp Gln Ser Ser Pro Ser Leu Glu Asn Pro Ser Ser Leu
7085 7090 7095

Pro Ser Leu Leu Ser Leu Pro Ala Thr Thr Ser Pro Pro Pro Ile
7100 7105 7110

Ser Ser Thr Leu Pro Val Thr Ile Ser Ser Ser Pro Leu Pro Val
7115 7120 7125

Thr Ser Leu Leu Thr Ser Ser Pro Val Thr Thr Thr Asp Met Leu
7130 7135 7140

His Thr Ser Pro Glu Leu Val Thr Ser Ser Pro Pro Lys Leu Ser
7145 7150 7155

His Thr Ser Asp Glu Arg Leu Thr Thr Gly Lys Asp Thr Thr Asn
7160 7165 7170

Thr Glu Ala Val His Pro Ser Thr Asn Thr Ala Ala Ser Asn Val
7175 7180 7185

Glu Ile Pro Ser Ser Gly His Glu Ser Pro Ser Ser Ala Leu Ala
7190 7195 7200

Asp Ser Glu Thr Ser Lys Ala Thr Ser Pro Met Phe Ile Thr Ser
7205 7210 7215

Thr Gln Glu Asp Thr Thr Val Ala Ile Ser Thr Pro His Phe Leu
7220 7225 7230

Glu Thr Ser Arg Ile Gln Lys Glu Ser Ile Ser Ser Leu Ser Pro
7235 7240 7245

Lys Leu Arg Glu Thr Gly Ser Ser Val Glu Thr Ser Ser Ala Ile
7250 7255 7260

Glu Thr Ser Ala Val Leu Ser Glu Val Ser Val Gly Ala Thr Thr
7265 7270 7275

Glu Ile Ser Arg Thr Glu Val Thr Ser Ser Ser Arg Thr Ser Ile
7280 7285 7290

Ser Gly Ser Ala Glu Ser Thr Met Leu Pro Glu Ile Ser Thr Thr
7295 7300 7305

Arg Lys Ile Ile Lys Phe Pro Thr Ser Pro Ile Leu Ala Glu Ser
7310 7315 7320

Ser Glu Met Thr Ile Lys Thr Gln Thr Ser Pro Pro Gly Ser Thr
7325 7330 7335

Ser Glu Ser Thr Phe Thr Leu Asp Thr Ser Thr Thr Pro Ser Leu
7340 7345 7350

Val Ile Thr His Ser Thr Met Thr Gln Arg Leu Pro His Ser Glu
7355 7360 7365

Ile Thr Thr Leu Val Ser Arg Gly Ala Gly Asp Val Pro Arg Pro
7370 7375 7380

Ser Ser Leu Pro Val Glu Glu Thr Ser Pro Pro Ser Ser Gln Leu
7385 7390 7395

Ser Leu Ser Ala Met Ile Ser Pro Ser Pro Val Ser Ser Thr Leu
7400 7405 7410

Pro Ala Ser Ser His Ser Ser Ser Ala Ser Val Thr Ser Leu Leu
7415 7420 7425

Thr Pro Gly Gln Val Lys Thr Thr Glu Val Leu Asp Ala Ser Ala
7430 7435 7440

Glu Pro Glu Thr Ser Ser Pro Pro Ser Leu Ser Ser Thr Ser Val
7445 7450 7455

Glu Ile Leu Ala Thr Ser Glu Val Thr Thr Asp Thr Glu Lys Ile
7460 7465 7470

His Pro Phe Ser Asn Thr Ala Val Thr Lys Val Gly Thr Ser Ser
7475 7480 7485

Ser Gly His Glu Ser Pro Ser Ser Val Leu Pro Asp Ser Glu Thr
7490 7495 7500

Thr Lys Ala Thr Ser Ala Met Gly Thr Ile Ser Ile Met Gly Asp
7505 7510 7515

Thr Ser Val Ser Thr Leu Thr Pro Ala Leu Ser Asn Thr Arg Lys
7520 7525 7530

Ile Gln Ser Glu Pro Ala Ser Ser Leu Thr Thr Arg Leu Arg Glu
7535 7540 7545

Thr Ser Thr Ser Glu Glu Thr Ser Leu Ala Thr Glu Ala Asn Thr
7550 7555 7560

Val Leu Ser Lys Val Ser Thr Gly Ala Thr Thr Glu Val Ser Arg
7565 7570 7575

Thr Glu Ala Ile Ser Phe Ser Arg Thr Ser Met Ser Gly Pro Glu
7580 7585 7590

Gln Ser Thr Met Ser Gln Asp Ile Ser Ile Gly Thr Ile Pro Arg
7595 7600 7605

Ile Ser Ala Ser Ser Val Leu Thr Glu Ser Ala Lys Met Thr Ile
7610 7615 7620

Thr Thr Gln Thr Gly Pro Ser Glu Ser Thr Leu Glu Ser Thr Leu
7625 7630 7635

Asn Leu Asn Thr Ala Thr Thr Pro Ser Trp Val Glu Thr His Ser
7640 7645 7650

Ile Val Ile Gln Gly Phe Pro His Pro Glu Met Thr Thr Ser Met
7655 7660 7665

Gly Arg Gly Pro Gly Gly Val Ser Trp Pro Ser Pro Pro Phe Val
7670 7675 7680

Lys Glu Thr Ser Pro Pro Ser Ser Pro Leu Ser Leu Pro Ala Val
7685 7690 7695

Thr Ser Pro His Pro Val Ser Thr Thr Phe Leu Ala His Ile Pro
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Pro Ser Pro Leu Pro Val Thr Ser Leu Leu Thr Ser Gly Pro Ala
7715 7720 7725

Thr Thr Thr Asp Ile Leu Gly Thr Ser Thr Glu Pro Gly Thr Ser
7730 7735 7740

Ser Ser Ser Ser Leu Ser Thr Thr Ser His Glu Arg Leu Thr Thr
7745 7750 7755

Tyr Lys Asp Thr Ala His Thr Glu Ala Val His Pro Ser Thr Asn
7760 7765 7770

Thr Gly Gly Thr Asn Val Ala Thr Thr Ser Ser Gly Tyr Lys Ser
7775 7780 7785

Gln Ser Ser Val Leu Ala Asp Ser Ser Pro Met Cys Thr Thr Ser
7790 7795 7800

Thr Met Gly Asp Thr Ser Val Leu Thr Ser Thr Pro Ala Phe Leu
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Glu Thr Arg Arg Ile Gln Thr Glu Leu Ala Ser Ser Leu Thr Pro
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Gly Leu Arg Glu Ser Ser Gly Ser Glu Gly Thr Ser Ser Gly Thr
7835 7840 7845

Lys Met Ser Thr Val Leu Ser Lys Val Pro Thr Gly Ala Thr Thr
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Glu Ile Ser Lys Glu Asp Val Thr Ser Ile Pro Gly Pro Ala Gln
7865 7870 7875

Ser Thr Ile Ser Pro Asp Ile Ser Thr Arg Thr Val Ser Trp Phe
7880 7885 7890

Ser Thr Ser Pro Val Met Thr Glu Ser Ala Glu Ile Thr Met Asn
7895 7900 7905

Thr His Thr Ser Pro Leu Gly Ala Thr Thr Gln Gly Thr Ser Thr
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Leu Ala Thr Ser Ser Thr Thr Ser Leu Thr Met Thr His Ser Thr
7925 7930 7935

Ile Ser Gln Gly Phe Ser His Ser Gln Met Ser Thr Leu Met Arg
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Arg Gly Pro Glu Asp Val Ser Trp Met Ser Pro Pro Leu Leu Glu
7955 7960 7965

Lys Thr Arg Pro Ser Phe Ser Leu Met Ser Ser Pro Ala Thr Thr
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Ser Pro Ser Pro Val Ser Ser Thr Leu Pro Glu Ser Ile Ser Ser
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Ser Pro Leu Pro Val Thr Ser Leu Leu Thr Ser Gly Leu Ala Lys
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Thr Thr Asp Met Leu His Lys Ser Ser Glu Pro Val Thr Asn Ser
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Thr Val Thr Asp Val Gly Thr Ser Ser Ser Gly His Glu Ser Thr
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Thr Pro Gly Phe Phe Glu Thr Ser Arg Ile Gln Thr Glu Pro Thr
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Thr Gly Ala Thr Ala Glu Val Ser Arg Thr Glu Val Thr Ser Ser
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Glu Thr Ser Thr Glu Thr Ile Thr Arg Leu Pro Thr Ser Ser Ile
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Met Thr Glu Ser Ala Glu Met Met Ile Lys Thr Gln Thr Asp Pro
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Pro Gly Ser Thr Pro Glu Ser Thr His Thr Val Asp Ile Ser Thr
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Thr Pro Asn Trp Val Glu Thr His Ser Thr Val Thr Gln Arg Phe
8225 8230 8235

Ser His Ser Glu Met Thr Thr Leu Val Ser Arg Ser Pro Gly Asp
8240 8245 8250

Met Leu Trp Pro Ser Gln Ser Ser Val Glu Glu Thr Ser Ser Ala
8255 8260 8265

Ser Ser Leu Leu Ser Leu Pro Ala Thr Thr Ser Pro Ser Pro Val
8270 8275 8280

Ser Ser Thr Leu Val Glu Asp Phe Pro Ser Ala Ser Leu Pro Val
8285 8290 8295

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Gly Ile Ser Arg Glu Pro Gly Thr Ser Ser Thr Ser Asn Leu Ser
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Ser Thr Ser His Glu Arg Leu Thr Thr Leu Glu Asp Thr Val Asp
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Thr Glu Asp Met Gln Pro Ser Thr His Thr Ala Val Thr Asn Val
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Ser Ile Ser Ser Ser Pro His Pro Val Thr Ala Leu Leu Thr Leu
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Gly Pro Val Lys Thr Thr Asp Met Leu Arg Thr Ser Ser Glu Pro
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Asp Gly Ile
10430

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